



# **STIC Search Report**

## **Biotech-Chem Library**

**STIC Database Tracking Number: 204048**

**TO: Ruixiang Li**  
**Location: rem/4D75/4C70**  
**Art Unit: 1646**  
**Friday, October 13, 2006**  
**Case Serial Number: 10/668767**

**From: Dwayne Hill**  
**Location: Biotech-Chem Library**  
**REM-1A41**  
**Phone: (571)272-8972**

**Dwayne.Hill@uspto.gov**

### **Search Notes**

Examiner Li,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Dwayne Hill  
STIC Biotech/Chem Library  
(571)272-1972

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78733

10-324

204048

114

STIC-Biotech/ChemLib

From: Li, Ruixiang  
Sent: Friday, October 06, 2006 11:40 AM  
To: CRFF STIC-Biotech/ChemLib  
Subject: Sequence search of Application No.10/668,767

Please do a standard search on:

aa 5128

- (i). SEQ ID NO: 128 against interference amino acid databases;
- (ii). SEQ ID NO: 127 and ~~128~~ against interference nucleic acid databases.

Thank you very much!

Ruixiang Li  
GAU 1646  
REM 4D75  
Mail Box 4C70  
(571) 272-0875

127 na 15387

Seq ID 127 1-5000

Em ☒  
Leg ☒

Me

\*\*\*\*\*  
Searcher: 10/14  
Searcher Phone: \_\_\_\_\_  
Date Searcher Picked up: \_\_\_\_\_  
Date completed: \_\_\_\_\_  
Searcher Prep Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

\*\*\*\*\*  
Type of Search  
NA# \_\_\_\_\_ AA# \_\_\_\_\_  
S/L: \_\_\_\_\_ Oligomer: \_\_\_\_\_  
Encode/Transl: \_\_\_\_\_  
Structure #: \_\_\_\_\_ Text: \_\_\_\_\_  
Inventor: \_\_\_\_\_ Litigation: \_\_\_\_\_

\*\*\*\*\*  
Vendors and cost where applicable  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIT: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (Specify): \_\_\_\_\_

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Li, Ruixiang

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From: Hill, Dwayne (ASRC)  
Sent: Tuesday, October 24, 2006 1:52 PM  
To: Li, Ruixiang  
Subject: Sequence Search Results for 10/668767 Seq. ID 128 (1-1700)

Dear Examiner,

I just checked SCORE and the results for your sequence search are there now.

\*\*\*\*\*

<http://es/ScoreAccessWeb/GetItems.action?ApplId=10668767&ItemType=4&VersionNo=10>

After downloading files, use **Microsoft Word** to view, manipulate and print.

\*\*\*\*\*

If you have any problems, please do not hesitate to call me for assistance.

Please let me know if you have any questions. Thank you for using STIC services.

Dwayne Hill  
STIC/Biotech Library  
REM1A64  
X28972



search  
feedback form.d

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GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: October 6, 2006, 23:32:44 ; Search time 87 Seconds  
(without alignments)  
5159.277 Million cell updates/sec

Title: US-10-668-767-128

Perfect score: 26800

Sequence: 1 MAEAGGAGSEDDVFLRTE.....WDFPPVGDGCRKQYEDLMGE 5128

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

- 1: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/5\_COMB.pep.\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/6\_COMB.pep.\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/7\_COMB.pep.\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/H\_COMB.pep.\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/PCTUS\_COMB.pep.\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/RE\_COMB.pep.\*
- 7: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	11887.5	44.4	4968	2	US-09-424-783-5
2	11386.5	42.5	4872	2	US-09-424-783-3
3	11349	42.3	5037	2	US-09-424-783-4
4	11325.5	42.3	5032	2	US-09-538-092-979
5	11295.5	42.1	4866	2	US-09-424-783-2
6	658	2.5	2749	2	US-09-385-222A-4
7	654	2.4	2713	5	PCT-US96-01735-1
8	336.5	1.3	240	1	US-08-114-555A-8
9	336.5	1.3	240	2	US-08-559-397A-14
10	334.5	1.2	240	1	US-08-114-555A-6
11	334.5	1.2	240	2	US-08-559-397A-12
12	313.5	1.2	2262	2	US-09-949-016-8849
13	308	1.1	3259	2	US-09-949-016-6507
14	305.5	1.1	5024	2	US-09-710-279-2964
15	305	1.1	2733	2	US-09-949-016-11433
16	303.5	1.1	10182	2	US-09-134-001C-3159
17	302	1.1	3878	2	US-09-914-259-11
18	288	1.1	3248	1	US-08-353-700-1
19	288	1.1	3248	5	PCT-US95-16216-1
20	285	1.1	3210	2	US-09-538-092-1154
21	276.5	1.0	2954	2	US-09-150-867-1
22	276.5	1.0	2954	3	US-09-724-584-1
23	263	1.0	200	2	US-10-104-047-3679
24	259.5	1.0	2349	2	US-09-538-092-914
25	255.5	1.0	3433	2	US-09-538-092-1136
26	249.5	0.9	2482	1	US-08-328-254-6

ALIGNMENTS

RESULT 1

US-09-424-783-5

; Sequence 5, Application US/09424783

; Patent No. 6780508

; GENERAL INFORMATION:

; APPLICANT: Hakamata, Yasuhiro

; APPLICANT: Nishimura, Seichiro

; APPLICANT: Barsoumian, Edward Leon

; TITLE OF INVENTION: Human Type 3 Ryanodine Receptor Protein

; TITLE OF INVENTION: and DNA Molecules Coding Therefor

; FILE REFERENCE: 0652.2000000

; CURRENT APPLICATION NUMBER: US/09/424,783

; CURRENT FILING DATE: 1999-12-01

; PRIOR APPLICATION NUMBER: PCT/EP98/02926

; PRIOR FILING DATE: 1998-05-18

; PRIOR APPLICATION NUMBER: DE 197 22 317.6

; PRIOR FILING DATE: 1997-05-28

; NUMBER OF SEQ ID NOS: 11

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 5

; LENGTH: 4968

; TYPE: PRT

; ORGANISM: Oryctolagus cuniculus

US-09-424-783-5

Query Match 44.4%; Score 11887.5; DB 2; Length 4968;

Best Local Similarity 46.7%; Pred. No. 0;

Matches 2459; Conservative 903; Mismatches 1455; Indels 451; Gaps 92;

QY	4	AEGGASEQDDVSFLRTEDMVCLSSTAT----	GERVCLAAEGFGNRHCFLENIAD-KNI	58
DB	2	ADGEGE-DEIQFLRTDDEVVLQCTATTHKEQ	QKCLAAEGFGNRLCFLESTNSKNVPP	60
QY	59	DLSCQVFIEQALSVRALQELVTAAGSETGK	-----TCSGHRITLLYGNAI	104
DB	61	DLISCTFVLEQSLVRALQEL-ANTVEKSE	QVDVEKWKFMKMTAQGGHRTLLYGNAI	119
QY	105	LLRLHNSDMYLACLSSTS--SSODKLA	FDVGLQOHSGEGACWMTLHPASKQRSE	163
DB	120	LLRHYSQGMVLCCLSTSRSSSTDKLA	FDVGLQEDTTGEACWMTIHPASKQRSE	179
QY	164	DLILVSVATERLYLHTTKNEVSVIN	ASPHVTHWSVQPGTGISRMKVVYVFGD	223
DB	180	DLILVSVSSRYLHLSYNGSLHVDAA	FQQTLSVPATISSGSEAAQ--GYLIGD	237
QY	224	HGG-DECLTIPSTWTKGQGNIVYEG	SVMQARSRLRLEARTKWAGGFINWHP	282
DB	238	HGHMDECLTVPSEGBGEQRRTVH	YEGGAVSHARSRLRLETLRVANS	297



Db 2275 QSCQMLVSKGYPDIGWNPVEGERYLDLFLURFAVFCNGESVEENANVVVRLILRRPECFGPA 2334  
Qy 2457 LRGE-GEGLLXAI V DANKWMSRIADRRKLRMEQBGDVFNSHLPES-----DEDE 2506  
Db 2335 LRGEQGNLLAMEBAIKAE-----DFSROGSPSTSGSKTLDTEEBED 2379  
Qy 2507 DYIDTGAAILNFYCTVLDLGRCAPDAGVIALGKNESLRARAILRSVLPLEDLQGVLSLR 2566  
Db 2380 DTIHMGNAIMFYAALIDLLGRCAPEMHLIHAGKEAIRSILRSILPLDGLGVVISIA 2439  
Qy 2567 FTLNNPAAGERPKSDMPGSLIPGHQSVGLFLERVYGIETQBELFYKLLBEAPFLDLRAA 2626  
Db 2440 FQMPTIARDGNVPEMDGAGCPDHKAAMVFLDRVYGIQVQDFLLHLLVGVFLPDLRAA 2499  
Qy 2627 TMLDRNDCESDMALSMRYTGNSTLPLLIKHAYPNEAENVASILLDATLHTVYRLSKNR 2686  
Db 2500 ASLDTAALASADMALALNRYLCTVAPLTLTRCAPLFACTEHHASLIDSLLHTVYRLSKGC 2559  
Qy 2687 MLTKQREAVSDFLVALTSAMQPSMLLKLRLKLTVDVSKLSEYTTVALRLTLHYERCAC 2746  
Db 2560 SLTKAQRDSIEVCLLSICQLRPPSMQHLRLVFDVPLLNEHAKMPLKLLTNHYERCWK 2619  
Qy 2747 YYGSTGAGGAFGASDEKRLTMMFLFSNIFDSLSKMDYBELFKALPCLAIAGCALPP 2806  
Db 2620 YYCLPG-GWGNFGAASEBELHLSRKLFWGIFDALSQKYEQELFKALPCLSAVAGALPP 2678  
Qy 2807 DYSLSKNYDDPEYKGEQAAGLDNDPOYDPOPISTSSVALNNDLNTIVOKFSEHYHDWAS 2866  
Db 2679 DY-MESNVYSWM--BKQSSMDSEG-NFNPQPVDTNIIIPKLEYFINKYAEHSHDKWSM 2734  
Qy 2867 RKIENGWYVGEWSQKTHPRKLPYNMLNDEKERYKEPVRESLKAALLAIGWSVEHSEV 2926  
Db 2735 DKLANGWYGEIYSDSSKIQPLMKPYKLLSEKEIYRWPIKESKTMLANGWRIERTR- 2793  
Qy 2927 DIPSNRSMRRQSKGGRPEIVTDSATPDYNPHPVDMNTLTLRSQMNAERLADNA 2986  
Db 2794 ---EGDSMALYNRTTRISQTSQVSDAA--HGYSPRADMSNVTLRSDLHAMAEMNAENY 2848  
Qy 2987 HDIWAKKKEELVYNGGIHQVLPYDILLTQKEKKKDERQOEFLKYLOYGYKHLRPSK 3046  
Db 2849 HNIWAKKKLELESKGGGNHPLVYPDTLTAKAKAKREKAQDILKFLQINGYAVSRGFK 2908  
Qy 3047 APOSTEQTTGVAJELRFAYSLLEKLIQYIDRATINMKLLKPSFTFSRRRSFKTSTRDI 3106  
Db 2909 DLELDT-----SIEKFPAYSLQOLIRYVDEA--HQYILEFDGGSKSGEHPPEYGEI 2960  
Qy 3107 KFFSXAFLPLMEKYFSTHRNFIYAVAT-ATNNVGAASLKEKEMVAALFCKLASLSRLA 3165  
Db 2961 KFFAKVWLPLIDQYFKNHRLYFSLASRPLCSGGHASNKEKEMVTSLFCKLGLVVRHRIS 3020  
Qy 3166 APGPDVITVRCLQVLVKGIDAKSLVKNCPPEPIRTSMITFFNNVADDVGHITMLODKY 3225  
Db 3021 LFGNDATSI VNLCHLIGOTLDARTYMTKGLSVKSALRAFLDNAAEDLEKTMENLKQGOF 3080  
Qy 3226 AHLRGTHLKTSLGVINGVLLPILITAKFDHLANCEYGAIDLDDIIOVASYKMLGSLVAL 3285  
Db 3081 THTRNQPRGVTOIYNTVALLPMLSSUFEHIGQHOFGEDELLILEVQSVCRILTSIAL 3140  
Qy 3286 GTDASLTHDRKYLKTEIERHKKPALGSCGAFSTFPFVAPLEPHLNKRNQFSLNRIADHS 3345  
Db 3141 GTSKSI-----YVERQSALGECLEAAAFAGAPVAFLETHLNKNIYSIYNTKSSRE 3191  
Qy 3346 LEAQDIMQKOEQ-C--MPTLETILGEVQOFVESDKTYNEAPHIIDVPLICSYLPFWWA 3402  
Db 3192 RAALSIPANVEDVCPNIPSEKLMBEIVELAESGIRYTMQPHMEVILFPLMCSYMSRWWE 3251  
Qy 3403 QCPDNVPTGGNHVTWTAHNNOLLKNVLKLIKNIGNENAPWTRIATVTOQIIINS 3462  
Db 3252 HGPENPGRAEMCCCTALNSDEWNTLLGNILKLIYNNLGDIGEGAWKRLAVFSQPIINKVK 3311  
Qy 3463 BELLRDSFLPLAERYKRTDNNMFHEESLRGFIKSTDDTSQVESQIQEDMOLLVRDIYS 3522  
Db 3312 POLLKTHFLPLMEKUKKKAAMVVSSEDLKA---EARGDMSAEALLILDEFTTLARDLYA 3368

Qy 3523 FYPLLIKYVDLQRNHWLNRNVPEAEELYNHVAEIFNIWKSQYFLKEBEQNFIANEIDNM 3582  
Db 3369 FYPLLIREFVDYNRAKWLKEPTPEAEELFRMAEVEFIWYKSHNPKREBEQNFVQNEINNM 3428  
Qy 3583 VLMPTATRRVT---AVTDGTPQGGGKKKKHRRDKRDKKEVQASLMAVACLKRLPLPYGLN 3640  
Db 3429 SFLITDTTKSKMSKAASD-----QERKMKRKGDRL-YSMQTSLIIVAAALKRLLPIGLN 3479  
Qy 3641 LFAGREOELVQHCKDRFLKWMSEODVAEFAKTOLTLTPDKI--DPADEMSWQHYLSKLGSK 3699  
Db 3480 ICAPGDELLALAKNRSRLKODTEDEVDDIIRNNIHLQCKLEDPA--IRWQWALY-----K 3532  
Qy 3700 SKSNITVETAENKAKIIDDTVERIVAMSKVLFGI-----HMIDHPQMSKNVY 3747  
Db 3533 DLPNRTEETSDP-----EKTVERVLDIANVLFHLEQSKFPIGRYRYNLVEHPQSRKAVM 3587  
Qy 3748 RSVVSIORQKRAVIACFRQTSLSHSLPRHACNIPARTYVELWLE--EENIGQEWMLDITQS 3806  
Db 3588 HKLLSKQRKAAVACFRMAPLYNLPRHAVNLFLQGYEKSWIETEEHYFEDKLIEDLAK- 3646  
Qy 3807 FEDAEELKSDVVEGEKPDPLTOLVTTFCRGAMTERSALQOEDPLYMSYAHIIAKSCGEE 3866  
Db 3647 -PGAEPPEED--EVTKRVDPULHQIILLFSRTALTTEK- KLEEDFLYAYADIMAKSCHDE 3702  
Qy 3867 BEEGGEEEGGGEAEAEDEGRASIHQEMEKQKLLFHQARLADRGAEMVLLHLISASKG 3926  
Db 3703 EDDGGESEVK-----SFEKEMEKQKLLYQARLHDRGAEMVLTQISASKG 3749  
Qy 3927 LPSBMWKTTLQGLISILRGKNIDIQOMGLNHLKDKKDVGPPTSAGLWNSSCVLDDLAPE 3986  
Db 3750 ETGPMVAATLKLGIAILNGGNSVTQQKMLDYLKEDKDVFPFQSLAGLQMSVLDLNAPE 3809  
Qy 3987 RNTKAEGLGVGLEGAAGEKNMHDAEFTCALFRFTQLTCEGHNLDQWYLRTOAGNTTVN 4046  
Db 3810 RQNKAEGLGMVTEGSGEKVLQDDFEFTCDLFRFQLQICEGNSDFQNYLRTQTGNNTTVN 3869  
Qy 4047 VVICTVDYLLRLOESIMDFYWHYSSKELIDPAGKANFFKAIGVASQVFNLTLEYIQGPCT 4106  
Db 3870 IIISTVDYLLRVOESISDFYWYSGKVIDEQGQNFSKAIQAVAKQVFNLTLEYIQGPCT 3929  
Qy 4107 QNOQALSHSLRWDVAGVGFLFLFSHQDKLSKHSQVOLLKELLNLOKDMI PMMLSMLEGN 4166  
Db 3930 GNOQSLAHSRLWDVAVGFLFVFAHMQMKLSQDSQIELLKELMDLQKDMVVMMLSMLEGN 3989  
Qy 4167 VVNGTIGKQWYDITAVESASNVELLILKYFDMFLKDLTSSASFQBIANNQWVLPKDPK 4226  
Db 3990 VVNGTIGKQWYDMLVESNNVEMTLKPFDMFLKDLTSSDTFKBYDDPGKGIISKRDHF 4049  
Qy 4227 EKMEQKSYTPPEETEFLLACCETNHDGKLDYIGCDFRHEPAKEIGFNLA VLLTNLSEHM 4286  
Db 4050 KAMESHKHYTQSETEFLLSCAETDENETLDYEEFVKRFHEPAKDIGFNVA VLLTNLSEHM 4109  
Qy 4287 PNEPLARLETAGSVLNYFEPFLGRIEIMGSGKRIERVYFEI KESNTEQWEKQPKESK 4346  
Db 4110 PNETRLQTFLEAESVLNYFOPFLGRIEINGSAKRIERVYFEI SESSRTQWEKQPKESK 4169  
Qy 4347 RAFPYSIVTEGGDEKLEAFVNFCEDAIFEMTHASGLMAASESVG-GTKNREASMYMG 4405  
Db 4170 RQFIDVNVNEGGEKMBELFVNFCEDTIFEMQLAAQI---SESDLNESKANSERSEK --- 4223  
Qy 4406 DDDDERAGKDPF-----RRGLQSVKQGVATAPASSLSPSNIKAKIADMQQPPPAELAVGF 4459  
Db 4224 ERPEEQPGMGFFSVLTVRSALPAIRNYLTLRMLSLSKLSKKQMKKMKMTVKDMVTAF 4283  
Qy 4460 FPMFIFYLPLYGYGVVVRVYIFGVLLGLMRGPQTDDEPP-----PEPTEEBKI 4507  
Db 4284 FSSYWSIFMTLLHFVASVFRGFPRIVCSLLGGSLVEGAKKIKVAELIANMPDPTQDEVR 4343  
Qy 4508 QQ----LHRLLATQSSRHLPALPPADDTGQWQVSATFGLDITKEDNGQIQVKPHESPSTS 4563  
Db 4344 GDGEBEGRKPMETTLPSEDLTDLKELTSDESLLSDIFGLDL-KREGGQYKLIPH----- 4396



Qy 1129 WAPGYNEEKVYSGNTESFGKQWAGVDVGVFLDLIDKTTISFSLNGELLMDALGGETFA 1188  
Db 1121 LCLKAAG-ASVGTKVVGILGVPMQPGDVGVMGINLDASIMFTLNGELLITNKSELAFA 1179  
Qy 1189 DVQGDN-FVPACTLGVCGKARLTYYGQDWNILKYFTTTCGLQEGYPPFCVNMKRDVTHWYTK 1247  
Db 1180 DYEIENGFPVTCISGLSIGRMNLTGDTASTFKFTYTCGLQEGYPPFAVNMNRDVMWFSK 1239  
Qy 1248 DOPIFENTDEMIDRIDVTRIPAGSDTPPCILKISHNTFETM-EKANVEFLRLSLPVLICHN 1306  
Db 1240 RLPTFVWPK-DPHIEVRIIDGTWDSPPCLVKTHKTFGTGNSNANIYCELSNPVCHS 1298  
Qy 1307 EFIDEAEKARWBEIKDRQQILMKEAVEAQAHPAHIDQIMRSGFTMNDIKGLHYEDNQEEL 1366  
Db 1299 SF----- 1300  
Qy 1367 PSSKMKRLPSRPPKRGSMTRGVTTQNNYNLQPGQVGMHRSTSEAMAKYDLGAQGLTPD 1426  
Db 1301 ----- 1300  
Qy 1427 DKDKRGSPKFFRSKRGESSDRAKSKSTPDPFSDTEVSPERGARRPNPQIKVSOAN 1486  
Db 1301 -----SHSPCLDSEA----- 1310  
Qy 1487 QRYNGMNAARPSRTNLYGSQVGLNMATPTQDRKQMTTSTLAQATETVGNEIFDAECLKLI 1546  
Db 1311 -----FOKEKQM-QEILSHITT-----QC----- 1328  
Qy 1547 NEYFYGVRIYPGQPTHYVIGWVTQVHLHSEKDNQSKVTKSSVIIITDDYDRVVENNRQ 1606  
Db 1329 ---FYSIRIFAGQDPCVWGVMTPDVHLYSEKFDLNKNCVTVTVLGDERGRVHESVKRS 1385  
Qy 1607 SCYVRADELNEYMAEATAGACQMGFICGSVDTSVSGVFTCEGKDTSKFKWEPETK 1666  
Db 1386 NCYVMWGDV---VASSQSRSSRVNDLEIGCLVLMAGMLSPSANGKELGTCYQVEPNTK 1442  
Qy 1667 LPFAIFVEATSKETILOELGRSATSLPLSAAVLPTSDKHVTPQPPRLKVCQLKPHOWAR 1726  
Db 1443 VPPAVFLOPTSTSLFQFELGKLKXAMPLSAAIFKSEENPVQCPPLDLVQTIQPVLSR 1502  
Qy 1727 VPNOSLQVHALKSLDIRGWSLMCEDAVSMLALHIPEEDRCIDILEPIEMOKLSLFSHTL 1786  
Db 1503 MENSFLKVETERSERHGVVQCLEPLQWMLHIPEENRCVDILELCEQEDLMQFHVHTL 1562  
Qy 1787 TLYAALCVQSNYRAAHALCTHVDQKOLLYATQSQVMSGPIRQGFVDLLIALHLSSHATTM 1846  
Db 1563 RLYSAVCALGNSRVAYALCSHVDLSQLFHAIDNKYLPGLLRSGFYDLLISITHLANAKERK 1622  
Qy 1847 EACKNEFVPLGPPELK--ALYEEDPMGHSLRSLOTES--VRQMKWTDIAESIT-EISNLY 1902  
Db 1623 LMKNEYIIPITSTTRNIRLVPDESKKGLPGVGPRTCLKFGPKFSTPCFVVTNEERQKQ 1682  
Qy 1903 SPYFPLEVARBFVMOALAEAVETNOVHNRPVGGSNENLFLPLIKLVDRLLLVGMNRDED 1962  
Db 1683 SPEPLELTKMKALSMLTEAVQCSGAHIRDVPGGSVEFQFVPLKLVGTLLVMGVFCDD 1742  
Qy 1963 VEKLLIMTNPETW-DPSFD-KEGKDEHR-----KGLLHMK 1995  
Db 1743 VRQIILLADPSVFGHSDATBEGAEBEVSQVEEKAVEAGEKTSKEARKEAPVRGLLQTR 1802  
Qy 1996 MAEGKALQWCVLQHLNDIQLRHRVEALIAFAHPDVGDLQDOLRRYTEIKQS-DLPSAV 2054  
Db 1803 LPESVKLQWCELLSYLDCOELOHRVEAIVAFGDIYVSKLOANQKFRYNELMQALNWSAAL 1862  
Qy 2055 AAKTRERFCPPREOMNAILSPKHLSEEDKENCPCGEBELIARMNEFHTLMAHVSLSHALQ 2114  
Db 1863 TARKTRERFSPQEQINMLNF-----QLGENCPCEIREELDYDFHEDLLVHCGV---- 1913  
Qy 2115 EPDAAENGEPEAKPAFGKLYNINIVKLEBEEAKAIEBPKKTPPEEK-----FRKVL 2167  
Db 1914 --PLEEEEEEDTWTGKLRVLVYKI-----KGPPEKEQEPTSEERCPPTLKELI 1964  
Qy 2168 IQTIVNNAEESQIETPKLVREMFSLLRQYDAVGELIRALEKTYVINAKTKLDVAEMVVG 2227

Db 1965 SQTMIWAQSDQODAEVMMFNLRQYDSIGELLQALRKTYTISHASVSDTINLAA 2024  
Qy 2228 LSOIRALLPVQMSQEEBELMRKELWKLNNHHTFQHPDLIRVLRLVRNVMVMMNTLGR 2287  
Db 2025 LQOIRSLLSVRMGREBELLMINGLDIMNNKVYQHPNLRVLGMHETVMEVWVVLG-- 2082  
Qy 2288 AQAQSDAQSSQVPAEDSEKEDTSHEMVAVACCRFLCYFCRTGRQONQKAMDHPDFLENS 2347  
Db 2083 -----TEKSQIAFPKMWASCCRFLCYFCRISRQONQKAMEFHLSYLLENS 2126  
Qy 2348 NIILSRPSLRGSTPLDVAYSSLMTELALAEHYLEKIAVLSRCLGLOSNESELVKGY 2407  
Db 2127 SVGLASPMRSGSTPLDVAASSVMNDELALGLSEPDLEKVVVYIAGCGLSCPMLLAKGY 2186  
Qy 2408 PDLGMDPVEGERYDLRFVFCVWNGSVSEENANLIVIRLLIRRPCECLPALRGE-GEGLLK 2466  
Db 2187 PDVGNPIEGERYLSFLRFVAVFVNSEVENASVVVKLLIRRPCEFCPALRGECCGGLA 2246  
Qy 2467 AIVDANKMSRIADRRKLRMEQEGDVNFSHPIPE-SDEDEDYIDTGAAILNFCTIVDL 2525  
Db 2247 AMQGAIKISSPA-----LDLPQSG---YKREVPEDGEEEEEIVHMGNAIMSFYSALIDL 2298  
Qy 2526 LGRCAPDAGVIALGKNESLRARAILRSLVPLEDLOGVLRLFTLNPNNAAGEERPKS--DM 2583  
Db 2299 LGRCAPEMHIQTKGGAIRIRSILRSLVPTEDLVGIISIPKL--PSLNKDGSGSVSPDM 2356  
Qy 2584 PSGLIPGHKOSVGLFIERVVYGIETQELFYKLEAEFLPDRAATMLDRNDNDCESDMALSM 2643  
Db 2357 AANFCPDHKAAMPWFLDORVIGIKQOTFLHLHLEVGFPLDRASASLTVALSTTESALAL 2416  
Qy 2644 NRYIGNSILPLLKHAYFYNEAENYASLLDATHVTYRLSKNRMLTQKOREAVSDFIVAL 2703  
Db 2417 NRYICSAVPLLRFCAPLEFAGTEHYTSLIDSTLQTVRLSKGRSLTQAQRDTIECLLAI 2476  
Qy 2704 TSAMQPSMLKLRLKTLVDVSKLSEYTTVALRLTLHYERCAYKYGSGTAGCQAGFASDD 2763  
Db 2477 CNHLRPSMLQQLRLRFLVDVPQLNDYCKMPLKLLTNHFEOCKWY-CLPSGWSYGLAVE 2535  
Qy 2764 EEKRLTMWLSNFTSDSKMDYEPFLGKALPCILAIAGCALPPDY-----SLSKNYDD 2816  
Db 2536 EELHTEKLFWGIWIPDSUSHKKYDPLFRMSLPCUSALAGALPPDYLOTRITATLEK---- 2591  
Qy 2817 EFGYKEQAAGDLNPQDPQOPINTSSVALNNDLNTIVQKFESEHYHDAAWASKIENGWYVG 2876  
Db 2592 -----QVSDADG-NFDPKPINTINFSLPEKLEVIIVTKVAESHDKWACEKSGWKYG 2644  
Qy 2877 EGWSDSQKTHPRLPKYNMLNDYKERYKEPVRESLKALLAIGWSVEHSE-----VDIPSN 2931  
Db 2645 ISLDENVKTHPLIRFPFKTLTEKEKEIYRWPARESLKTMLAVGWTVERTKEGEALVOLREN 2704  
Qy 2932 NRSSMRQSGSGRPPPELVTDSATPFDYNPHPDVDMTNLTLSREMONMAERLADNAHDIA 2991  
Db 2705 EKLRSVQTSQGN-----SYNPAPLDLSNVVLSRELQGVMEVVAENVHNLIWA 2751  
Qy 2992 KKKKEELVTNGGGTHPOLVPYDLTLTKKKKDRERSQEFKLYQYQGYKLRHPSKAPQSD 3051  
Db 2752 KKKKLELESKGGSGHPLVPYDTLTAKKFDREKAQDLFKFLQVNGVIVSRGKMDMELD 2811  
Qy 3052 TEQTTTGVAIELRPAYSLLEKLIQYIDRATINMKLLKPSTTFFSRSSSKTSTRDKIFPSK 3111  
Db 2812 -----AFSMEKRFAYFKKILKYVDSAQBFIAHLE-AIVSSGKTEKSPHDQEIKFFAK 2864  
Qy 3112 AVLPLMEKYPFSTRNYFI-AVATATNNVGAASLEKEMVAALFCKLASLSRSLAAFGPD 3170  
Db 2865 VLLPLVDQYFTNRLYFLSSPLKPLSSSGYASHKEKEMVASLFCCKLAALVRRHSLSFGSD 2924  
Qy 3171 VRITVRCLOVLKVGIDAKSLVKNCPERTSMLTFFNNVADDVGHTINMLQDGKYAHLRG 3230  
Db 2925 STTWVCSLHILUAQIOLDRTRVNMKSELVKAGLRAFFESAEDLEKTSNKLKGFTHSR- 2983  
Qy 3231 THLK-TSTSLGYINGVLLPILTAKFHDHLANCEYGAADLLDLBIQVASYKMLGSLYALGTD 3289

Db	2984	TOIKGVSONITYTVALLPILTSIFEHVAHQHQFQVDDLGLDGVQVCSVRILCSYLSIGTGK	3043
Qy	3290	SLTHDRKYLKTEIERBHRKPALGSCILGAFSSTFPVAFLEPHLNKHNQFGLLNRIADHS--L	3346
Db	3044	NI-----YVERQRPALGECCLASLAAALPVAFLPTLNRYNALSVFNTKTPRERSIL	3094
Qy	3347	EAQIMQMEOCMPTLETILGEVDQFVESDKTYNEAPHIIDVLPPLCSYLFPFWAQQGD	3406
Db	3095	GMPTVBE MCPDI PQLEGLMKEINDLAESAARGYTEMPHVIEVILPMLCNLYLSYMERGPE	3154
Qy	3407	NVPTGGNHVMTVAEHNOLLKNVLKLIKNGENENAPMWTATVTOQIILNSBEEL	3466
Db	3155	NLSPTGPCCSKVTSEHLSLITGLNLIKINNUGIDEASWMKRIATVVAQPIISKAPDLL	3214
Qy	3467	RDSFLPLAERVRKRTDNMFKEESLRGFIKSSSTDTSQVESQIOEDQOLLIVRDIYSFYL	3526
Db	3215	RSHPITPLEKLKXKAVKTVQEEBOLKA--DGKGDTOEAEILLIDEPAILICRDLYAFPM	3271
Qy	3527	LIIKYVDLQRNHLRNPNPEABEELYNHVAEIEFNWKSQYFLKEBQNFISANEIDNMVLIM	3586
Db	3272	LIRVYDNNRSNWLKSPGDSQDLPRMVAEVLWCKSHNFKEBQNFVIOQNEINNLAFLT	3331
Qy	3587	PTATRVATVDGTPOGGGKKKXKROKDKDKEQVQASLMVACLKELLPVGLNLPAGRE	3646
Db	3332	GDSKS KMSKAMQ--VKSGGQDQERKRTKRIGDLYSIQTSILVAAKMKMLPGLNMCTPGD	3389
Qy	3647	QELVQHCKDRFLKQMSQDVAEFAKTOLTUTPKDT-DPADEMSWQHYLYSKLGSKSKSNIT	3705
Db	3390	QELISLAKRSYSDTDDEBVEKHLRNHLHLOEKSDDPA--VKWQLNLY-----KDVLK	3440
Qy	3706	VETAENKAKIIDDTVERIVAMSKVLFGLHMDHPQMSKNYRSVSVSIQRKRAVIACFRQ	3765
Db	3441	SEEPSNPEK---TVERVQRIISAAPVHLEQVEQPLRSKKAVWHKLLSKQRKRAVACFRM	3496
Qy	3766	TSLSHLRPRACNTPARTYYELWLE-BENTGOEVMIEDLTQSFDEDAELKSKDVVEBGEKP	3824
Db	3497	APLYNLPRHRSINLFLHGYOFWETIEBSYFEELKVQDLAKS---PRVEBEEBEMEKPQ	3553
Qy	3825	DPLQLVTTFCRGAMTERSGALQSDPLVMSYAHIIAKSC--GREERGGGEEBEGGEAE	3882
Db	3554	DPLHQIILHFSRNALTFRS-KLEDDPLYTSYSSMMWAKSCSGEDEEB---EDKE-----	3603
Qy	3883	AEDEGRASIIHEQEMEKQKLLFHQARLADRGAEMVLLHHSASKGLPSEVMYKTLQLGISI	3942
Db	3604	-----KTFPEKEKEKQKLYQARLHERGAAEMVLQWISASKGEMSPMVVETLKLGLAI	3657
Qy	3943	LRGNIDIQMGWMLNHLKDKDVGFETSIAGLWNSCSVLDDADAFERNYKASGLGVGLEGAA	4002
Db	3658	LNGCNAGVQQKMLDLYLVKKDAGFPQSLGSLMQSCSVLDLNAFERQNKABGLGMVTEGT	3717
Qy	4003	-----GEKNMHDAEFTCALPRFTQLTCEGHNLDMQNLVTRTQAGNTTIVNVLTVDYLL	4056
Db	3718	LIVREGEKVLQNDDEFTRDFRFLQLICEGHNSDFQNLRTQMGNTTIVNVLTVDYLL	3777
Qy	4057	RLOESIMDFYWHYSKELLIPAGKANFFKAIGVASQVFNTLITEVIOGPTCQNQOALAHSR	4116
Db	3778	RLOESISDFYWYSGKDIIDBSGGHNSKALAVTKQIFNSLITEVIOGPTCIGNQOOLAHSR	3837
Qy	4117	LWDAVGGLFLFUSHMQDKLSKHSSQVLLKELLNLQKDMI PMMLSMLEGNVNGTIGKQM	4176
Db	3838	LWDAVGFLHFVFANMQMKLSQDSSQIPELLKELLDLLQDMVVMLLSILLEGNVNGTIGQM	3897
Qy	4177	VDTLVESASNVELLIKVFDMPFLKDLITSSASFOEIDANNDGWVLPKDPEKMEQOKSYT	4236
Db	3898	VDTLVESSTNVEMILKPFDMFLKDLITSSDTFKEYDPDGKGLISKKEFOKAMEGQOXYT	3957
Qy	4237	PEETIEFLACCEETHNDGKLDYIGFCDFRHEPAKIEGNLAVLLTNLSEHPNBPRLARFL	4296
Db	3958	QSEIDFLLSCAEBANDMFWYIDVDFRHEPAKDIGFNVAVLLTNLSEHPNDSRLKCLL	4017
Qy	4297	ETAGSVLNYFPFLGRIEIMGGSKRIERVYFEIKESNIEQWEKQIKESKRAFFYSIVTE	4356
Db	4018	DPASVNLNYPFYLGRTEIMGAKKIERVYFEISSERTOWEKPOVKESKROTFIDVYNE	4077

Qy	4357	GGDKKELEAFVNFCEDAIFEMTHASGLMAAS-----BESVGGTKNREASVM--YMGDDDD	4400
Db	4078	GGQEKWELFVNFCEDTIFEMQLASQISBDSADRPEEBEG---DRESSYVLINGEBEE	4134
Qy	4410	ERA--GKDPRRGLOQSKGVATAPFSSLSPSNIKAKIADMQMPPAELAVGFFKMPFYL	4467
Db	4135	DKSFESASAFAMACASUKRNIWNLRKATLKNLRKYRVNVKMTAKELVKVFFSFWMLF	4194
Qy	4468	YYLGYGVLVVRYIFGVLL-----GLMRGPQT-----DEPPP-----EP	4501
Db	4195	VGLFQLFFTTIVGGIFOLLNSTVFGGLVEGAKNIRVTKILGDMDPDTQFGIHHDDAMEAR	4254
Qy	4502	TESEKIG--QLAHRLLA---TQSRHPALPPADDTGOMQVSAFGLDITKEDNGQIQV	4554
Db	4255	AEVAEAGITTELVHFVKYBERGDTFELMSDIFGLHPKXEGGVKHGPEVGLGDLSIIIGK---	4311
Qy	4555	KPHESPST--STPSSGEEAEVSPDESADITHEEORPPS-LIDLGGEOAKQAOERMEAQA	4611
Db	4312	---DEPPTLESTVTKRKKAQA--ETKAEHAEGKVESEKADLEDGEKEDKAKEERAEYL	4367
Qy	4612	AQAAMSAIEAESKAVQGPAPSALSOVDLSQVTRRAVSFLARNFYNLKVVLVLPFCIN	4671
Db	4368	WAEVTYKKRRRRGQVKEKPEAFMANFPGKLEIYQTKLLHLYARNFYNLRFLAFLVAFAIN	4427
Qy	4672	FVLLFYKVS--TLDGEGGSGIGLDIIAGGSGSGAGSGDGSSEGEDDDDALEVVID	4729
Db	4428	FILLFYKVTETPEEESTEDVANLWN-----SLNDEEESAMVFFVLQ	4469
Qy	4730	EDFFYMEHVIKMAALVHSIVSLAILGYIYHLKVPLAIFKREKEIARKLEPDGLYIAEQPE	4789
Db	4470	ESTGYMPTLRALAVVHTIISLCVVGYCYLKVPLVVFKEKEIARKLEPDLGYIVTEQPS	4529
Qy	4790	DDDLKSHWDKLVTSAKSPFVNVYWDKVKKKVKRAKYSETYDPDSISNMLGMEKTS--FSAQ	4847
Db	4530	EDDIKGQWRVLINTSPSPHNYWDKFKVRKVINKYGLDYGAERIAELLDGDKNALDFSPV	4589
Qy	4848	EEGSK--GLIHYIINIDWRYQWKAGVTTIDNSFLYSLWYFSGVMGNFNFFFAAHL	4905
Db	4590	EETTAAASLVSWLSSIDMKHIXLKGUVFTDNSFLYLAWYTTWSVLGHYNNFFFAAHL	4649
Qy	4906	DVAVGFKTLRTLIQSVTHNGKQLVLTVMLTIIIVYTVIAFNFRKFY-VQBEDDEVNR	4964
Db	4650	DIAMGFKTLRTLISSVTHNGKQLVLTVGLLAVVVYLVTVVAFNFRKFYKNSDDDBPDM	4709
Qy	4965	NCHDMLTCFVFNLYKVRAGGGTDELEPDGDDSEVYRIIFDISRFFFTIIVILLAIQ	5024
Db	4710	KCDMMTCVLFHMYGVRAGGGTGBIEDPAGDPYEMYRIVFDITTFPHFVIVILLAIQ	4769
Qy	5025	LIIDAEGELRDQLESVKEDMESNCFICGINQOYFDKVPYHGFDTHTVOREHNLANYMFLMH	5084
Db	4770	LIIDAEGELRDQEOQVEDMETKFCIGINDYFDTTPHGFTHTLQEHNLANYLFLMY	4829
Qy	5085	LINKPTEYTGQTYVNNMYTQRCWDPFFPVGDGCFRQYEDLMG	5127
Db	4830	LINKDTEHTGOSYVWYMOESCWDPFFPAGDCFRKQYEDQLG	4872

RESULT 3  
US-09-424-783-4  
; Sequence 4, Application US/09424783  
; Patent No. 6780608  
; GENERAL INFORMATION:  
; APPLICANT: Hakamata, Yasuhiro  
; APPLICANT: Nishimura, Seiichiro  
; APPLICANT: Barsoumian, Edward Leon  
; TITLE OF INVENTION: Human Type 3 Ryanodine Receptor Protein  
; TITLE OF INVENTION: and DNA Molecules Coding Therefor  
; FILE REFERENCE: 0652.2000000  
; CURRENT APPLICATION NUMBER: US/09/424, 783  
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TYPE: PR1

ORGANISM: Oryctolagus cuniculus

US-09-424-783-4

Query Match 42.3%; Score 11349; DB 2; Length 5037;

Best Local Similarity 44.9%; Pred. No. 0;

Matches 2395; Conservative 906; Mismatches 1517; Indels 516; Gaps 106;

Qy	5	EGGASEQDDVFLRTEDMVCISCTAT---GERVCLAAEGFNGRCHFLNIAD-KNIPPD	59
Db	3	DGSEGE-DEVOFLRTDDBVLQCSATVLKEQLKCLAAEGFNGRCHFLNIAD-KNIPPD	61
Qy	60	LSQCVFVIEQALSVRALQELV---TAAGSETGKTGSGHRTLLCYNAILLRHLNSDMYLA	116
Db	62	LAICCFTLEQSLSVRALQELMANTVEAGVSSQ---GGHRTLLYGHAILLRHHRMYLS	119
Qy	117	CLSTSSQ-DKLAFDVGLQHQSGEACWTLHPASKQSEGEKVRVGGDDLILVSVATERY	175
Db	120	CLTTSRSMTDKLAFDVGLQEDATGEACWTLHPASKQSEGEKVRVGGDDLILVSVSSERY	179
Qy	176	LHTTKENEVSIVNASFVHTWSVOPYGTGIRSMKVVGVVFGDVLRFPHGG-DECLTIPS	234
Db	180	LHLTASGELQVDASFQWTLNMPN---ICSCCEEGYVVGHLRULPHGHMDSECLTI-S	234
Qy	235	TWTGKGQNIIVVYEGGVSQARSILRLLEARTKWAGFINWYHPMRIRHITTYGRLGVN	294
Db	235	AADSDQRLVYEGGAVCTHARSILRLLEPLRISWSGSHLRWGQPLRIRHTTYGRLALT	294
Qy	295	DONELYLSRBEATTASACFLRKEQDQKQVLEKDLLEVIGAPIIKYGDSTVIVQHSET	354
Db	295	EDQGLVVVDACKAHTKATSFVRVSK-EKLDTPAKRDVEGMPPEIKYGESLFCFVQHVAS	353
Qy	355	GLWLSYKSYETKKGVGVKESKQAILHEEGQMDGLDPSRQSESRRTARVIRKCSLFT	414
Db	354	GLWLTAAAPDPKALRLG-VLKKKAILHQEGHMDALFLTRCQSEQAARMIHSTAGLYN	412
Qy	415	KFINGLETLOENRRHSMFPA---SVNLGBMVNCLIEDLINFYAQPDDEMBHEKQKFRALR	472
Db	413	QFIKGLDSFKSPKSGPPAGPALPIEAVILSLQDLICFYFPPEELQHEKQKLSLR	472
Qy	473	NRQDLFQEGILNLILEAIDKINVITSQGFAGFLAGDESQGSWEMISGYLYQLAAIIK	532
Db	473	NRQSLFQEGMLSLVNLICDLRLNVVTTAAHFAEY-AGEEAAESWKEIVNLLYELLASLR	531
Qy	533	GNHTNCAOFANSRLNWLFSRLGS-OASGEGTGMDLVHCVLIDSPEALNMMRDEHIKVI	591
Db	532	GNRANCALF--STNLDWVVSRLDLAS--SGILEVLYCVLIESPEVINTIIOENHIXSI	586
Qy	592	LSLEKHKGRDPKLVLCVLCVNGVAVRSNNICDVLPGKLLLOTALVDHVSSVRP	651
Db	587	LSLDKGRHKKLVLCVLCVNGVAVRSNQDLITENLLFGRELLLTQNLINIVTSIRP	646
Qy	652	NIFVGRVSGSAVYRKWYFVETMDHIEK-TTHMPLHRIGWANTTGYVPYGGKMGNG	710
Db	647	NIFVGRAGSQTQYKWKYFVWVDEVVVPLTAQATHLRVGMALTEGYSYPYGGGEGWNG	706
Qy	711	VGDDLYSGFDGAYLWSGKRTPPVNRTHAEBPYIRKGDVIGCALDLYPIINFPNGVRV	770
Db	707	VGDDLYSGFDGLHMTGHVAPV--TSPGQHLAPEDVWSCCLDSVPSISFRINGCPV	764
Qy	771	TGSEFTNENLGFFPVVISCSSKLSRFLGGBHRLRYAAPGYSPLVESILLPOOISLE	830
Db	765	QGVFAFNLDGLFFPVVSFAGVKVFLGGHGBEFKFLDPGYPACHEAVLPRERLRE	824
Qy	831	PCFYFENLSKRA--LAGPPLVQDDTAFVPTVDTLQITLPTVVEQIRKLAENIHEMMAM	888
Db	825	PIKEYRREGPRGPHLVGSRCLSHSTDFVPCPVDTVQIVLPHLERIREKLAENIHELWAL	884

Qy	889	NKIEAGMWYGDQREDLHKIHPCLVPPFLPPAERKRYDIQAVQTLKTILALGYISL--D	946
Db	885	TRIEQGWYTGVRDNNKRLHPCLVNFHSLPEPERNYNLOMSGETLKTLLALGCHVGMADE	944
Qy	947	KPPARIRNVRLPNEPFPMSNGYKAPLDLSAVLTPQMDLVDQALBENTHNLHARERIOQ	1006
Db	945	KAEDNLKTKLP-KTYMMSNGYKAPLDLSHVLRTPAQTTLVDRLAENGHNVDWARDVAQ	1003
Qy	1007	GWYGLNEDSDMHSRPHLVYPKVDDAIKKANDTASSETVRLTVVGYMLDPPPTGEQHEA	1066
Db	1004	GWYSIAVQDIPARRNPLVYRLDDEATKSNRDSLCOAVRTLGLGYNYIEPPDQERS--	1061
Qy	1067	LLLEASKQKQAD-FRTYRAEKNYAVSSGKWFYFEFELTAGPMRVYGAHADMAPGMMLQD	1125
Db	1062	---QVENQSRWDVRIFRAEKSIVTQSGRWYFEFAVTTGEMRVGMARPELRDPVELCAD	1118
Qy	1126	ENSWAFDGYNEEKVYNGNTESFGKQWAGVDVGVFLDLIDKITSFSLNGELLMDALGET	1185
Db	1119	ELAYVFNHGRQWRHLG-SEPFGRPMQSGDVGVGCMIDLITENTIIFTLNGEVLMSDSGET	1177
Qy	1186	TEADVQ-GDNFVPACTLGVGQKARLTVGDVNTLKVFYTTCLQSGYEPFCVNMKRDVTHW	1244
Db	1178	AFREIEIGDGLPVCSLGPGQVGHNLGQDVSSLRFPFACLOQEGFEPFALNMORPVTTW	1237
Qy	1245	YTKDQPIFENTDEMIDTRIDVTRIPAGSDTPPCPKISHNTEFETMEK-ANNEFLRLSLPVI	1303
Db	1238	FSKSLPQFEPVPE-HPHYEVARMGDVTDTPCLRLAHRWTGSONSLVEMFLRLSLPVQ	1296
Qy	1304	CHNEFIDEAKRWRWEIKORQOILMKEAVEAOMPAAHDIQIMRSGFTWIDIKGLHYEDNQ	1363
Db	1297	FHQHFRCTA-----GAT-----	1308
Qy	1364	ELPSSKWKRLPSRPRKSGMTRGVTIQNYNNLQPGQVNGMHRSTSEAMAKYDLGAQGL	1423
Db	1309	-----PLAPP-----GLQP-----PADE-----ARAA	1326
Qy	1424	TPDDKDKGRSPFKFRSKRGESSDRAKSKTDPDFSDTEVSPERGARRPNQIKVS	1483
Db	1327	EPDPDYENLRSSAGGWEAGEGEGTAKETPGTGPQ--GVEAQP--VRAENEKDAT	1381
Qy	1484	QANQRYNGMNAIPSRNTLYSGVGLNMTATPDQRKQMTTSTAQSATETV-GNEIFDAEC	1542
Db	1382	EKNKK-----RGFLFAKKAAMMTQPP-----ATPALRPLPHDVPADNRDPEI	1426
Qy	1543	LKLINEFYGVRIYVPGODPTHVYIGWTTQVHLHSKDFNOSKVTSSVIIITDDYDVVEN	1602
Db	1427	ILNTTYYVVRVFPAGQEPSCVWGVWTPDYHQHDMFDSLKVRAVVTMGDEQNVHSS	1486
Qy	1603	VNRQSCYVRADELYNEVMAEATAKASQGFICGSVDSTSGVSFTCEGKDTSFKXME	1662
Db	1487	LKSCNRYWGGDF--VSPQOQGRISHTDLVIGCLVDLATGLMTFTANGKESNTFFQVE	1543
Qy	1663	PETKLPFAIVFVETSKELQIELGRSATSPLSAVLPTSDKHVIFOPPPRLKQVCLXPH	1722
Db	1544	PNTKLPFAVFLPHQNVIFELGKQKNIMPLSAAMFELSERKNPAPCPPELVEQMLMPV	1603
Qy	1723	QWARPVQSLQVHALKLSLDIRGWSMLCEDAVSMALHHPEDRCIDILEPIEMDKLISFH	1782
Db	1604	SWSRMPNHLQVETRRAGERLIGWAVQCCODPLTMALHHPENRCMDLLELSELDLQRFH	1663
Qy	1783	SHTLTLAALCYQSNYRAAALCTHVQKOLLYAIQSOYMSGRLRQGFYDLILALHLESH	1842
Db	1664	SHTLRLRVACALGNRVAAHLSHVQAOALLHALEDALHPLPLRAGYDYLILSHLESA	1723
Qy	1843	ATTMEACKNEFVPLGPELKALYBEPP-----MHSRLSL-OTESVROPQMKMTD----	1890
Db	1724	CRSRRSLSEVIVPLTPETRAITLTPFGKGNARRHGLPGVGTTSRLRPHHSPPCFV	1783
Qy	1891	---TAEISITELSNLYSPFFLEVAREFVMOALAEAVETNOVHNRDPVCGSNENFLPLIK	1947
Db	1784	AALPAAGVAEAPARLSIPAIPLEALRDKALRMLEGEVRDGGQGHARDPVGSGVEFQVPVLK	1843







2504 FLDRVYGIENQDFLLHVLVDFGLPDMRAAASLDTATFTSTTEWALAVNRYLCLAVLPLITK 2563  
2658 HAYFYNEAENVASLADLTHTYRSLKRMULTKQREAVSDFLVALTSAMOPSMLLKLLR 2717  
2564 CAPLFAGTEHRAIMVDSMLTYRSLRGRSLTKAQRDVIEDCLMSLCRYIRPSMLQHLRL 2623  
2718 KLTVDVSKLSEYTTVALRLTLHYERCAYKYGSTGAGOGAFASDEKRLTMMFLSNIF 2777  
2624 RLVDVDPILNEPAKMLKLLTNHYERCWKY--CLPTGWANFGVTSEEBLHLTKLFWGIF 2682  
2778 DSLKMDYEPFLFGKALCLIAIGCALPPDYSLSKNYDDEFYKGEOAGDLD--NPQYDPQ 2836  
2683 DSLAHKKYDPELYRWAMPCLCAIAGALPPDY-----VDASYSSKAEKATVDAEGNFDPR 2737  
2837 PLNTSSVALNNDLNTIVOKFSBHYHDWASRKIENGWYVGEWSDSKTHPRLKPYNNMLN 2896  
2738 PVETLNVIIPEKLDSEFNKFABYTHEKWAFLKQNNWSYGENIDEELKTHPWLRYKTF 2797  
2897 DYKERYKEPVRESIKALLAIGWSVEHGEVDIPSNNRSMRQSKSGRPPPEIVTDSATP 2956  
2798 EKDKIIRWPIKESLKAMIAEWITIE-----KAREGEEKTEKKTKAKISQSAQT 2847  
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2848 YDPREGYNPPDLSAVTLRSRELOAMAEQLAENYHNTWGRKKKQBLEAKGGGTHPLLVPI 2907  
3013 DLLTDKEKKKOREROEFLKYLQYOGYKHLRSKAPQSDTEQTTGTGVAIELRFAYSLLK 3072  
2908 DTLTAKEKARDREKAQELLKFLQMGYAVTRGLKDMELDSS-----SIEKRFAGFLQQ 2961  
3073 LTYQIDRATINMKLAK--PSTTFSSRRSPKTRDIFKFSKAVLPLMBKYSFSTRNYFIA 3130  
2962 LIRWMD--ISOEFTAHLEAVSSGRVEKSPEHEQIKFPAKILLPLINQYFYNHCLYFLS 3018  
3131 V-ATATNNVGAASLKEKEMVAALPKLASLRSRLAAGPDVRIIVTRCLQVLVKGIDAKS 3189  
3019 TPAKVLGSGCHASNEKEKEMITSLFKLAALVHRVSLFQTDAPAVVNCILHILARSLDART 3078  
3190 LVKNCPEFIRTSMLTFNNAVDDVGHITMNLQDGVAHLRGTHLKTSTSLGVINGVLLPI 3249  
3079 VMKSGPEIVKAGLSRFFESASEDEKMNVENLGLKVQARTQVKGQNLTYTTVALLPV 3138  
3250 LFAKDHLANCYBGADLLDETOVASYKMLGSLYALGDASLTHDRKYLKTEIERHKPAL 3309  
3139 LTLTFOHIAHQFGDDVLDDVQVSCYRCLSIYSLGTKN-----TYVEKLRPAL 3189  
3310 GSCLAGFSSTFPVAFLEPHLNKHQFSLNLRADHS--LEAQDMQKMEQCMPTLETIL 3366  
3190 GECLARLAAAMPVAFLEPQLNEYNACSVYTTKSPRERAILGLPNVSEBMCPIPVLERLM 3249  
3367 GEVDQFVESDKTYNEAPHIIDVVLPLLCYSLPFWWAQGD---NVTPTGG-NHVTWMTAE 3422  
3250 ADIGGLAESGARYTEMPIHVEITLPLMLCSYLPWRMERGPEAPSPALPAGAPPPCAVTSD 3309  
3423 HNNOLLKNVLKLIKKNIGENAPWMTRIATYTOQIIINSSEELLRDSFUPIAERYKRTD 3482  
3310 HLNSLLGNLRLIIVNGLGDEASWMLKLAFAQPIVSRARPELLQSHFPTIGRLRKAG 3369  
3483 NMFHKEESLRGFKSTDDTSQVESQIQEDWOLLVRDIYSFYPLLIKYVDLQORNHLRN 3542  
3370 KVVSEEEQALEAKA---EAQEGELLVRDEFVLCRDLVALYPLLIYRYVNNRAQWLTEP 3426  
3543 VPEABELYNHVAIFINWKSQVFLKEBQNFISANEIDNMVLIIMPTATRTAVTDGTTPQ 3602  
3427 NPSAEELFRMVGEIFTYWSKSHNFKEEQNFVQNEINNMSFL--TADNK-----SKAK 3479  
3603 GGGKKKKHDKRDKKEVQSLMVACLKLLPLVGLNLFAGREQSLVCHCKDRFLKKWS 3662  
3480 SGSDQERTKKKRRGDRYSVQTSLIVATLKKMLPIGLNWCAPTDQDLITLAKTRALKDT 3539  
3663 EODVAEFAKTQTLTKPIDPADEMSWQHYLYSKLSKSNITVETAENKAKIIDDTVER 3722  
3540 DEEVREFLHNLHLQKRGESPLRWOMALYRGVPGRE-----EDADDPKXI----VPR 3589

3723 IVAMSKYFLGLHMTIDHPQOMSKNRYRSVSVIQRKRAVIACFRQTSLSLSLPHRACNIFAR 3782  
3590 VQEVSAVLVYLDQTEHPYKSKKAVWHKLLSKORRAVAVCFRMTPLYNLPHTRACNMFLE 3649  
3783 TYIELW--LEBENIQOEVMIEDLTCSPEDAELKKSDVVEEGEKDPDLQTLVTTFCRGAWTE 3841  
3650 SYKAAWTLTDHSDPEDRMIDDLKAGQEE--EEEEVEE--KKPDLHLQVLVHFSELTALTE 3706  
3842 RSGALQBDPLVMSYAHIIAKSCGEBEEGEGEAEAEDEGRASIEHQEMEKOKL 3901  
3707 KS--KLDELYMAVADIWAKSC-----HLEEGENGEGAEVEVEVSPEEKQMKQRL 3756  
3902 LFHQARLADRGVAEMVLLHISAKGLPSEMVMKTLQLGISILRGNDIDIOGMMLNHLKDK 3961  
3757 LYQCARLHTRGAABWMLQMSACKGETCAMVSSTLKLGISILNGNAEVOQKMLDYLKDK 3816  
3962 KDVGFFTSIAGLNMNCSVLDDLDAFERNTKAEGLG-VGLEGAA-----GEKNMHDAEFTCA 4015  
3817 KEVGFQSIQALMQTCSVLDLNAFERQNKAEGLGMVNDGTVINRQNGEKYMADEFTQD 3876  
4016 LFRFIQLTCEGHNDWQNYLRTQAGNTTVMNVICTVDYLLRLQBSIMDFYWHYSSKELI 4075  
3877 LFRFLQLLCEGHNDWFQNYLRTQGTNTTINIICTVDYLLRLQBSISDFYWHYSGKDI 3936  
4076 DPAGKANFFKAIGVASQVFNLTLEVIQGPCTQNOQALAHSLRDLWDAVGFLFLFSHMOKL 4135  
3937 BEQGRNFSKAMSVAQVFNLSLTVIQGPCTGNQOQSLAHSRLWDAVVGFLHVFHMMML 3996  
4136 SKHSQVDLLKELLNLQKDMIPMMLSMLEGNVNGTIGKQWVDTLVSASNVLLIKYFD 4195  
3997 AQDSQIELLKELLDLQKDMVYMLSLLEGNVNGMARQWMLVSESSNVEMILKFFD 4056  
4196 MFLKDLTSSASFOEIDANNQWVLPKDPKEKMEQOKSYTPPEITEFLACETNHDGKL 4255  
4057 MFLKDLKILVGEARQDYVTDPRGLISKDFOKANDSQFQSGPELOFLLSCSEADENMI 4116  
4256 DYIGCFDRFHPAKEIGFNLAULLNLSEHNPRLARFLETAGSVLNYPEPFGRIEI 4315  
4117 NCEEFANRFQEPARDIGFNVAULLNLSEHVPDPRLHNLFLAELSILEYFRPYLGRIEI 4176  
4316 MGGKRIERTVFEKESNIEQWEPQIKESKRAFFYSIVTEGGDKKLEAFNFCEDAIF 4375  
4177 MGASRRIRIYFEISETNRAQWEMPQVKESKROQIFDVVNEGGEAKRMLFVSPCEDTIF 4236  
4376 EMTHASGLMAASESVGCTKNREASYMYMGDDDERACKDPFRRLQSVKQDVA----- 4429  
4237 EMQIAAQISEPEGBP-----ETDEDEGAG--AAEAGAEAGAEAGLEGTA 4280  
4430 -----TAFSSLSPSNIIKAKIADMQMPAPBLAVGFFHFFYLYLYLGYG 4473  
4281 ATAAAGATARVVAAAGRALRGLSYSLRRRVRRLRLTAREATAVAALLWAAVTRAGAA 4340  
4474 VLVVVRYIFGVLLGLMRGFTDDEPP-----PEPTEEKIGQLRHLLATQSSR 4521  
4341 GAGAAAGALGLLWSLFGGLVEGAKKVTVTTELLAGMPDPTSDEVHGE----- 4388  
4522 HLPALPPADDTGQWQVSAGFLDIKEDNGQIQVXPHE----- 4559  
4389 -QPAGPGGDADG--EGASEGADGAABGDBEEAVHEAGPGGADGAVAVTGGPPRPEGA 4445  
4560 -----PSTSTSSGAEAVSP-----DESADHTEQRPPLSLDLLGGEQAKTKQAQRMBAQ 4610  
4446 GGLGDMGDTTFAEPPTPGSPILKRLKGLVDGVVEELPPE----PEPEPEPELEPEKADAE 4501  
4611 AAQQAAMSAIBAESKAVQGPAPSALSQV-----DLSQVTRRAVSFLARNFYMLKYVA 4663  
4502 NGKEEVPEPTPEPKKQAPPSPPKBEAGGEFWELEQVQVKFPLNLSRNFYTLRFLA 4561  
4664 LVLAFCINFVLLFYKVTLDGEG-----EGSLGDIAGGGSGSAGSGSGSGESGSD 4719  
4562 LFLAPAINFILLFYKVS--DSPPGDDMEGSAAGDV---SGAGSGSGSGWGLGAGEBAG 4616

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Qy 4720 DDALEVVH--IDEDFFYMEHVWKMAAVLHISVSIALIIGYHYHLKVLPLAIKREKEIARKL 4777
|: : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :|
Db 4617 DEDENMYVYFLEESTGYMEPALRCLSLHLTVAFLCIIGYNCCLKVPLVIFKREKELARKL 4676
|: : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :|
Qy 4778 EFDGLYIAEOPEDDDDLKSHWDKLVISAKSPFNVDKVFVKKVRKAKYSEYDFDPSISNML 4837
|: : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :|
Db 4677 EFDGLYITEQEDDDVKGWDRVLVNTSPSPSNVDKVFVKRVLDKHGDIYGRERAEALL 4736
|: : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :|
Qy 4838 GM-----EKTFSFAQEBEGSKGLIHYIINIDRWYQVWKAGYITIDNSFLYSLMYFSFVM 4892
|: : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :|
Db 4737 GMDLATLEITAHNERKENPPGLLTLMSIDVKYQIWKFGVIFPTDNSFLYGLWYVMWSLL 4796
|: : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :|
Qy 4893 GNFNFFFAHLLDVAVGFKTLRLILOSVTHNGKQLVLTVMMLTIYIYIVTVAFNFRK 4952
|: : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :|
Db 4797 GHYNNFFFAHLLDIAMGVKTLRLTILSVTHNGKQLVMTVGLLAVVYVLYTVVAFNFRK 4856
|: : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :|
Qy 4953 FYVQED-DEVNRNCHDLTCFVNLKYGVRAGGIGDELEPPDGDSEVVRIFIIDISFF 5011
|: : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :|
Db 4857 FYNKSEDEDEPMKDDMTCYLFHMVYGVVRAGGIGDEIEDPAGDYEYLYRVVFDITFF 4916
|: : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :|
Qy 5012 FFIIVILLAIQGLIIDAFAGBLRDQLESVKEDMESNCFICGINKDYFDKVPHGFDTHVQR 5071
|: : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :|
Db 4917 FFIIVILLAIQGLIIDAFAGBLRDQSQVKEDMETKCFICGIGSDYFDTPPHGFETHLE 4976
|: : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :|
Qy 5072 EHNLYNMFHMLHINKPDTBYTCQETVYVNMVYTORCWDFFPVGDCFRKQYED 5124
|: : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :|
Db 4977 EHNLYNMFHMLYLINKDETEHTQESYVWKYQERCWDFPAGDCFRKQYED 5029
|: : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :|

RESULT 5
US-09-424-783-2
; Sequence 2, Application US/09424783
; Patent No. 6780608
; GENERAL INFORMATION:
; APPLICANT: Hakamata, Yasuhiro
; APPLICANT: Nishimura, Seiichiro
; APPLICANT: Barsoumian, Edward Leon
; TITLE OF INVENTION: Human Type 3 Ryanodine Receptor Protein
; TITLE OF INVENTION: and DNA Molecules Coding Therefor
; FILE REFERENCE: 0652.2000000
; CURRENT APPLICATION NUMBER: US/09/424,783
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: PCT/EP98/02926
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: DE 197 22 317.6
; PRIOR FILING DATE: 1997-05-28
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 4866
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-424-783-2

Query Match 42.1%; Score 11295.5; DB 2; Length 4866;
Best Local Similarity 44.6%; Pred. No. 0;
Matches 2350; Conservative 908; Mismatches 1457; Indels 559; Gaps 93;

Qy 4 AEGGASQDDVSFLRTEDMVCLSCTAT-----GERVCLAAEGFGRNHCFLFNAD-KNIPP 58
|: : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :|
Db 2 AEGGEGGEDEIQFURTEDEVVLQCIATIHKEQRFCLAAEGLGRLCFLFPTSEAKYIPP 61
|: : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :|
Qy 59 DLSCQCFVIEQALSVRALQELVTAAGSETGKGT--GSGHRTLLYGNAILLRHLNMSMYLA 116
|: : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :|
Db 62 DLVCNCFVLEQSLSVRALQELMANTGENGGEAGAGGGHRTLLYGHAVLLRHSPSGMYLT 121
|: : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :|
Qy 117 CLSTSSQ- DKLATFVGLQHQSGEACWTTLHPASKQORSEGEKRVGDDILILSVATERY 175
|: : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :|
Db 122 CLTTSRSQTKLAFDVLGRHATGEACWTLTHPASQORSEGEKVRIGDDLILSVSSRY 181
|: : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :|
Qy 176 LHTTKENEVSIVNASFHVTHWSVOPGTGIGSRMKYGVGVFGDVLRFPHGDECLTIPST 235
|: : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :|
Db 182 LHLVSNGNTIQVDASFQGLTNVHPTCSGSIEB--GYLLGGHVVRLLPHGDECLTIPST 239
|: : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :|
```

```
Qy 236 WTKDGGQNIWVEGSGVMSQARSLRLELARTWKAGGFINWHPMEIRHITTTGRYLGVND 295
|: : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :|
Db 240 DQNDQSHRRIFFYBAGAGGATRAHSLRVEPLRISWSGSINRWGQAFRLRHLLTHGHYLALE 299
|: : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :|
Qy 296 QNELYLVSRREEATTASCACLRQEKDDQKQVLED---KOLEVIGAPIIKYKGDSTVIVQHS 352
|: : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :|
Db 300 DQGLLIQDRAKSDTKTAFSFRASK-ELKEKLDSSHKRDIEGMGVPEIKYKGDVSCVQHI 358
|: : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :|
Qy 353 ETGLMTLSYKSYETKKKGVGKVEEKQAILHEBEGMDGLDFSRSQEBESRTARVIRKSSL 412
|: : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :|
Db 359 ASGLAVTYKAQDAKTSRLGPLKPK-VILHQEGHMDGLTLQRCQREESQAARIIRNTAL 417
|: : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :|
Qy 413 FTKFINGLETQBNRRHSMFFASVNLGEMVMCMLEDLINYFAQDDEMEHEEKONKPRALR 472
|: : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :|
Db 418 FSQFVSG-----NNRTAAPi--TLPIEEVLQTLQDLIAYFPPEEERHEDHKNKURSLK 470
|: : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :|
Qy 473 NRQDLFOEBGILNLIIEADIKINIVTSQGFAGFLAGDESQGSQSWEMISGYLYQLLAAAIK 532
|: : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :|
Db 471 NRQNLFKEGMLALVLCIDRLNVNSVAHFAG-IAREESGMAMKEILNLLYKLLAALIR 529
|: : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :|
Qy 533 GNHTNCAQAFANSRLNMLFSRLGSQASGEGTGMLDVLHCVLIDSPBALNMRRDEHIKVII 592
|: : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :|
Db 530 GNRNNCAQF--SNNLDWLISKDLRLS--SSGILEVLHCLITESPALNLIASGHKSI 585
|: : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :|
Qy 593 SLLEKKGRRPKVLDVLCISLVGNGVAVRSNNICDYLPGKNLLIQLTALVDHVSSVRPN 652
|: : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :|
Db 586 SLLDKGRNRKVLDDILCSLCNGVAVRANQNLCDNLLPRRNLLOTLRLINDVTSIRPN 645
|: : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :|
Qy 653 IFVGRVGSADVRYKWFYEVMTMDHIEKTHMPP-HLRIGWANTTGYVPYGGGKWKQNGV 711
|: : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :|
Db 646 IFLGVAEGSAQYKWFELIIQVDFLTAEPHLAVGHASSSGYAPYFGGEGWGGNGV 705
|: : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :|
Qy 712 GDDLVSYGFDGAYLWSGGRKTPVNRTHABEPIYKGDV-----TGCALDVLTPINFM 764
|: : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :|
Db 706 GDDLVSYGFDGLHLWSG--RIPRAVASINQHLRLSDVGKLLPGPRGC-----PASHSA 757
|: : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :|
Qy 765 FNGVRVTGFTNPNLEGMPFVIVSCSKLSRFLGGEGRRLYAAPEGVSPLVESLPPQ 824
|: : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :|
Db 758 SMGSPCRGCLNFNTDGLFFVPMFSAGVKVRFMLMGRRHGFELFPSPGAPCYEALLPK 817
|: : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :|
Qy 825 QILSLPFCVFGNLSK--BALAGPPLVQDDTAFVPTPVDTLQITLTYVEIQIRDKLAENI 882
|: : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :|
Db 818 EKRLEPVEYKRDADGIRDLGTTQFLSQASIFPCPVDTSQVILPHLEKIRDLAENI 877
|: : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :|
Qy 883 HEMWAMNKIEAGWYGDQREDLHKHPCLVPFPFPAEKRYDIQLAVQTLTKTILALGYX 942
|: : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :|
Db 878 HELWGMNKIELGWTFGKIRDDNKRQHPCLVEFSLKPEKYNVLMQSTETLTKLLTLGCH 937
|: : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :|
Qy 943 ISLDKPPAR--IRNVLPNEPFMQSNQYKPAPLDLSAVTLTPKMDLVDOLAENTNLWA 1000
|: : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :|
Db 938 IAHVNPAAEEDLKKVKLPKN-YMMSGYKPAPLDLSVLLPQELIIVDKLAENHNVWA 996
|: : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :|
Qy 1001 RERIQQWYGLNEDSDMHSRPHLVVPYKVDVDAIKKANRDTASSETVRTLLVYGMIDPPT 1060
|: : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :|
Db 997 KDRIKQWYIGIQDDLKNRKNPRLVYALLDERTKKNSRDSLREAVRTFVGYNIEPSD 1056
|: : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :|
Qy 1061 GEQHEALLLEASKQKQADFRTYRAEKYAVSSGKWFYFEFELTAGPMRVGWAHADMAPGM 1120
|: : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :|
Db 1057 QELADSAVEKVSIDK--IRFPRVERSYPRVSKWYFEFEVVTGGDMRVGMARPGCRPDV 1113
|: : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :|
Qy 1121 MLQODENSNAFDGYNBEKYVSGNTSEFGKWAVGDVGVFLDLIDKTIISLNGELLMWA 1180
|: : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :|
Db 1114 ELGADDQAFVFEENRQRWHQG--SGYFGRTWQPDVGVGMINLDDASMIFTLNGELLITN 1172
|: : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :|
Qy 1181 LGGETTFADVQGN-FVPACTLGVGQKARLYGQDVNTLKYFTTCGLQEGYEPFCVNMKR 1239
|: : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :|
Db 1173 KGSALAFADVEIEENGVPICCLGLSQIGRMNLGTASTFKFYTCMGLQEGFEFPAVNMNR 1232
|: : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :|
Qy 1240 DVTHWYTKQOPIFENTDEMIDTRIDVTRIPAGSDTPCLPKISHNTEFTM-EKANWFEPLR 1298
|: : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :|
Db 1233 DVAMWFSKRLPTFVNVPK-DHPHIEVMRIDGTWDSPPCLVKTHKTFCTQNSNADMIYCL 1291
|: : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :| : : : : :|
```

QY 1299 SLPVICHNEFIDEAEKARRWEIKDROQILMKEAVEAQMPAHIDQIMRSGFTMNDIKGLH 1358  
 Db 1292 SMPVECHSSF----- 1301  
 QY 1359 YEDNOBELPSSKMKRLPSRPPRKGSMTRGVTIQYNNLPQGVNGMHRSTSEAEWAKYDL 1418  
 Db 1302 ----- 1301  
 QY 1419 GAQGLTPDDKXDKRGSRPPKFRSKRGESSDRAKSRSKTPDPFSDDTEVSPIRGARRNP 1478  
 Db 1302 ----- SHSPCLDSEA----- 1311  
 QY 1479 QIKVSQANQYNGMNAEPSRTNLYGSQVGLNMAPTQDRKQMTTSTLAQSATETVGNBIF 1538  
 Db 1312 ----- FQKRQOM-QEILSHTT----- 1327  
 QY 1539 DAECLKINEYPYGVRIIPGODPTHVYIGWTTQTHLHSDKPNQSKVTKSSVITDDYDR 1598  
 Db 1328 --QC-----YYAIRIFGQDPPSCVWVWTPDYHLYSEKFDLNMKNCTVTVLGDERGR 1378  
 QY 1599 VVENNRSCYMRADDELNYEMAEATAKASQGMFGICSDTSGSVSFTCEGKDTSEK 1658  
 Db 1379 VHESVRSNCRVWVGDDI---VASSQRNRNRNDVLEIGCLVDLWGLMUSFSANGKELGTC 1435  
 QY 1659 FMKEPETKLPFAIFVEATSKELQIELGRSATSPLSAVLPTSDKHVIPPFPRLKVQC 1718  
 Db 1436 YQVENTKVFAVFOPTSTSLFQFELGLKNAMPLSAAIIRSEBENFVPCPRLLDVQT 1495  
 QY 1719 LKPHQWARVQNSLOVHAKLSDIRGWSMLCEDAVSMLALHIPEDRCDIDILEPIEMDKL 1778  
 Db 1496 IQPWLWRMPNSFLKVFETERSERHGVVQCLEPQMMALHIPENRNCVDILECEQEDL 1555  
 QY 1779 LSPHSHLTLYAALCYQSNYRAAHALCTHVDOKLXYAIQSYNGSPQRQFYDLLIALH 1838  
 Db 1556 MRFYHTLRLYSAVCALGNSRWAYALCASHVDLSQLFYAIDNKLPLGLRSFGFYDLLISIH 1615  
 QY 1839 LESHATTMEACNVEFVILGPBLK--ALYEEPDGMGHSLSRSIQTES-VRPQMKMTDIAESI 1895  
 Db 1616 LASAKERKLMKNVEIITSTTRNICLPDESKEHGLPGVGLRCLCPGRFSTPCFV 1675  
 QY 1896 T-EISNLSPYPPELVAREFVQALAEAVETNQVNRDPVGGSNENLFLPLIKLVDRLLL 1954  
 Db 1676 TGEDHQKSPPEIPLSRLTKALSMLEAVEQCSGAHIRDVPGSVSEFQVPLVLIKTGLLV 1735  
 QY 1955 VGMWDEDEKLLIMTNPETWD-----PSFDKSGKDEHRGL 1991  
 Db 1736 MGVFDDDDVRQILLIDPSVFGESAGTEGAEBSEVTQVEKAVEAGEKAGKAPVKGL 1795  
 QY 1992 LHMKAEGAKLQMCYLLQHLNDIQLHRVEAIIAFADHFDVGLQTDQLRRYTEIKQS-DL 2050  
 Db 1796 LOTRIPESVKLQMCCELLSVLDCLOHRVEAIVAGDIYVSKLOANQKFRYNELMQALNM 1855  
 QY 2051 PSAAAKTTRPCPPREOMNAILSFKHLSEEDKNCPCGEBELIARMNEFHTLMAHVS 2110  
 Db 1856 SAALTARKTKFSPPEQINMLNF----QLGENCEPCPEIRBELYDFHEDLLHCGV 1910  
 QY 2111 HALQEPDAENQPEAKGAPFKLYNIINTVKELEBEAKAIEPPKPTPEEK-----F 2163  
 Db 1911 -----PLEEBEEBEDTSWTGKCALVYKI-----KGPPKPEKEQPTPEEERCPTTL 1957  
 QY 2164 RKVLQTIWNABEQIETPKLVREMFSLVRQYDAVGBELIRALEKTYVINAKTKLDVAE 2223  
 Db 1958 KELISQTHICWAQEOQIQDSELVRMFLNRLRQYDSIGELLOALRKYTISHTSVSDIIN 2017  
 QY 2224 MWVGLSQIRALLPVQMSQEEELMRKRLWKLNNHTFFQHPDLIRLVRHENVMVMMNT 2283  
 Db 2018 LLAALQIRISLLSVRMGKEELLMINGLDIMNNKVYQHPNLMRVGLMHETVMEVMNV 2077  
 QY 2284 LGRAQAQSDAQSPSQPAEDSEKDDTSHVMVACCRFLCYFCRTGRQONKAMPDFDL 2343  
 Db 2078 LG-----TEKSQIAPPKMVASCCREFLCYFCRISRQNKAMFHLISYL 2119  
 QY 2344 LENSNIILLRSPRGSTPLDVAISSIMMENTELALALREHYLEKIAVYLSRCGLQNSSELV 2403

Db 2120 LENS SVGLASPSMRGSTPLDVAASSVMDNDELALSLEEDPKVVTYLAGCGLQSCPMLL 2179  
 QY 2404 EKGYPDLGMDPVEGERYLDLFCVWVNGSVENANLIRLLIRRRPECLGPAURGE-GE 2462  
 Db 2180 AKGYPDVGMPPIEGERYLSLRFVAVFVNSSEVENASVVVKLLIRRRPECFGPAURGEGN 2239  
 QY 2463 GLKAIIVDANKMSER----IADRRKLRMEQEGGVNFSHPLPESDEDEDYIDTGAALNF 2518  
 Db 2240 GLLAAMQGAIKISENPALDLP SQGYKEVSTEDD-----EIEEEI VHMGNAIMSF 2289  
 QY 2519 YCTVLIDLLGRCAPDAGVIALGKNESLRARAILRSLVPLEDLOGVLRSFRTLNPAAGEER 2578  
 Db 2290 YSALIDLLGRCAPEMHIIQTKGEAIRSIRSLVPTEDLVGIIISIPKL--PSLNKDG 2347  
 QY 2579 PKS--DMPSGLI PGHKQSVGLFLERVYGIETQELFYKLEBAFLPDLRAAATMLDRNDGCE 2636  
 Db 2348 SVSEPDWAGNFCPDHKA PMVFLDRVYGIKQDTLLHLLEVGFLPDLRAASLDTVSLST 2407  
 QY 2637 SDMAISNRNYIGNSILPLLIKHAIFYNEAENYASLLDATLHTVYRLSKNRMLTQGBEAV 2696  
 Db 2408 TEAALANRYICS AVPLPITFCAPLFGGTEHCTSLIDSTLTQTVRLSKGRSLTKAQRDTI 2467  
 QY 2697 SDFVALVTSAMQPSMLLKLRLKLTVDVSKLSEYTTVALRLTLHYERCAKYGSTGACQG 2756  
 Db 2468 BECLLAI CNHLRPSMLOQLRLRLVDFVQPNLEYCKMPLKLLTNHYBOCKY-CLPSCWG 2526  
 QY 2757 AFGASSBEKRLTMMFLSNIPDSLSKMDYBELPGKALPCIIAIGCALPPDYSLSKNYDD 2816  
 Db 2527 SYGLAVSEELHTEKLPWGIIDLSHKKYDDLPFPMALPCLSAIAGALPPDY-----JDS 2581  
 QY 2817 EFGY--KEQAAGDLDNPDYDPOPINTSSVALNNDLNTIVQKFSHYHDAMASRKIENGW 2874  
 Db 2582 RITATLEKQISVDAGD-NFDPKPI NTWNFSLPEKLEYIVTKYAEHSHDKMACDSQSCKW 2640  
 QY 2875 YGEGMSDQKTHPRLPKYNMLNDYKERYKEPVRESIKALLAIGNSVEHSE-----VDIP 2929  
 Db 2641 YGISLDENVKTHPLIRPFKLTLEKEKITYRPAESLKTMLAVGTVERTKEGALVQOR 2700  
 QY 2930 SNNRSMRQSKSGRPPEIVTDSATFPDYNPHVDNTNLTLSEMONMARLADNAHDI 2989  
 Db 2701 ENELKRSVSQANQN-----SYSPAPDLJNSNVLSRELQMGVEVAENYINI 2747  
 QY 2990 WAKKKEBELVTNGGIIHPQLVPYDLLTKEKKKDRERSQEFKYLQYQGYKLRHPSKAPQ 3049  
 Db 2748 WAKKKLELESKGGSHPLVPYDITLTAKEKFKDREKAQDLFKFLQVNGIIVSRGMKOME 2807  
 QY 3050 SDTSQTTGTVAELRFPAYSLEKLIQYIDRATINMKLKPSTTFSRRSSFT--STRD-- 3105  
 Db 2808 LDAS-----SMEKRFYGFYKILKYVDSQAQEFIAHLEAIV-----SSGKTEKSPDOE 2856  
 QY 3106 IKFESKAVLPMEKYFSTHRNYFI-AVATATNNVGAASLKEKEMVAALFKCLASLLSRSL 3164  
 Db 2857 IKFPAKVLPLVDQYFTSHCHYIFLSSPUKPUSSGSGYASHKEKEMVAGFCUKLAALVRURI 2916  
 QY 3165 AAFGPDVRITVRCLQVLVKGIDAKSLVKNCEPFI RTSMLTFNNVADDVGHITMNLQDGK 3224  
 Db 2917 SLFSDSTTWVSLCHILAAQTLDTRTVMKSGSELVKAGLRAFFENAAEDLEKTSENLKGK 2976  
 QY 3225 YAHLRGTHLK-TSTSLGVINGVLLPILTAKEPDHLANCEYGADLLDEIQVASYKMLGSLY 3283  
 Db 2977 FTSHR-TQIKGVSNINYTTVALLPILTSIPEHVTQHOGMDLLLDGVQISCYHTLCSLY 3035  
 QY 3284 ALGTDASLTHDRKYLKTEIERHKBALGCLGAFSSTFPVAFLEPHLNKNHOFSLNRIAD 3343  
 Db 3036 SLGTGKNI-----YVERQORFALGECGLASLAAAIPVAFLEPTLNRYNPLSVNTKTP 3086  
 QY 3344 HS---LEAQDQIMQKMEQCMPTLETILGEVDQFVESDKTYNEAPHIIDVVLPLLCSLYLPFW 3400  
 Db 3087 RERSILGMPDVEDKCPDIPOLEGKLMKEINDLASGARYTEMHPHIEVILPMLCNLYSYW 3146  
 QY 3401 WAQGPDNVTPGNGHVTMTVAHNMQLKNVLUKIKKIGNENAPMWTRIATYTOQIIIN 3460







Db 27 ISTLGL---VDRCVVQPEAGDLNPPKFRDCLF-----KLCPMNRYS----- 68  
Qy 1807 HVDQKQLLYAIQSYMSGFLRQGYD--LLIALHLESHATTMEACKNE-----FVIP 1856  
Db 69 ---QKQFWKAK-----PGANSTTDAVLLNKLH--HAADLEKKQNETENRKLGTVIQ 116  
Qy 1857 LG-----PELKALYEBPDMGHSLRSLOTES-----VRPQWMTDIABSI 1895  
Db 117 YGNVIQLHLKSNKYLTNKRLLPALLEKNAMRVTLDEAGNEGSWFYIQPFYKLRISIGDSV 176  
Qy 1896 TEISNLYSPYPLEVAREFVQALAEAVETNOVNRDPVGGSNENLFLPLIKLIDRLILLV 1955  
Db 177 -----VIGDKVVLNPNVAGQPLHASSH-----OLVDN---P 204  
Qy 1956 GMMRDEDEVE---KLLIMTNPEITWDPSPDKGKDEHRKG--LLHMMAEAGAKLQMCYLL 2008  
Db 205 GCNEVNSVNCNTSWKIVLFMK---W-----SNKDDILKGDVVRLFAEAEQEKFTCD-- 254  
Qy 2009 QHLNDIQLRHRVEAIIAFAHDFVGLQDQLRRYTEIKOSDLPSSAFAAKTREFRCPPRE 2068  
Db 255 -----EHRKK-----QHVF-----RTTGRQS-ATSATSSKALWEVEVQHD 290  
Qy 2069 -----QNNAILSPKHLEEDKENCPCGEBELIARNEFHDTLMAHVSJHALQEPDAAEN 2121  
Db 291 PCRGGAGYWNLSLFRFKHL-----ATGHYLAESV-----DPD----- 321  
Qy 2122 QPEPAKPGAFGLYNIINTVKELEBEAKAIEBPCKTPEE-----KFRKVLLOTIVN 2173  
Db 322 -----FEEE---CLEFQPSVDPDQDASRSLRNAQEKWYSLVS 357  
Qy 2174 WAEESQIET-----PKLVREMFSLIVRODAGELIRALEKTYVINAKTKLDVAB----- 2223  
Db 358 VEGNDISSIFELDPPTLRGGDSLVR--NSVYRLHLCTNTWVHSTNIPDKBEEKPVM 415  
Qy 2224 MWVGLSQR-----ALLPVQMSQEBE-----ELMRKRLWK 2253  
Db 416 LKIGTSPLKEDKEAFAIVPSPAERVRLDLDANDASKVLGSIAGKLEKGTITQNERRSVTK 475  
Qy 2254 LVNNHTF-----QHPDLIRV-----LVHENVMAMVMTLGRRAQASDAQP 2296  
Db 476 LLEDLVYFVTGNSQGVLEVVFSKPNREROKLMBEQNILKQIFKLQAPPTDCGDG-- 533  
Qy 2297 SSQVAEDSKEDTSHEMVAVACRFLCYFC-----RTGRQONAKMDFHDFLENSNILL 2351  
Db 534 ---PMLREELQORHAPRHICR-LCYVRLRHSQODYRKNQEIYAKQGFQMK----- 583  
Qy 2352 SRPSLRGSTPLDVAYSSLMENTELALAREHYLEKIAVYLSRCGLOSSELVEKGYDILG 2411  
Db 584 -----QIGYDVLAEDTITAL-----LHNNRKLLEKHITAAE 614  
Qy 2412 WDPV-----EGERYLDPLR-FCVWNGESV-----EENANLVI--RLILR 2448  
Db 615 IDTFVSLVRKNRPRFLDYLSCVSMN-KSPIVTQELICKAVLNPNTNADILIEITKLVL 673  
Qy 2449 RPECLGPALRGEGELLLKAIVDANKM-----SERIADRKLREMEQEGDVNFSPHLPES 2502  
Db 674 REPEFGVS---TGENALEGEDEBEVWLFWRDSNKEIRSXSVELAQDAKEG-----Q 723  
Qy 2503 DEDEDYIDTGAAILNFCYTL-----VDLLGRCAPDAGVIALGNESLR 2545  
Db 724 KEDRDILSYRYQLNLFARMCCLDRQYLAINEISGQLDVLILRCMSDENL-----PYDLR 778  
Qy 2546 A---RAILSLVPLEDQVLSLRLFTLNNPAAGEPRKSDMPGSLIPGHKQSVGLFLERV 2602  
Db 779 ASFCRLMLMHVDRDPQEQVTPVKA-----RLMSEIFEISAIIDDYDSSGTSKD-- 827  
Qy 2603 YGIELOELFKLLE--EAPLPDLRAATMLDRDGCESDMALSMNRYIGNSILPLLIKAY 2660  
Db 828 ----EIKERFAQTMFEVEEYLRDV-VQORPFDSDKEKNKLTFFVNNLARNLI-----YFG 877  
Qy 2661 FYNEAENYASLILDAT-----LHTVYLSKNRMLTKQGEAVSDFLVALTSAMQP 2709  
Db 878 FY---NFSDLLRLTKILLAILDCVHTVITFIPISK---MTKGEENKNGSNWMSIHGVE- 929

Qy 2710 SMLKLJLRKLTVDVSKLSEYTTVALRLLTLHYERCACKYGSTGAGQG-AFGASSDEEKRL 2768  
Db 930 -----LMTQVVLRGGGFLPMTMA-----AAPEGNVKQAEPEKEDIM 966  
Qy 2769 TMLFNSNIFSL-----KMDYEPFELFGKALPCLIIAIGCALPPDYSLSKNYDDDEFYKGEQ 2823  
Db 967 VMDTKJIIIEILOFILNVRLOYR-----ISCULCI-----FKREFEDES----- 1004  
Qy 2824 AAGDLNPQVDPQPIINTSSVALNNDLNTIVQKFSHYHDAMASRKIENGWYVGEWSQSD 2883  
Db 1005 -----NSQSESTSS-----GNS 1017  
Qy 2884 KTHPLRKYPMNLNDYKERYKEPVRESLKALLAIGWSEHSEVDIPSNRSMRQSKSG 2943  
Db 1018 QEGSPNVGAL--DFEH-----IEEQABGI--FGGSEENTPLDLDDH-----G 1056  
Qy 2944 GRPPEIVTDSATPDYDNPHPVDWNTNLTLSRBMQNAERLADNAHDIWAKKKKEELVTNGG 3003  
Db 1057 CRTFLRLLHLTHMDYPP-----LVSGALQLLFRHSQORQEVLOQAFKQVOLLVTS-- 1106  
Qy 3004 GIHPQLVPYDLTDTKEKKKORERSQEFKLYIQGYKLRHPSK-----APOSDEOTTTG 3058  
Db 1107 -----QVDNRYKQIKQDLQURSIVKSELWYKQGPDEPMDGASGENEHKKTREG 1158  
Qy 3059 VAIELRFAYSLLKLIQVIDRATINMKLLKPESTTFSRRSSPKTSTRODIKFESKAVLPLME 3118  
Db 1159 TS-----KPLXHEST---SSY----- 1171  
Qy 3119 KYFSTHRYFATAVATANNVGAASLKEKEMVAALFCKLASLLRSLAALFAGPDVITVRCL 3178  
Db 1172 -----NYRV-----KEIL-----IRLSKLCV 1188  
Qy 3179 QVLYKGIDAKSLKVNKPEFIRTSMLTFPNNVADDVGHITMNLQDGKYAHLRGTLTKSTS 3238  
Db 1189 Q-----ESASVRKS-----RKQOORLLRN-----GAH----- 1211  
Qy 3239 LGYINGVLLPILTAKFHLANCEYGADLLLDIEIQVASYKMLGSLYALGTDSLTHDRKYL 3298  
Db 1212 -----AVVLELLOIPY-----EKAEDTKMQEIMRLAHEFLQNF----- 1244  
Qy 3299 KTEIRHKPALGCLGAPSSTFPVAFLEPHLKNQNSLLNRIADHSLEAQDIMQKMQC 3358  
Db 1245 -----CAGNQONO---ALLKHINLFLKPGILEAVTMOHI---FMNMFQUC 1284  
Qy 3359 MPTLETILGEVDQFVESDKTYNEAPHIIDVVLPLLCVLPFWAQQPDNVPTGNGHYTM 3418  
Db 1285 SEINERV---VOHFV-----HCIE-----THGRNVQY 1308  
Qy 3419 VTAHMMNOLLKNVLKLIKKNIGENAPMMTRIATYTOQIIINSSEELL-----RDSFLPL 3473  
Db 1309 I--KFLQTIKVAEGKFIK-----QDMVMAELVNSGEDVLVFNDRASFOTL 1354  
Qy 3474 AERVKRTDNM-----PHKESLRGFTKSTDDTSQVESQIOEDWQLLVRDIYFY 3524  
Db 1355 IQMRSERDRMDENSPLMYHILVELL-----AVCTEKNYVTEIKNSLLPLDDIVRV 1409  
Qy 3525 -----PLLIKYYVDLQBNHMLRNVPABEEL--NHVABEIPNIWKSQYFLKBEQNFIS 3575  
Db 1410 THEDCIPEVKIAYINF-LNHCVYDTEVEMKEIYTSNMMWKLFL-----ENFL- 1454  
Qy 3576 ANEIDNNMVLIMPTATRRVTAVTGTPQGGKKKKKRRDKRDK-DKEYQASLMV----- 3628  
Db 1455 ---VD-----ICRACNNTSD-----RGHADSILEKYVTEIVMSIVTTFSP 1493  
Qy 3629 -----ACLKRLPLVGLNLFAGREQLVOHKDRFLKXMSQDV-----BEFAKTO-LT 3675  
Db 1494 FSDQSTTLQTRQPFVQLQGVFR--VYHC--NMLMPSQKASVESCIKRVLSDAKSAIRA 1549  
Qy 3676 LPDKID-----PADENSWOYLYSLKGSKSNIT-----VETAENKA 3713  
Db 1550 IPVDLDSQVNNLFLKSHNIVOKTALNWR--LSARNAARRDSVLAAASRDYRNIIERLQDIV 1607

QY 3714 KIIDTVIRIV-AMSKVLFGHLMIDHPQOMSKNIVRSVVSQIKRAVIACPRQTSLSLSP 3772  
DB 1608 SALEDRLPLVOAELSVL--VDVLRHPPELL-----FPENTDARRK-----CESGGFICKLI 1656  
QY 3773 RH-----RACNIPARTYYELWLBEENIGOVEMIEDLTQSFEDAELKKSQWVE--- 3819  
DB 1657 KHTQKLEENEKUCIKVQLTLEBMTWKDORGGEKQISID--ESENALPQAPAEANST 1713  
QY 3820 --EGEKPDLTQLVTTFCRGAMTFRSGALQBDPLMYSAHIIAKSCGEEEB----- 3868  
DB 1714 EOELEPSPLQLEB-----HKRGEALRQILVNRVYGNI--RPSGRRESLTSGNGPL 1764  
QY 3869 EGGEEBEGGEAEAEDEGRASIEHQEMEKQKLLFHQARLADRGVAEWL--LHISASKGL 3927  
DB 1765 SPGGPSKPGGG--GGGPGSSSTGRGEMSLAEV--OCHLDKEGASNLVIDLIMNASS-- 1816  
QY 3928 PSEWMKTLQGISLRGNIDIQMGLNHL--KQKQDVGF----- 3967  
DB 1817 -DRVFHESILLALLEGNTTIOHSFPCRLTEDEKKEFKFYFDRMKVAQOEIKATVT 1875  
QY 3968 --TSIAGLMNSCSVLDDAFERNKAEGL----- 3994  
DB 1876 VNTSDGNKKKDDVDRDAPSKKAKEPTQITEEVRDQLLEAGAAATKATFTTERRADP 1935  
QY 3995 -----GVGLEGAAGEKNMHDABETCA-----LFRFQLTCEGHNDWQNYLRTQAGNT 4042  
DB 1936 DDHYQSGEGTO-ATTDKAKDDELSAVITIMQPIRLFLQLLCEHNRDLQNLFCQ--NNK 1993  
QY 4043 TTVANVICVDYLLRLQES-----IMDFVHYSSKELIDPAGKANFKAIGVASQVNT 4096  
DB 1994 TYNLNVCTLOFLDCICSGTTGGGLGLLYNE-----KNVALINQTL 2038  
QY 4097 LTEVIQSGPCTQQAALAHSLRDWAVGGFLFLFSHMQDKLSKHQSQVLLKELLNLQKMI 4156  
DB 2039 LTEYCGGCHENQNCIA-----THESNGIDIITAL--ILNDIN 2074  
QY 4157 PMMLSMLEGNVNGTIGQMVDTLIVESASNVLELILKYFDMFLKLDLTSSASFQEIANN 4216  
DB 2075 P-----LGKRMDDLVLKKNNAKLL-----LAIMESRHDSENAERIILYN- 2114  
QY 4217 DGWVLPKDFKEKMEQOOSTYPEETEFLLACETNHDGKLDYIGFCDFRHEPAKEIGFNL 4276  
DB 2115 --MRPKELVEVI--KRAYMOGEVEF-----EDGENGE-----DGAASP-RNVGHIY 2156  
QY 4277 VLLTNLSHMPNEPLARFLTAGSV-----LNYFEPFLGRIEIMGSKRIERYVFEIKE 4331  
DB 2157 ILAHLARH--NKELOTMLKPGQVGDGDEALEFVAKHTAQIEIVRLDRMTMEQIVFPV-- 2211  
QY 4332 SNIQEWKPOI-----KESKAPFYSIVTEGGDK-EKLEAFVNFCEDAIPEMTHASGLMA 4385  
DB 2212 -----PSICEFLTKEKSLRIYVT--TERDEQSGKINDFFLRSEDLFNEMNWQKKLRA 2261  
QY 4386 ASESVGCTKNREASYMYMGDDDDERACKDPFRRLGSLQKGVATAPFSSLSPSNIKAKIA 4445  
DB 2262 -----QPVLWCARNMSFW--SSISFNLA 2283  
QY 4446 DMQOMPAPALAVGPFKMFYLYLGYGLVYVRYIFGVLLGLMRGPQTDPEPPPEPTEE 4505  
DB 2284 VLMNLLVA-----FFYPFKVGRTGL----- 2304  
QY 4506 KIGQLRHLLATQSRHLPALPPADDTGQMVSAGFLDITKEDNGQIQVKPHESPSSTP 4555  
DB 2305 -----EPHWS----- 2309  
QY 4566 SSGEEAEVSPDESADHTEQRPSSLIDLLGGEQAKQOERMEAAQAQAAMSAIEAESK 4625  
DB 2310 ----- 2309  
QY 4626 KAVQGPAPALSQVDLSQYTRAVSFVLARNFYNLKYVALVAFINCVLLFYKYSTLDGE 4685  
DB 2310 -----GLLWTAMLJSLAIVIAL----- 2326  
QY 4686 GGEBSGLGDIITAGGSGSAGSGSGSGEDGDDDALEVHDEDFYMEHVIKMAVIL 4745

DB 2327 -PPHGIRALIA-----STIL 2341  
QY 4746 HSTVSLAI-----LIGYHLKVPLAIFKREKEIARKLEPDLGXYAEOPEDDDLKSHWDKL 4800  
DB 2342 RLIFSGLQPTFLGAFN-----VCNKIIF----- 2367  
QY 4801 VISAKSFPVNYWDKFVKKKVRAKYSYTDYFDSISNMLGMEKTSFSAQEESGSKLIHYII 4860  
DB 2368 -----LMSFVG 2373  
QY 4861 NIDWRYQVMKAGVTTITDNSFLYSILWYFSFVSGNF--NNFFFAAHLLDVAVGFKTLRLILQ 4919  
DB 2374 NCGTFRGRYA--WVLDFEFLYHLLYLICAMGLFVHEFFYSLLLPDLVYREETLLNVIK 2431  
QY 4920 SVTHNGQLVLTVMLLTIIVYIVIAFNFRKPYV----- 4955  
DB 2432 SVTRNGRSIILTAVLAILVYLSIVGYLFFKDDFILLEVDRLPNETAVPETGSLANDFL 2491  
QY 4956 -----QEEDEVNRNCHDMLTCTFVNLYKGVRAAGGGIGDE 4990  
DB 2492 YSDVCRVETGENTCTSPAPKEELLPAEBETEODKEHTCETLLMCIVTVLSHGLRSGGVGDV 2551  
QY 4991 LEPPDGDDS--EVYRIIFDISFFFIIVILAILQGLIIDAFGEIRDQLESVXEDMESNCF 5049  
DB 2552 LRPSKEEPLFAARVIYDLLFFFWVIIIVLNLIFGVIIIDTFADLRSEKQKKEILKTTCF 2611  
QY 5050 ICGINKDYFDKVPHPGDFTHVQREHNLANYNFMLHMLINKPDTYTGQETVVMNYTORCW 5109  
DB 2612 ICLERDKFDNKTVTPEEHIKEBNMWHYLCFVLVKVDSTYTGESYVAEMIRERNL 2671  
QY 5110 DFF 5112  
DB 2672 DWF 2674

RESULT 7  
PCT-US96-01735-1  
; Sequence 1, Application PC/TUS9601735  
; GENERAL INFORMATION:  
; APPLICANT: Marks, Andrew R.  
; TITLE OF INVENTION: HUMAN T CELL INOSITOL 1,4,5,-TRISPHOSPHATE  
; NUMBER OF SEQUENCES: 8  
; TITLE OF INVENTION: RECEPTOR  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Brumbaugh, Graves, Donohue & Raymond  
; STREET: 30 Rockefeller Plaza  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10112-0228  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US96/01735  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/386,039  
; FILING DATE: 09-FEB-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kole, Lisa B  
; REGISTRATION NUMBER: 35,225  
; REFERENCE/DOCKET NUMBER: A30042 - 165/30555  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-408-2628  
; TELEFAX: 212-765-2519  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:



Db 1357 IQMRSRDRMDNSPLMYHILVELL-----AVCTEKNVYTEIKNSLLPLDDIVRVV 1411  
Qy 3525 -----PLLIKYYDLQNRHWRNNVPAEBLY--NHVAEIFNTWSKSQVFLKEEQNFIS 3575  
Db 1412 THEDCIPEVKIAYINF-LNHCVYDTEVEMKEIYTSNH-----NWKLVENFLVD----- 1458  
Qy 3576 ANEIDNMVIMPTATRRVAVTDGTPQGGGKKKKHKKDK-DKEVQASLMV----- 3628  
Db 1459 -----ICRACNNTSD-----RKHADSILEKYVTBIVMSIVTTFPSSP 1495  
Qy 3629 -----ACLKRLPLVGLNLFAGREQLYQHCKDRFLKMMSEODV-----AEFAKTO-LT 3675  
Db 1496 FSDOSTTLOTROPVQLQVFR--VYHC--NWLMPQSQKASVESCIRVLSDVAKSRAIA 1551  
Qy 3676 LPDKIDPADENSWOHYYLSKLGSKSNITVETAENKAKIIDDTVER--IVAMSKVLFLG 3733  
Db 1552 IPVLDL-----SOVNNLFLK-----SHSIVQKTAMNWLRSARNAARRDSVLAASR----- 1596  
Qy 3734 HMIDHPQMSKNVYRSVVSIOKRAVIACFR-----QTSLSHL--PRHR----- 3775  
Db 1597 -----DYRNI--IERLQDIVSALEDRPLVQAELSVLDVLRPELPPENT 1642  
Qy 3776 -----ACNIFARTYVELMBENIGOEVMIEDLTQSPEDAELEKSDVVVEGE-- 3822  
Db 1643 DARRKCSGGFICKLIKHTKQ-----LLEEN--SEKLCIKVLOTLEMTKRGYGEKEAL 1697  
Qy 3823 -----KPDPLTQLVTPFCRGAMTERSALQEDPLMYSYAHIAKSCGEBEEB 3870  
Db 1698 RQVLVNRYYGNVPSGRRESLTSFGNG-----PL-----SAGGPKGPG 1735  
Qy 3871 GGBEEBGGGAEBDEGRASIHBOEMEKQKLLFHOARLARGVAMV-----LLHISASKGL 3927  
Db 1736 GG-----GGG-----SGSSMSRGEMLAEV--QCHLDKEGASNLVIDLIMNVSSDR-- 1780  
Qy 3928 PSEVMKTLQILGAGGNIDIQWMLNHL-KDKQDVGP----- 3967  
Db 1781 ---VFHESILAIALLGGNTTIOHSPFCRLTEKKEKFKVYDRMKVAQOEIKATVT 1837  
Qy 3968 --TSIAGLMSCSVLDLDAFERNTKAEG----- 3994  
Db 1838 VNTSLGNKKKDDVEDRDPSPKKAKEPTTQITEVRDQLLEASAATKAPTTPREADP 1897  
Qy 3995 -----GVGLEGAAGEKMHDAETCA-----LFRFIQLTCEHNLWDQNYLRTQAGNT 4042  
Db 1898 DDHYQPGEGTO-ATADKAKDLEMSAVITIMQPIRLFLQLLCEHNRDLQNLFCQ--NNK 1955  
Qy 4043 TTVNVVICTVDYLLRLOES-----IMDFYWHYSSKELIDPAGKANFFKAIGVASQVNT 4096  
Db 1956 TYNVLVCTQLQDCIGSTTGGGLGLLYNE-----KVALINQTL 2000  
Qy 4097 LTEVIQPGCTONQQAHLRLMDAVGGFLFLFSHMQDKLSKHQSQVDLLKELNLQKMI 4156  
Db 2001 LTEYCQGPCHENQNCIA-----THESNGIDIITAI--ILNDIN 2036  
Qy 4157 PMMLSMLEGNVNGTIGKQWQDVLVBASVVELILKYFDMFLKLDLTSSASFOEIDANN 4216  
Db 2037 P-----LGKRRMDLVLEKLNASKLL-----LAIMESRHDSENAERILYN- 2076  
Qy 4217 DGWVLPKDFKEMKQKSYTPEETIEFLLACETNHDGKLDYIGFCDFRHPKAEIGNLA 4276  
Db 2077 ---MRPKELVEVI--KKAIMOGEVEF-----EDGE--DGAASP-RVNGHNY 2118  
Qy 4277 VLLTNLSHEMPNEPRLARFLTAGSV-----LNYFEPFLGRIEIMGSKRIERYFFBIKE 4331  
Db 2119 ILAHLARH---NKELOSLKPGQVGDGEALEFYAKHTAQIEIVLDRMTQEVFPV-- 2173  
Qy 4332 SNIEQWKPQI-----KESKAFYYSIVTEGDKLEAFVNFCEDAIFENTHASGLMAA 4386  
Db 2174 -----PSICEFLTKEKSLRIYTT----- 2191  
Qy 4387 SEESVGTKNEASWYMGDDDRAGKDPFRGRGLQSKDGVATAFSSLSPSNIKAKIAD 4446  
Db 2192 -----TERDSQG-----SKIND 2203

Qy 4447 MQOMPAPLAVGFFKFFFYLYYLVGVVVVRYIFGVLLGLMRGPOTDEPPPEPTEEEK 4506  
Db 2204 -----FF----- 2205  
Qy 4507 IGO LRHRLLATQSSRHLPALPPADDTGOMQVSAFGLDITKEDNGQIQVKHPESPSTSPS 4566  
Db 2206 ---LRSE-----DLFNMENW----- 2217  
Qy 4567 SGEEAEVSPDESADHTEQRPSPSLDILGGEQAKQERMEQAQAQAQAAMSAIEABSKK 4626  
Db 2218 -----OKKLRAQP----- 2225  
Qy 4627 AVOGPAPSALSQVDLSQYTRAVSFLARNPNLYVALVLAFCINFVLLF-YKVSTLDGE 4685  
Db 2226 -----VLYWCARNMSFWSSISFNLAVLMLNLLVAFVLPUGVRGG 2264  
Qy 4686 GGGSGGLDIIAGGSGGAGSGSGSGSGSGEDDDALEVVHIDEFFYMEHVHVKMAAVL 4745  
Db 2265 TLEPHWSGLLWTG----- 2277  
Qy 4746 HSTVSLAILIGYYHLKVPLAIFKREKEIAFKLEFDGLYIAEQPEDDDDLKSHWDKLVTSK 4805  
Db 2278 -MLISLGIVIG--LPNPHGI-----RAL-----IGSTILRLIFSVG 2310  
Qy 4806 SPVNTWDFKVKKKVRAKYSETYDFDSISNMLG-----MEKTSFSAQEEESKGLIHYIN 4861  
Db 2311 SQPALF-----LLGAFNVCKNIIF-----LMSFVGN 2336  
Qy 4862 IDWRYQVMKAGVITITNSFLYSLWFSFSGVGNF--NNFFFAAHLDDVAVGFKTLRTILQS 4920  
Db 2337 CGTFTGGRAMVLVDVEFLYHLLYLVICANGLFVHVFFYSLLLLLDLVYREESLLNVKS 2396  
Qy 4921 VTNGKQLVLTVMLLTIIVYTVIAFNPRKPYV----- 4955  
Db 2397 VTRNGRSIILTAVLALILVYLSIVGLVFPKDDFILEVDRPLPNETAVPETGESLSEFLF 2456  
Qy 4956 -----QEDDEVNRNCHDMLTCTFVFNLYKGVKAGGIGDEL 4991  
Db 2457 SDYCRVESGENCSPAPRELVPAEBTEQDKETCTLLMCIVTVLSHLSRSGGVDVL 2516  
Qy 4992 EPPDGDS--EVYRIIFDISPFFIIVILLAILQGLIIDAFLERDQLESVKEDMESNCFI 5050  
Db 2517 RKESKEPLPAARVVDLFFFWIIVLNLIFGVILDTADLRSEKQKKEILKTTCFI 2576  
Qy 5051 CGINKDYDFKVPFGFTHVQREHNLANYMFLMHLINKPDTYTGQBYTYVMNYTORCWD 5110  
Db 2577 CGLERDKFNDKTVTFEEHKEEHNMMWHLVLCFVILVKVKDSTYTGPSYVAEMIKERNLD 2636  
Qy 5111 FFP 5113  
Db 2637 WFP 2639

## RESULT 8

US-08-114-555A-8  
; Sequence 8, Application US/08114555A  
; Patent No. 5854392  
; GENERAL INFORMATION:  
; APPLICANT: Manly, Susan P.  
; APPLICANT: Kozlowski, Michael R.  
; APPLICANT: Neve, Rachael L.  
; TITLE OF INVENTION: CLONING AND EXPRESSION OF beta-APP-C100  
; TITLE OF INVENTION: RECEPTOR (C100-R)  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PENNIE & EDMONDS  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:

```
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/114,555A
; FILING DATE: 30-AUG-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 6013-115
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 240 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-114-555A-8

Query Match 1.3%; Score 336.5; DB 1; Length 240;
Best Local Similarity 34.7%; Pred. No. 2e-18;
Matches 82; Conservative 37; Mismatches 70; Indels 47; Gaps 4;

Qy 1879 TESVRPQMKMTD-----IAESITEISNLYSPYFPLEVAEFVYMQALAEAVETNQVNR 1931
Db 5 TTSLRPPHFPSPCFVAAALPAAGVAEAPARLSPAIPLEALRDKALRMGLGEAVRDGGQAR 64

Qy 1932 DPVGSNENLFLPLIKLVDRLLVGMMDDEVEKLLIMTNPETW-----DPSFDK 1981
Db 65 DPVGSVFQFVPLKLVSTLLVGMIFGDEVDVKILKMIPEVFTTEEEEEEEEEEE 124

Qy 1982 EGKDEHRK-----GLLHKMAEAGAKLQMCVYLLOHNL 2012
Db 125 EEEDEEKEDEEEKEDEAEKEEAEPEGEKEDLEEGLLQMKLPESVKLQMCNLLLEYFC 184

Qy 2013 DIQLHRVETAIIFAHDFVGLQDTDLRRYTEIKQS-DLPSAVAAKTREFRCPPR 2067
Db 185 DQELQHRVESLAFAERYVDKLOANQSRVALLMRAFTMSAAETARRTRFRSPQ 240

RESULT 9
US-08-559-397A-14
; Sequence 14, Application US/08559397A
; Patent No. 6083713
; GENERAL INFORMATION:
; APPLICANT: Manly, Susan P.
; APPLICANT: Kozlowski, Michael R.
; APPLICANT: Neve, Rachael L.
; TITLE OF INVENTION: CLONING AND EXPRESSION OF
; TITLE OF INVENTION: BETA APP-C100 RECEPTOR (C100-R)
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/559,397A
; FILING DATE: 15-NOV-1995
; CLASSIFICATION: 435

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/114,555A
; FILING DATE: 30-AUG-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 6013-115
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 240 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-559-397A-14

Query Match 1.3%; Score 336.5; DB 2; Length 240;
Best Local Similarity 34.7%; Pred. No. 2e-18;
Matches 82; Conservative 37; Mismatches 70; Indels 47; Gaps 4;

Qy 1879 TESVRPQMKMTD-----IAESITEISNLYSPYFPLEVAEFVYMQALAEAVETNQVNR 1931
Db 5 TTSLRPPHFPSPCFVAAALPAAGVAEAPARLSPAIPLEALRDKALRMGLGEAVRDGGQAR 64

Qy 1932 DPVGSNENLFLPLIKLVDRLLVGMMDDEVEKLLIMTNPETW-----DPSFDK 1981
Db 65 DPVGSVFQFVPLKLVSTLLVGMIFGDEVDVKILKMIPEVFTTEEEEEEEEEEE 124

Qy 1982 EGKDEHRK-----GLLHKMAEAGAKLQMCVYLLOHNL 2012
Db 125 EEEDEEKEDEEEKEDEAEKEEAEPEGEKEDLEEGLLQMKLPESVKLQMCNLLLEYFC 184

Qy 2013 DIQLHRVETAIIFAHDFVGLQDTDLRRYTEIKQS-DLPSAVAAKTREFRCPPR 2067
Db 185 DQELQHRVESLAFAERYVDKLOANQSRVALLMRAFTMSAAETARRTRFRSPQ 240

RESULT 10
US-08-114-555A-6
; Sequence 6, Application US/08114555A
; Patent No. 5954392
; GENERAL INFORMATION:
; APPLICANT: Manly, Susan P.
; APPLICANT: Kozlowski, Michael R.
; APPLICANT: Neve, Rachael L.
; TITLE OF INVENTION: CLONING AND EXPRESSION OF beta-APP-C100
; TITLE OF INVENTION: RECEPTOR (C100-R)
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/114,555A
; FILING DATE: 30-AUG-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 6013-115
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; TELEX: 66141 PENNIE
```

INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 240 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
US-08-114-555A-6

Query Match 1.2%; Score 334.5; DB 1; Length 240;  
Best Local Similarity 35.6%; Pred. No. 3e-18;  
Matches 84; Conservative 32; Mismatches 73; Indels 47; Gaps 4;  
Qy 1879 TESVRPQKMTD-----IAESTITEISNLSYFPFLEVARFVQALAEAVETNQVNR 1931  
Db 5 TTSLRPHHSPPCFVAALPAAGAAEAPARLSPAIPLALRDALKALMLGEAVRDGGQAR 64  
Qy 1932 DPVGSNENLFLPLIKLVDRLLVGMMDDEVEKLLIMTNPETW-----DPSFDKEGK 1984  
Db 65 DPVGSVEFQVPVKLVSTLLVMGIFGDEVDVKQILKMIPEVFTTEBEDEEEDDEE 124  
Qy 1985 DEHRK-----GLLHMKMAEGAKLQMCYLLQHLN 2012  
Db 125 DEBEKEDEEBETAQEKDEKEEBAEAGEKEGLEGLLQMKLPESVKLQMCHELLLEYFC 184  
Qy 2013 DIQLRHVEAIIAFADHFDVGLDQLDRLRY-TEIKQSDLPASAANKTREFRCPPR 2067  
Db 185 DQELQHRVESLAFAERYVDKLANQRSRYGLLIKAFSMTAAETARTREFRSPQ 240

RESULT 11

US-08-559-397A-12  
Sequence 12, Application US/08559397A  
Patent No. 6083713  
GENERAL INFORMATION:  
APPLICANT: Manly, Susan P.  
APPLICANT: Kozlowski, Michael R.  
TITLE OF INVENTION: CLONING AND EXPRESSION OF  
TITLE OF INVENTION: BETA APP-C100 RECEPTOR (C100-R)  
NUMBER OF SEQUENCES: 35  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10036/2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/559,397A  
FILING DATE: 15-NOV-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 6013-135  
TELEPHONE: 212-790-9090  
TELEFAX: 212-869-8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 240 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-559-397A-12

Query Match 1.2%; Score 334.5; DB 2; Length 240;  
Best Local Similarity 35.6%; Pred. No. 3e-18;  
Matches 84; Conservative 32; Mismatches 73; Indels 47; Gaps 4;  
Qy 1879 TESVRPQKMTD-----IAESTITEISNLSYFPFLEVARFVQALAEAVETNQVNR 1931  
Db 5 TTSLRPHHSPPCFVAALPAAGAAEAPARLSPAIPLALRDALKALMLGEAVRDGGQAR 64  
Qy 1932 DPVGSNENLFLPLIKLVDRLLVGMMDDEVEKLLIMTNPETW-----DPSFDKEGK 1984  
Db 65 DPVGSVEFQVPVKLVSTLLVMGIFGDEVDVKQILKMIPEVFTTEBEDEEEDDEE 124  
Qy 1985 DEHRK-----GLLHMKMAEGAKLQMCYLLQHLN 2012  
Db 125 DEBEKEDEEBETAQEKDEKEEBAEAGEKEGLEGLLQMKLPESVKLQMCHELLLEYFC 184  
Qy 2013 DIQLRHVEAIIAFADHFDVGLDQLDRLRY-TEIKQSDLPASAANKTREFRCPPR 2067  
Db 185 DQELQHRVESLAFAERYVDKLANQRSRYGLLIKAFSMTAAETARTREFRSPQ 240

RESULT 12

US-09-949-016-8849  
Sequence 8849, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: CL001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 8849  
LENGTH: 2262  
TYPE: PRT  
ORGANISM: Human  
US-09-949-016-8849

Query Match 1.2%; Score 313.5; DB 2; Length 2262;  
Best Local Similarity 23.9%; Pred. No. 1.2e-14;  
Matches 168; Conservative 110; Mismatches 263; Indels 163; Gaps 36;  
Qy 76 LQELVTAAGSETCKGTGSGHRTLL-----YGNAILRLHNSDMYLAC-LSTSSQDKLAF 129  
Db 36 LKKLQHAALAEQ-KQNESENKLLGIVKYSNVYQLLHKSNKYLTVNKLPALEKNAM 94  
Qy 130 DVLGLQHSQGEACWTLHPASKORSEKVRVGDLLVSVATERVYHTTK-----EN--- 182  
Db 95 RVSLDA-AGNEGSWFYIHPFWKLRSQDNVWGVKVPVNAQOPUHASNIELLDNPGC 153  
Qy 183 -EVSIVNASPHVTHWSVQPYGTGISRMKYGVY----VFGDVLRFPHGGDECLTIPSTWT 237  
Db 154 KEVNAVNCN---TSWKITLF-----MKYSSYREDVLKGGDVRLFAEQEKFLTCDEYE 204  
Qy 238 KCGGQNI-----VYEGGSVMSQARSWLRLLELA-RTKAGGFINWYHPMRIRHTTGYLG 292  
Db 205 KK--QHIFLRTTLRQSATSATSSKALWEIEVHVHDDPCRGAGQWNSLFRFKHLATGNLYA 262  
Qy 293 V-----NDONE-----LY-LVS-----REEATTAS 311  
Db 263 AELNPDYRDAQNEGKNVRCVPTSKKQKQAGKIMTTLVSVPHGNDIASLFDATLTQ 322  
Qy 312 CAFCLRQEKDDQKQVLEDKLEVIGAPIIKYGDSTVIVQHSSETGLWLSYKSY-----ETKK 367

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Db 323 RADCLVPR-----NSVRLRLHLCNTWTSTSIPIIDTDEER 358
Qy 368 KGVGKV-----EKKQALHEEGKMDGLDFRSQEEESRTARVIRKCSSLFTKFINGLE 421
Db 359 PVMKIGTCQTKEDKEAFIVSVPUSEVRDLDIFANDANKVLAATTVKLE-----NG-- 409
Qy 422 TLQENRRHSMPFASVNLGEMVCLDLINYFAQ--PDEMEHEE-----KONFRALRNQD 476
Db 410 TITQNERF-----VTKLLEDLFFVADVNNQGEVLDVVTIKPN-----RERQK 454
Qy 477 LFOBEGILNL-----ILEADKINVTISQGLAGFL--AGDESGQSWEMISGYLYQLLALIK 532
Db 455 LMREQNIIAQVFGILKAPKEK--AGEGSMRLLEDLGDQRYAPYKMLRLCYRVL----- 507
Qy 533 GNHTNCAQFANSRLNWLFSRLGSOASGEGTGL--DVLHCVLIDSPALNM--MRDEHIK 589
Db 508 -RHSQDVRKQEQYIAKPCVMSQSI-----GVDILAEDTITALLHNNRKLKEKHITAKEIE 563
Qy 590 VIISLEKHGRDPKVDLCSLCVNGVAVRSSQNNICDYLL--PGK-NLLLTQALVDRHS 647
Db 564 TFSVLLRN--REPRLDYLDLCSVNTTAPVTOELICKFMLS PGNADILITQKVSMQA 622
Qy 648 S--VRPNFVGRVGSAYVRKYFVPTWMDHIEKTHMMPHLRIG 689
Db 623 DNPMESSILSDIDDEEVWLYMIDSNKEPHGKAIRHLAQEAKEG 666

RESULT 13
US-09-949-016-6507
; Sequence 6507, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6507
; LENGTH: 3259
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6507

Query Match 1.1%; Score 308; DB 2; Length 3259;
Best Local Similarity 18.7%; Pred. No. 6.8e-14;
Matches 637; Conservative 557; Mismatches 1216; Indels 988; Gaps 171;

Qy 1283 NTFET-----MKNWFEURLSLPVICHN-----EFTDEAKA-RRWVEIKDRQOI 1327
Db 308 NTVTEREESKILLEKMELEVAERKLSF--HNLOBEMHLLHLEQFEQAGQAQAELESRYSA 365
Qy 1328 LMW--EAVEAQPAAHIDQIMRSG-----FTMNDIKGLHYEDNOEELPSS--KMKRLPS 1376
Db 366 LEQKHKAEMEETSHLSLQKTQBLQACDALKQNSKLLQDKNEQAVQSQTQQLED 425
Qy 1377 RPRKGSMTGRVTIONNNLQPGQVGMHRSTSEAMAK-YDLGAQGLTPDDPKDKRGRS 1435
Db 426 QIQKSK-----EISOFLNRLPLQ--QHETASQTSFPDVYNEGTQAVTEENIASLQKRV 477
Qy 1436 PKFPRSKRGESSDRAKSRKSTPDPFSDTEVSPERGARRPNPQIKVSOANQRYNGMAR 1495
Db 478 -----VELENEKGA----- 486
Qy 1496 PSRTNLYGSOVLNMAPTQDRKQMTSTFL--AQSATETVGNIEIFDAECLKLINEFYGV 1553
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Db 487 -----LLLSSTELB-ELKAENKLSQITLLEAQNRTGEADREVSSEISIVDIANKRSSA 540
Qy 1554 RIYPQDPTHYVIGWVTTQVHLHKSDFNQSKVTSSVLIITDYDRVVENVNRQSCYM-- 1610
Db 541 E-BEGQD-----VLENTFSQ-KHKLSVLLLE-----MKEAQEEATFLKLO 579
Qy 1611 ---VRADELYNEVMAEATAKAGSQCMFIGSVDSTSGVSFTCEGKDTSPFKMEP-BTK 1666
Db 580 LQGRAEAEADHEVLDDQEMK-QMEGEGI-----APIKMKVLEDTGDFPLMPNEES 630
Qy 1667 LPFAIFVEATSKETILOELGRSATSLPLS---AAVLPTSDGH-----VTPQP----- 1711
Db 631 SLPAVEKEQASTE-----HQSRSTSEISLNDAGVELKSTKQDQKSLSAVPDQCHQD 684
Qy 1712 --PLKVKQCLKP-----HQAARVPNQSLQVHALK----- 1738
Db 685 ELERLKSQILELENFHKAEIYKNDLDEKAKESLNLQLEEBFKQADNNSAFTALUSE 744
Qy 1739 -----LSDIRGWSMLCE--DAVSMALALHIPED--RCIDILEPIEMDKLLSFHSHLTLY 1789
Db 745 ERDQLLSQVKLSVMTELRAQVKOLEMNLAEARQRRLDYESTAHDNLLTEQIHSLSIE 804
Qy 1790 AALCYQSNYRAAHALCTHVDQKQLLYAIQS---QYMSGPLRQGFVDDLIAL-----HLSEH 1842
Db 805 A----KSKDVKIEVLQNELDDVQLQFSQSTLIRSLOSQQLQKSESEVLEGAEVRHISK 860
Qy 1843 ATTMEACKNEFVPIPLGPPELXALYEEDPMGHLSLSIOTESVRPQMKMTDIAESSIE-ISNL 1901
Db 861 VEELSQUALSQKELEITKMDQLLEKK---ROVETLQOTIEBKQOQVTTISFSMTKMQVL 917
Qy 1902 YSPYFPLEVAREFVWQAL-----AEAVETNOVHRDPV--GGSNENLFLPLIKLVDRLLLV 1955
Db 918 NEEKFSLGVEIKTLKEQLNLLSRAEAKKEQVEEDNEVSSGLKQN-----YDEMSPA 969
Qy 1956 GMMRDEDEVKLLIMTNPETWDPSPD---KEGKBHRKGLLHMKAAGKALOMCYLLQHLN 2012
Db 970 QOISKEELOH-----EFDLLKKENEQRKR-----LQAALINRKELLQVRS 1010
Qy 2013 DIQ-----LHRVEAITAFADHFVGDLOTD--QLARRYTEIKQSDLPASAVAAKTFRFCPP 2066
Db 1011 KLEELANLKDSEKKEIPLSETERGEVEEDKENKEYSE-----KCVTSKCQCIETYL 1062
Qy 2067 REOMN-AILSPKLEEDKENCPCGEELIARMNFHDTLMAHVSILHAHQEPDAENQ--- 2122
Db 1063 KQTISEKEVELQHTRKOLEEKLAAEQFQALVKQNNQTLQDKTNQIDLLQAEISENQAI 1122
Qy 2123 -----BPEAKPG---AFGKLYNIINT-----VKELBEEAKAIEBPCKTPEEKR 2164
Db 1123 QKLITSNTDASDGDVALVKETVVISPPCTGSSEHWPKEBELKILALEK-EKEQLQKKLQ 1181
Qy 2165 KVLJ--QTIVNWABESQ---IETPKLVREMSLLVRQYDA-----VGEILRALEKTVV 2212
Db 1182 EALTSRKAILKKAQEKERHLREELKQKQDDYNRLOEQFDEOSKENENIGDQLRQJQ--- 1237
Qy 2213 INAKTLDVAEMWVGLSQIRALLPVQMSQEBEL-----MRKRLWLKLVNHHPTFHQDPL 2266
Db 1238 IQVRESID-----GKLP---STDQESCSSTPGLEELPFKATEQH-----HTQP 1278
Qy 2267 IRVLRV-----HENVMVMNTLGRRAQASDQSPSPVAEDSKDTSHEMVVACC 2319
Db 1279 VLESNLCPDWPFSHESASALQGGTSVAQIKAL-KEIEAEKVELEKLVKSVSTTSELT--- 1333
Qy 2320 RFLCYFCTGRNQKAMDFDHFDFLENSNILLRSPSLRG-STPLDVAVSSL--MENTEL 2375
Db 1334 -----KSEEVFQEQINQKQLEIESTKTVSHEAEVHAESLQQLLESQ 1379
Qy 2376 ALALREHYLEKIAVYLSRCGLSQNSSELVEKGYPDLGWDPVGEERYLDFLFCVWVNGBSV 2435
Db 1380 QIAGLEHURE-----LQPKLELOKLIKKEEDVS-----YLSGQLS 1416
Qy 2436 BENANLV-IRLLIRPECLGPALRGEGGLKAI-----VDANKMSERIADRR-KLRBEN 2488
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Db 1417 EKEAALTKIQTEII-----EQEDLIKALHTOLEMQAKEDHRIKQLOVELCEMK 1465  
 Qy 2489 QEGDWNFSHPUPESDEDEYI-----DTGAAILNFYCTVLVLLGRCAPDAGVIALGKNE 2542  
 Db 1466 QK-----PEBIEESRAKQIQKQLQAALI-----SRKEALKENK 1500  
 Qy 2543 SLR-----ARAILRSLV-PLEDLOGVLSLRFTLNNPAAG-----ERPCK--SDMPSGLI 2588  
 Db 1501 SLOBELSLARGTIBRLTKSLADVESQVSAQNKEKDTVLGRLLAQLEBERDKLITEMDRSL 1560  
 Qy 2589 PGHK-----QVGLFLERVYGIETQELFYKLEBAFLPDRAATMLRDNDCESDMALSM 2643  
 Db 1561 ENQSLSSCESLKLAEGL--TEUKE--KLVKE--IESLKSSKIAESTEWEQKHKELOK 1613  
 Qy 2644 NRYIGNSILPLLIKHAYPNAENYASLLDNLTHVYRL-----SKNRLMTKGOBEAV 2696  
 Db 1614 EYEI-----LLQSVNVSNEARIQHVEAVRQEQELVYKLRSTANKETEKOLQEA 1667  
 Qy 2697 SDFLVALTSANQ---PSMLLKLR-----KLTVDV-----SKLSEYTTV--A 2733  
 Db 1668 EQEMEEMKEMKPKAKSQKQKILBEBENDRLRAEVHPAGDTAKECEMETLLSNASKMBE 1727  
 Qy 2734 LRLTLHYERCAKYVSTGAGOGAFGASSDEKRLTWMLFSNI-----FDSLSKMDYE-- 2786  
 Db 1728 LERVMEYETLSKKFQSLMSEKDSL---SEEVQDLKHQIEDNVSKQANLEATEKHNDQTN 1784  
 Qy 2787 -PELFGKALP-----CLIAIGCALPPDYSLSKNYD--DEFYG----- 2820  
 Db 1785 VTEEGTSIPGETEBOQSLSMSTRPTCSVPSSAKSANPAVSKDFSSHDEINNYLOQIDQ 1844  
 Qy 2821 -KEQAAGDLPQVDPQINTSSVALANDLNTIVQKSEHYHDWASRKENGHWYEGW 2879  
 Db 1845 LKERIAGLEBKQKKE-----FSQTLNEKNLTLSQIS-----TKOG----- 1882  
 Qy 2880 SDSOKTHPLKPYNMLNDYERKVPVRESLKALLAIGMSVERSEVDIPSNRRSMRQ 2939  
 Db 1883 -ELKMLQEEVTKMMLN-----QQIQEELSVTKLKTAEBEKDDLBERLMNQLAEL 1933  
 Qy 2940 SKSGRRPEIYVTSATPDPYNPVDMTNLTLSREMOMARLADNAHDIAWKKKEELY 2999  
 Db 1934 NSIGNYQDVTDA-----QIKNVELSESEMKNLKKVSE-----LEBEKQVLV 1976  
 Qy 3000 TN-----GGGIHPQVLPYDILLTDKEK-----KDRERSOEFL 3031  
 Db 1977 KERTKVESEIRKYLEIKTQAQKEPGNKSNAKEL--QELLKEQOEKQVLOKOCIRYQEKI 2035  
 Qy 3032 KYLOVQYKLRPSKAPQSDTEQTTGVA-----IELRPAYSILLEKLIQYIDRAT 3081  
 Db 2036 SALERTVKALEFVQTESQKDLITKENLAQAVEHRKKAQAEASFKVLDDTQSEAAARVL 2095  
 Qy 3082 I-NMKLLK--PSTTFSRRSPKSTRDIKFFSKAVLPLMEKYFSTHRNYFIATATANNV 3138  
 Db 2096 ADNLKLLKELQSNKESVKSMQKQDLE---RRLEQAEEKH----- 2134  
 Qy 3139 GAASLEKEMVAALFCKLASLLRSLAFAFGDPDVRITVRCLOVLV--KGIDAKSLVKNCP 3196  
 Db 2135 ---LKEKNQOE---KLDALRREKV-----HLEETIGEIQVTLNKKDKVEYQQLQENLDS 2182  
 Qy 3197 FIRTSMLTF---FNNVADDVGHIT-----MNLQDGKYAHLRGTHL 3233  
 Db 2183 TV-TQLAAFTKMSLSQDDRVRVDEAKKWERKFSDAIQSKEBIRLKEKDNCSVLKQDLR 2241  
 Qy 3234 KTSTSLGYINGVLLFIILTAQPDH-----LANCEYG-ADILLDEIOVASYKMLGS--- 3281  
 Db 2242 QMS-----IHMEELKINISRLHDKQIWESKAQTEVQLQKQVCDTLQENKELLSQLEET 2296  
 Qy 3282 --LVALGTD--ASLTHRKYLKTE-----IERHKPALGSCIGAF-----SSTFPV 3322  
 Db 2297 RHLVHSSQNELAKLESELKSLKQDLTDLNSLEKCEKQKGNLEGIIRQOEADIQSNKFSY 2356  
 Qy 3323 AFLPHLNKHNQFSLNRIADH-SLEAQDINQKMEQCMPTLETTLIGVDQFVESDKTYNE 3381  
 Db 2357 EQLETDLQASRE--LTSRLHEINNKQKQIISLSGKEEAIOVAIELRQ--QHDKEIKE 2412

Qy 3382 APHIIDVPLLCSYLPFWWAQCPDNVPTGNGHNVTMTVAEHMNNOLLKNVLIKKKNIGN 3441  
 Db 2413 LENLLS-----QEEENIVLEEENKAV---DKTNQJLME-TLKTIKK----- 2450  
 Qy 3442 ENAPMWTIRIATYTOOI--IINSSEELLRDSFLPLAER---VRKRTDNMFHK-----E 3488  
 Db 2451 ENIQQAQLDSFKVSSSLONDRDRIVGD--YQLEERHLSIILEKQOLIOEAAENKKLK 2509  
 Qy 3489 ESLRGFIKSTDDTSQVES-----QIQEDWOLLVRDIYSFYPLLIKYVDLQRNHLRN 3541  
 Db 2510 EETRIG-LRSHMDLNSENAKLDAELIQYREDLNAQVITIKDSQKQKLEL-VLOQONKELEN 2567  
 Qy 3542 NVPEAEELYNHVAEININWSKQYFLKERONFISANEIDNMVLMITATATRTVAVTDGTP 3601  
 Db 2568 KYAKLEBKLESEBEANEDLRRSFNAQOEKQDLS-KEISLKVSIQSOLTQVATLQBEGT 2626  
 Qy 3602 QGGGKKKKHRDKKDKKEVQ--ASIMVACLKRLLPVGLNLPAGREQUELVQHKORFLK 3659  
 Db 2627 LG-----LYHAQLKVKEEVHRLSALFSSQKRI-----AELEELV--CVQK--- 2667  
 Qy 3660 KMSEODVAFPAKTQLTLPDKIDPADEMSWOYHYLYSKGSKSNITVETAENK-AKIIDD 3718  
 Db 2668 -----EAAKKVGBIEDKL--KKELKHLHDAGIMRNET-----ETAERVAELARD 2711  
 Qy 3719 TVB--RIVAMSKVLFGHLMIDHPQOMKXNVYSVSIQKR-----AVI 3760  
 Db 2712 LVMEQKLLMTVTENKGL-----TAQISFGSMSSLQNSRDHANEELDELKRYDASL 2765  
 Qy 3761 ACFRQTSLSLPHRRACNTPARTYVELWLEEN-----IQOEVMIED-----LTQSFE 3808  
 Db 2766 KELAQLKEQGLNRRDALLSETAPSMNSTEENSLHLEKLNQOLLSKDLQLHLSQL 2825  
 Qy 3809 DA-----ELKXSDVVVEBEK-----PDPLT-----QLVTTFCRG 3837  
 Db 2826 DSYNQVSFSKAWASLQNERDHLWNELEKPRKSEEGKQSAAPSTSPAEVQSLKKAMSS 2885  
 Qy 3838 AMTERSGALQES-DPLYMSYAHIIAKSCGEEBEGGEGGEGGAEEADEGRA-SIHEQE 3895  
 Db 2886 LQNDRLRLKELKNLOOQVLOI-----NOBITELHPLKAO---LQBYQDKTKAFQIMQEE 2937  
 Qy 3896 MEKQKLLF-----HOARLA-----DRGVAEMVLLHISAKGLPSEMVMKTLQIGSILR 3944  
 Db 2938 LRGENLSWQHLEHQLRMEKSSWEIHERRMKEQYLMALS-----DKQOQLSHLQNLIRELR 2992  
 Qy 3945 GGNIDIQMGMLNHLKDKXDVGFFTSIA--GLMNSCSVLDDAFERNTKAEGLVGLEGA 4002  
 Db 2993 SSSSQTOPLKVQY---QROASPETSASPDGSONLVYETELLRTQLNDSL----- 3038  
 Qy 4003 GEKNMHDABFTCALFRPIQLTCEGHNLDQNYLRTQAGNTTNNVVICVDYLLRLOESI 4062  
 Db 3039 --KEIHQKE-----LRIQOL-----NSNFSQLLEEK-----NTLSIQICDTSQSURENQ- 3081  
 Qy 4063 MDPYWHYSS-----KELIDPAGKANFFKAIGVASQVNTL-----TEVIQGPC 4105  
 Db 3082 -----HYGDLNHCVALEKQVQEL--QAGPLNIDVAPG-APOEKNGVHRKSDPEELREP- 3132  
 Qy 4106 TQOQALAHSLRWDVAGGFLFLFSHQDKLSKHSQVDLLKELNLNLOKQK---IPMMLSM 4162  
 Db 3133 ---QQS-----FSEAQQQLCNTRQEVNELRKLLEBERDQVRAENALSV 3173  
 Qy 4163 LEGNV-----VNGTIGQMVDTLVESASN 4186  
 Db 3174 AESQIRRLHEHSEWDSRTPPIIGSCGTQEQALLIDLTSN 3211

RESULT 14

US-09-710-279-2964  
 ; Sequence 2964, Application US/09710279  
 ; Patent No. 6703492  
 ; GENERAL INFORMATION:  
 ; APPLICANT: KIMMERLY, WILLIAM JOHN  
 ; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS









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Qy 2629 LDRNDGCSNALSNNRYGNSILPLLIKHAIFYNEAENYASLLDATHVTYRL----- 2692
Db 1073 AESTWQEKHKELOKEVEI-----LQSYENVSEAEIRIQHVVEAVERQEKQELYGLKRS 1126
Qy 2683 -SKNRMLTKGQREAVSDFVALTSAMO---PSMLLKLLR-----KLTVDV----- 2723
Db 1127 TEANKKETEKQLOBAEQEMBEKMKRFAKSKQOKILELEENDRLRAEVHPAGDTAKE 1186
Qy 2724 ---SKLSEYTV--ALRLLTLHYRCAYKGSTGAGQAGFAGSDEBKRLTMMLFNSI-- 2776
Db 1187 CMETLLSSNASKBEELERVKMEYETLSKKFQSLMSEKDSL---SEVQDLKHQIEGNVSK 1243
Qy 2777 ---FDSLISKMYE---PELFQKALP-----CLTAIGCALPPDYSLSKNY 2814
Db 1244 QANLEATEKHNDQNTVTEGTSIPGETEBQDSLSMSTRPTCSVPSAKSANPAVSKDF 1303
Qy 2815 D--DEFYV-----KEQAAGDLDNPOYDPOPINTSSVALNNDLNTIVOKFSHYHDW 2864
Db 1304 SSHDEINNYLOQIDQLKERIAGLEEEKQKWE---FSQTLNENKNTLLSQIS----- 1352
Qy 2865 ASRKIEGWYVEGMSDSQKTHPLKPNYMLNDYEKERYKEPVRESLKALLAIGMSVEHS 2924
Db 1353 ---TKDG-----ELKMLQEEVTKNNLLN-----QQIQEELSRVTKLKETAEE 1392
Qy 2925 EVDIPSNRRSMRQSKSGRPPPIVTDSATPPDYNPHVPVDMTMTLSREMONMAERLAD 2984
Db 1393 KDDLEERLMNQLABELNGSIGNCYQDVTDA-----QIKNELLESEMKNLKKCVSE 1441
Qy 2985 NAHDIWAKKKEELVTN-----GGGTHPOLVPYDLTLDKKE- 3020
Db 1442 -----LEEEKOQLVKETKVESEIRKEYLEKIQOAKQEPGNKSHAKEL-QELLKEQOE 1494
Qy 3021 ---KDRERSQEFKLYQYGYKHLRPSKAPQSDTEQTITGVA-----IELRFA 3066
Db 1495 VKQLQKDCIRYOEKISALERTVKALEFVQTESQKDLITKENLAQAVEHRKKAQAELASF 1554
Qy 3067 YSLEKLIQYIDRATI-NMKLLK--PSTTFSRRSSFKTSRDIKFPFSKAVLPLMEKYFST 3123
Db 1555 KVLDDTQSEAAARVLADNLKLKELQSNKESVKSQMKQKQEDLE---RRLEQAEKHEH--- 1608
Qy 3124 HRNYFIAVATATNVNVAASLKEKMAAALFCKLASLLRSRLAAGPDVVRITVRCLOVLV- 3182
Db 1609 -----LKEKNQOE---KLDALAREKV-----HLEETIGEIQVTLN 1641
Qy 3183 -KGIDAKSLVNKCEPFI RTSMLTF---FNNVADDVGHITI-----M 3218
Db 1642 KKDKEVQOQLENLDSV-TQLAAFTKSMSSLODDRVIDEAKWKERKFSDAIOSKEEI 1700
Qy 3219 NLQDKVAHLRGTHLKTSTSLGYINGVLLPLTAKFDH-----LANCEYG-ADLLLDE 3270
Db 1701 RLKEDNCSVLKQDLRQMS-----IHMELKINISRLBHDKQIWSKQATEVQLOQKYCDT 1755
Qy 3271 IQVASYKMLGS-----LYALGTD--ASLTHDRKVLKTE-----IERHKPALGSCGLGA 3315
Db 1756 LQGENKELLSQLEBETHRLHYSSQNELAKLELSKLDQDLTDLNSLEKCKEKGKQNLGI 1815
Qy 3316 F-----SSTFFVAFLPHLNKHQFSLNRIADH-SLEAQDIMQMEQCMPTELTIL 3366
Db 1816 IRQOEADIQNSKFSYEQLETDQASRE-LTSRLHEEINMKKEQKIISLLSGKEAIOVAI 1873
Qy 3367 GEVQOFVESDKTYNEAPHIIDVLPILCSYLPFWAQGPDPNVTPTGGNHVTWMTAEHMNQ 3426
Db 1874 AELRQ--QHDKEIKELLENLLS-----QEEENIVLEENKXAV---DKTNQ 1914
Qy 3427 LLKNVLKLIKNIGENAPWMTRIATVTOOI--IINSSEELLRDSFLPLAER---VRKRT 3481
Db 1915 LME-TLTKTIK-----ENIQQAQALDSFVKSSSLQNDRDRIVGD-YOOLEERHLSIILEK 1968
Qy 3482 DNMFKH-----EESLRGFIKSTDDTSQVES-----QIQEDWQLLVRIYSFYPL 3526
Db 1969 DQIQEAAAAENNKLEKEIRG-LRSHMDDLSNENAKLDAELIQYREDLNQVITIKDSQOKQ 2027
Qy 3527 LIKYVDLQRNHWLRNNVPEAEELNHNVAEIPNINWSKQYFLKEEQNTISANEIDNMVLIIM 3586

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Db 2028 LLE-VLOQNKELNRYAKLEEKLKSESEANEDLRRSFNALQEBEKQDLS-KEIESLKVSI 2085
Qy 3587 PTATRRVTAVTDTGTPGGGKKKKHRDKKRDKDKEVO--ASLMVACLKRLPLPVLGNLNFAG 3644
Db 2086 SOLTQVOTALQEBGTILG-----LYHAQLKVKEEVHRLSALFSSQKRI-----AE 2131
Qy 3645 REBELVQHCKDRFLKXMSQODVAEPAKTQTLTPDKIDPADEMSMQHWLYLYSKLSKSKSNI 3704
Db 2132 LEBELV--CVQK-----EAAKKGVEIEDKL--KKELKHLHHDAGIMNET----- 2172
Qy 3705 TVETAENK-AKIIDDTVE---RIVAMSKVLFGHLHMDHPQOMSKNVVSVVSQQRK--- 3757
Db 2173 --ETAERVAELARDIVEMEOKLLMTWKENKGL-----TAQIOSFGRSMSSLSQNSRDHA 2224
Qy 3758 -----AVIACFRQTSLSHSPHRACNIFARTYVELWLEEN-----IQGEV 3798
Db 2225 NEELDELKRYDASLKELAQLEQGLNRRERDALLSETAFPMNSTEENSLHLEKLNQOL 2284
Qy 3799 MIED-----LTQSFEDA-----ELKKSQVVEGEK---PDPL 3827
Db 2285 LSKDEQLHLSSQLEDSYNQVQFSKAMASLQNERDHLNLELEKFRKSEEGKORSAQPS 2344
Qy 3828 T-----QLVTTFCRGAMTERSQALQF-DPLYMSYAHIIAKSCGEEBEEGGGEEGGEA 3881
Db 2345 TSPAQVQSLKAMSSSLQNDRLDRLLKELKNLQOQYLOI-----NQEITELHPLKAQ---LQ 2396
Qy 3882 EADEGRA-SIHQOEKQKLLF---HQARLA-----DRGVAEMVLLHISASKGLPS 3929
Db 2397 EYQDKTKAFQIMQEELRQENLSHQHELHQLRMEKSSWEIHERRMKEQYLMAS-----DK 2451
Qy 3930 EYMKTLQIGISILRGNDIOQMMLNHLKDKXDVGFFTSIA--GLMNSCSVLDDDAFER 3987
Db 2452 DQQLSHLQNLIRELSRSSSQTPKLVQY---ORQASPETSASPDGSONLVYETELLRTQL 2508
Qy 3988 NTKAEGVLGVEGAAGEKNHDAEFTCALFRPQLTCEGHNLWDQNYLRTQAGNTTIVNV 4047
Db 2509 NDSL-----KEIHOKE-----LRIQOL-----NSNFSQLEEK---NLISI 2541
Qy 4048 VICTVDYLLRLQESIMDFYWHYSS-----KELIDPAGKANFFKAIGVASQVFN 4095
Db 2542 QLCDTSQSLRENQ-----HYGDLNLNHCVALEKQVQEL--QAGPLNIDVAPG-APQEK 2592
Qy 4096 TL-----TEVIQGPCTQNOQALAHSLRWDVAVGGFLFLFSHMQDKLSKSSQVOLLKELLN 4150
Db 2593 GVHRKSDPEELREP---QOS-----FSEAQQQLCNTROEVNELRKLE 2632
Qy 4151 LQKDM--IPMMLSLMEGNV-----VNGTIGKQMVDTLIVESASN 4186
Db 2633 EERDQVAAENALSVABEQIRLLEHSEWDSSRTPPIIGSCGTQEQALLIDLTSN 2685

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Search completed: October 6, 2006, 23:35:39

Job time : 144 secs

GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: October 6, 2006, 23:58:04 ; Search time 465 Seconds  
(without alignments)  
5108.314 Million cell updates/sec

Title: US-10-668-767-128

Perfect score: 26800

Sequence: 1 MAEAGGAGSEDDVSFLRTE.....WDFPPVGDGCRKQYEDLMGE 5128

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:

- 1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US07\_PUBCOMB.pap.\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_PUBCOMB.pap.\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US09\_PUBCOMB.pap.\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10\_PUBCOMB.pap.\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10B\_PUBCOMB.pap.\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_PUBCOMB.pap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	26800	100.0	5128	4	US-10-668-767-128
2	26716	99.7	5134	4	US-10-668-767-130
3	26644	99.4	5142	4	US-10-668-767-144
4	26506	98.9	5100	4	US-10-668-767-146
5	26469	98.8	5142	4	US-10-668-767-2
6	21630	80.7	5127	4	US-10-668-767-8
7	21403	79.9	5127	4	US-10-668-767-122
8	21376	79.8	5113	4	US-10-668-767-121
9	21360	79.7	5127	4	US-10-668-767-120
10	21326	79.6	5109	4	US-10-668-767-10
11	21270.5	79.4	5107	6	US-11-097-143-22563
12	21234.5	79.2	5112	4	US-10-668-767-125
13	21218.5	79.2	5126	4	US-10-668-767-56
14	21218.5	79.2	5126	4	US-10-668-767-124
15	21191.5	79.1	5112	4	US-10-668-767-126
16	21175.5	79.0	5126	4	US-10-668-767-123
17	21046	78.5	5104	4	US-10-668-767-6
18	20932.5	78.1	5101	4	US-10-668-767-4
19	20422.5	76.2	4868	4	US-10-668-767-57
20	12129	45.3	5317	4	US-10-668-767-59
21	11938.5	44.5	5071	4	US-10-668-767-58
22	11887.5	44.4	4968	4	US-10-668-767-61
23	11868	44.3	4967	4	US-10-668-767-62
24	11840	44.2	4967	4	US-10-668-767-60
25	11561	43.1	5107	4	US-10-369-493-6377
26	11453.5	42.7	4868	6	US-11-044-111-24
27	11407.5	42.6	4870	4	US-10-764-425-144

28	11347.5	42.3	5038	5	US-10-723-860-1310	Sequence 1310, Ap
29	11347.5	42.3	5038	5	US-10-756-149-5039	Sequence 5039, Ap
30	11347.5	42.3	5081	5	US-10-450-763-35328	Sequence 35328, A
31	11338.5	42.3	5081	4	US-10-276-774-1850	Sequence 1850, Ap
32	11325.5	42.3	5032	4	US-10-408-765A-26	Sequence 26, Appl
33	11325	42.3	4899	5	US-10-450-763-42673	Sequence 42673, A
34	11222	41.9	4934	5	US-10-450-763-53705	Sequence 53705, A
35	10863.5	40.5	4767	4	US-10-276-774-1902	Sequence 1902, Ap
36	8109	30.3	3647	4	US-10-408-765A-2436	Sequence 2436, Ap
37	7530.5	28.1	3375	6	US-11-044-111-23	Sequence 23, Appl
38	4953	18.5	2055	4	US-10-276-774-1795	Sequence 1795, Ap
39	2709.5	10.1	1056	6	US-11-044-111-22	Sequence 22, Appl
40	1146.5	4.3	1425	5	US-10-450-763-53703	Sequence 53703, A
41	847	3.2	249	5	US-10-784-004-338	Sequence 338, App
42	730.5	2.7	323	5	US-10-450-763-35329	Sequence 35329, A
43	723.5	2.7	616	5	US-10-450-763-53704	Sequence 53704, A
44	712	2.7	1232	5	US-10-450-763-34060	Sequence 34060, A
45	698.5	2.6	599	5	US-10-450-763-53702	Sequence 53702, A

## ALIGNMENTS

RESULT 1  
US-10-668-767-128  
; Sequence 128, Application US/10668767  
; Publication No. US2004017114A1  
; GENERAL INFORMATION:  
; APPLICANT: Caspar, Timothy  
; APPLICANT: Cordova, Daniel  
; APPLICANT: Gutteridge, Steven  
; APPLICANT: Rauh, James  
; APPLICANT: Smith, Rejane  
; APPLICANT: Tao, Yong  
; APPLICANT: Wu, Linong  
; TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors  
; FILE REFERENCE: B1533 US NA  
; CURRENT APPLICATION NUMBER: US/10/668,767  
; PRIOR FILING DATE: 2003-09-23  
; PRIOR APPLICATION NUMBER: 60/412,795  
; PRIOR FILING DATE: 2002-09-23  
; PRIOR APPLICATION NUMBER: 60/427,324  
; PRIOR FILING DATE: 2002-11-18  
; NUMBER OF SEQ ID NOS: 149  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 128  
; LENGTH: 5128  
; TYPE: PRT  
; ORGANISM: Heliothis virescens  
; FEATURE:  
; OTHER INFORMATION: pXL-Hv7  
; US-10-668-767-128

Query Match	100.0%	Score	26800	DB	4	Length	5128
Best Local Similarity	100.0%	Pred. No.	0	Mismatches	0	Indels	0
Matches	5128	Conservative	0				
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DB	1	MAEAGGAGSEDDVSFLRTE	DMVCL	SCTAT	GERVCL	AAEGFGRHCF	LEN
QY	61	SQCVPVIBQALSVRALQELVTAAGSETGKGTSGHRTLLYGNAILLRHNSDMYLACLS	120				
DB	61	SQCVPVIBQALSVRALQELVTAAGSETGKGTSGHRTLLYGNAILLRHNSDMYLACLS	120				
QY	121	SSSQDKLAFDVLGLOQHSQGEACWMTLHPASKORSEKVRVGGDDILVSVATERVLTHTK	180				
DB	121	SSSQDKLAFDVLGLOQHSQGEACWMTLHPASKORSEKVRVGGDDILVSVATERVLTHTK	180				
QY	181	ENEVSIVNASFHVTHWSVOPGTGTSRKMKYGYVGGVLPFFHGGDECLTIPSTWTXDG	240				
DB	181	ENEVSIVNASFHVTHWSVOPGTGTSRKMKYGYVGGVLPFFHGGDECLTIPSTWTXDG	240				

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Db	241	QONIVVYEGGVSQARSLWLELARTKWAGGFINWYHPMRIRHITTTGRYLGVDNQNELY	300
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Db	301	LVSREEATTASCFCLRQEKDDQKQVLEDKLEVIGAPIIKYIGDSTVIQVHSETGLWLSY	360
Qy	361	KSJETKKGVKVKBEKQALHEBGMDDGLDFRSQBEESHTARVIRKCSLSLTFKFINGL	420
Db	361	KSJETKKGVKVKBEKQALHEBGMDDGLDFRSQBEESHTARVIRKCSLSLTFKFINGL	420
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Qy	661	SAVRYKMYFEVTMDHIEKTHMPLHRLIGWANTTGYVPYPGGGEKVGNGVGDLLYSYGF	720
Db	661	SAVRYKMYFEVTMDHIEKTHMPLHRLIGWANTTGYVPYPGGGEKVGNGVGDLLYSYGF	720
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Db	841	RALAGPPLVQDDTAFVPTTQITLTPTTYVEQIRDKLAENIHBMWAMNKIEAGWYGDQ	900
Qy	901	REDLHKIHPCLVPPERLPPAEBKRYDIQIQAOTLKTILALGYIISLDKPPAIRNVRLPNE	960
Db	901	REDLHKIHPCLVPPERLPPAEBKRYDIQIQAOTLKTILALGYIISLDKPPAIRNVRLPNE	960
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Db	961	PFMQSNQYKPAPLDL SAVTLTPKMDLVQDLAENHNLWAPERIQOQWTYGLNEDSDMHR	1020
Qy	1021	SPHLVPYPKVDDAIKKANRDTASVTRTLTYGYMLDPPPTGEQHEALLLEASKQKQADF	1080
Db	1021	SPHLVPYPKVDDAIKKANRDTASVTRTLTYGYMLDPPPTGEQHEALLLEASKQKQADF	1080
Qy	1081	TYRAEKNYAVSSGKWYFEFEILLTAGPMRVGAHADMAPGMMLGQDENSWAPDGYNEBKVY	1140
Db	1081	TYRAEKNYAVSSGKWYFEFEILLTAGPMRVGAHADMAPGMMLGQDENSWAPDGYNEBKVY	1140
Qy	1141	SGNTESFGKQWAGDVGVFLDLIDKLTISFSLGELLMDALGGTTADVOGDNFVPACT	1200
Db	1141	SGNTESFGKQWAGDVGVFLDLIDKLTISFSLGELLMDALGGTTADVOGDNFVPACT	1200
Qy	1201	LGVGOKARLTYYQDVNTLYKFTTCGLOBGYPPFCVNMKRDVTHWYTKDQPIFENTDEMD	1260
Db	1201	LGVGOKARLTYYQDVNTLYKFTTCGLOBGYPPFCVNMKRDVTHWYTKDQPIFENTDEMD	1260
Qy	1261	TRIDVTRIPAGSDTPPCLKISHNTFETMEKANWBFRLSLPVI CHNEFIDEAEKARWVE	1320
Db	1261	TRIDVTRIPAGSDTPPCLKISHNTFETMEKANWBFRLSLPVI CHNEFIDEAEKARWVE	1320
Qy	1321	IKDRQQILMKEAVEAQMPAHIDQIMRSQFTMNDIKGLHYEDNQBELPSSKMKRLPSRPPR	1380

Db	1321	IKDRQQILMKEAVEAQMPAHIDQIMRSQFTMNDIKGLHYEDNQBELPSSKMKRLPSRPPR	1380
Qy	1381	KGSMTRGVITONTNLIPOQGVNGMHRSTSEAEWAKYVDLGAQGLTPDDKDKRGRSPKFF	1440
Db	1381	KGSMTRGVITONTNLIPOQGVNGMHRSTSEAEWAKYVDLGAQGLTPDDKDKRGRSPKFF	1440
Qy	1441	RSKRGSSSDRAKSRKSKTDPFSDTIVSPERGARRPNPQIKVSOANORYNGMARPERTN	1500
Db	1441	RSKRGSSSDRAKSRKSKTDPFSDTIVSPERGARRPNPQIKVSOANORYNGMARPERTN	1500
Qy	1501	LYGSOVGLNMATPTQDKQMTTSTLAQSATETVGNEIFDAECLKLINEFYGYVRIYPGQD	1560
Db	1501	LYGSOVGLNMATPTQDKQMTTSTLAQSATETVGNEIFDAECLKLINEFYGYVRIYPGQD	1560
Qy	1561	PTHVYIGWVTTQVHLHSKDFNQSKVTKSSVIIITDDVDRVVENVNRQSCYVRADELNEY	1620
Db	1561	PTHVYIGWVTTQVHLHSKDFNQSKVTKSSVIIITDDVDRVVENVNRQSCYVRADELNEY	1620
Qy	1621	MAEATKAGASQGMFIGCSVDTSFGSVFTCEGKDTSFKPMPEPETKLPFAIFVEATSKEI	1680
Db	1621	MAEATKAGASQGMFIGCSVDTSFGSVFTCEGKDTSFKPMPEPETKLPFAIFVEATSKEI	1680
Qy	1681	LQIELGRSATSPLSAAVLPTSCKHVIPOPPRLKVQCLKPHQWARVPNQSLQVHALKLS	1740
Db	1681	LQIELGRSATSPLSAAVLPTSCKHVIPOPPRLKVQCLKPHQWARVPNQSLQVHALKLS	1740
Qy	1741	DIRGSMLCEDAVSMLALHIPEEDRCIDILEPIEMDKLLSFHSHHTLTLYAALCQSYNRA	1800
Db	1741	DIRGSMLCEDAVSMLALHIPEEDRCIDILEPIEMDKLLSFHSHHTLTLYAALCQSYNRA	1800
Qy	1801	AHALCTHVQKQLLYAIQOYMSGPLRQGYFDLLIALHLESHATTMEACKNEFVILPGPE	1860
Db	1801	AHALCTHVQKQLLYAIQOYMSGPLRQGYFDLLIALHLESHATTMEACKNEFVILPGPE	1860
Qy	1861	LKALYEEPPDMGHSLSRLQTESVRPQMKMTDIAESIISNLSYSPYPPLEVAREFVMQALA	1920
Db	1861	LKALYEEPPDMGHSLSRLQTESVRPQMKMTDIAESIISNLSYSPYPPLEVAREFVMQALA	1920
Qy	1921	EAVETNQVHNRDPVGGSNENLFLPLKLVDRLLLVGMREDDEVKLLIMTNPETWDSFD	1980
Db	1921	EAVETNQVHNRDPVGGSNENLFLPLKLVDRLLLVGMREDDEVKLLIMTNPETWDSFD	1980
Qy	1981	KEGDKHRKGLLHKWAEAGAKQMCVYLQHLNDIQLRHRVEAIIAFAHDFVGLDQTDQLR	2040
Db	1981	KEGDKHRKGLLHKWAEAGAKQMCVYLQHLNDIQLRHRVEAIIAFAHDFVGLDQTDQLR	2040
Qy	2041	RYTEIKQSDDLPSAAVAAKTRFRCPPREQMNAILSPFKHLEEDKENCPCGGEELIARMNEF	2100
Db	2041	RYTEIKQSDDLPSAAVAAKTRFRCPPREQMNAILSPFKHLEEDKENCPCGGEELIARMNEF	2100
Qy	2101	HDTLMAHVSJLHALQEPDAAENQPEAKPGAFGLKYNIIINTVKELEBEAKAIEBPPKKTPE	2160
Db	2101	HDTLMAHVSJLHALQEPDAAENQPEAKPGAFGLKYNIIINTVKELEBEAKAIEBPPKKTPE	2160
Qy	2161	EKERKVLITOTIVNWAESQIETPKLVREMPSLLVROYDAVGELIRALEKTYVINAKTJLD	2220
Db	2161	EKERKVLITOTIVNWAESQIETPKLVREMPSLLVROYDAVGELIRALEKTYVINAKTJLD	2220
Qy	2221	VAEMWVGLSOTIRALLPVQMSQBEELMRKELKLVNNHTFFQHPDLIRLVRHENVMAVM	2280
Db	2221	VAEMWVGLSOTIRALLPVQMSQBEELMRKELKLVNNHTFFQHPDLIRLVRHENVMAVM	2280
Qy	2281	MNTLGRRAQAQSDAQSSQPVABDSKEKOTSHEMVWVACCRFLCYFCBTGRQNKAMPDHF	2340
Db	2281	MNTLGRRAQAQSDAQSSQPVABDSKEKOTSHEMVWVACCRFLCYFCBTGRQNKAMPDHF	2340
Qy	2341	DFLLENSNILLSPRSRGSTPLDVAYSSSLMENTELALAREHYLEKIAVYLSRCLGLOSNS	2400
Db	2341	DFLLENSNILLSPRSRGSTPLDVAYSSSLMENTELALAREHYLEKIAVYLSRCLGLOSNS	2400
Qy	2401	ELVEKGYPDLGWDPVBGERYLDLFRFCVWVNGSVSEENANLVIRLLRIRRECECJGPAURGE	2460

Db 2401 ELVEKGYFDLGMWPVEGBRYLDLRFVWNGESVEENANLIVIRLLIRRPCLGPAURGE 2460  
Qy 2461 GEGLLKAIIVDANKMSERADRKKLRREMEQBGDNFSPHLPESDEDEDYIDTGAALNFYC 2520  
Db 2461 GEGLLKAIIVDANKMSERADRKKLRREMEQBGDNFSPHLPESDEDEDYIDTGAALNFYC 2520  
Qy 2521 TLVDLLGRCAPDAGVIALGKNESLRARAILRSLVPLEDLQGVLSLRFITLNNPAAAGEERP 2580  
Db 2521 TLVDLLGRCAPDAGVIALGKNESLRARAILRSLVPLEDLQGVLSLRFITLNNPAAAGEERP 2580  
Qy 2581 SDMPGSLIPGHKQSVGLFLERYGTETQELFYKLLLEAFPLDPLRAATMLDRNDGCESDMA 2640  
Db 2581 SDMPGSLIPGHKQSVGLFLERYGTETQELFYKLLLEAFPLDPLRAATMLDRNDGCESDMA 2640  
Qy 2641 LSMNRYIGNSILPLLIKHAYFYNEAENVASLLDATHVTYRLSKVRMLTKGOREAVSDFL 2700  
Db 2641 LSMNRYIGNSILPLLIKHAYFYNEAENVASLLDATHVTYRLSKVRMLTKGOREAVSDFL 2700  
Qy 2701 VALTSAMQPSMLLKLRLKLTVDVSKLSBYTTVALRLLTLHYERCAKYYGSTGAGOGAFGA 2760  
Db 2701 VALTSAMQPSMLLKLRLKLTVDVSKLSBYTTVALRLLTLHYERCAKYYGSTGAGOGAFGA 2760  
Qy 2761 SSDEKRLTMMLFNSIFPSLSKMDYEPBLFGKALPCLIAIGCALPPDYSLSKNYDDEFY 2820  
Db 2761 SSDEKRLTMMLFNSIFPSLSKMDYEPBLFGKALPCLIAIGCALPPDYSLSKNYDDEFY 2820  
Qy 2821 KEQAAGDLDNPOYPQINTSSVALNNDLNTTVQKFSHYHDMAASRKIENGWYGEQMS 2880  
Db 2821 KEQAAGDLDNPOYPQINTSSVALNNDLNTTVQKFSHYHDMAASRKIENGWYGEQMS 2880  
Qy 2881 DSQKTHPRLPKNMNLNDYKERYKEPVPRESIKALLAIGWSVEHSEVDIPSNRRSMRQOS 2940  
Db 2881 DSQKTHPRLPKNMNLNDYKERYKEPVPRESIKALLAIGWSVEHSEVDIPSNRRSMRQOS 2940  
Qy 2941 KSGGRPPEIVTDSATPFDPNPHVDMTNLTLSREMNMAERLADNAHDIWAKKKKEELVT 3000  
Db 2941 KSGGRPPEIVTDSATPFDPNPHVDMTNLTLSREMNMAERLADNAHDIWAKKKKEELVT 3000  
Qy 3001 NGGGTHPOLVPYDLITDKEKKDRSOFELKLOYQGYKLHRPSKAPQSDTEQTTGVA 3060  
Db 3001 NGGGTHPOLVPYDLITDKEKKDRSOFELKLOYQGYKLHRPSKAPQSDTEQTTGVA 3060  
Qy 3061 TELRFAYSILLEKLIQIDRATINMKLLKPSITTFSSRSFKTSTRDIKFFSKAVLPMBEKY 3120  
Db 3061 TELRFAYSILLEKLIQIDRATINMKLLKPSITTFSSRSFKTSTRDIKFFSKAVLPMBEKY 3120  
Qy 3121 FSTHRNYFIATATNNVGAASLKEKEMVAALFCKLASLLRSRLAAGPDVRIITVRCLQV 3180  
Db 3121 FSTHRNYFIATATNNVGAASLKEKEMVAALFCKLASLLRSRLAAGPDVRIITVRCLQV 3180  
Qy 3181 LVKGIIDAKSLVKNCPDEFIRTSMLTFPNNVADDVGHITIMNLQDGKYAHLRGTHLKTSTSLG 3240  
Db 3181 LVKGIIDAKSLVKNCPDEFIRTSMLTFPNNVADDVGHITIMNLQDGKYAHLRGTHLKTSTSLG 3240  
Qy 3241 YINGVLLPLTLAKFDHLANCEYAGDALLDEIOVASYKMLGSYLALGTASLTHDRKLYKT 3300  
Db 3241 YINGVLLPLTLAKFDHLANCEYAGDALLDEIOVASYKMLGSYLALGTASLTHDRKLYKT 3300  
Qy 3301 EIERHKPALGSLGAFSSTFPVAFLEPHLNKINQPSLLNRIADHSLEAQDIMQKMEQOMP 3360  
Db 3301 EIERHKPALGSLGAFSSTFPVAFLEPHLNKINQPSLLNRIADHSLEAQDIMQKMEQOMP 3360  
Qy 3361 TLETLIGEVQDQVESDKTYNEAPHIIDVVLPPLCSYLPFWMAQQPDNVTPTGNGHVMTVT 3420  
Db 3361 TLETLIGEVQDQVESDKTYNEAPHIIDVVLPPLCSYLPFWMAQQPDNVTPTGNGHVMTVT 3420  
Qy 3421 AEHMQNQLKNVLLIKKNGINENAPMPTIATYTOOIIINSFELLRDSFLPLAERVRKR 3480  
Db 3421 AEHMQNQLKNVLLIKKNGINENAPMPTIATYTOOIIINSFELLRDSFLPLAERVRKR 3480  
Qy 3481 TDNMFHKEESLRGFTIKSSTDDTSQVESQIQEWDQLLVDRDIYSFYPLLKYVDLQRNHMLR 3540  
Db 3481 TDNMFHKEESLRGFTIKSSTDDTSQVESQIQEWDQLLVDRDIYSFYPLLKYVDLQRNHMLR 3540

Qy 3541 NNVEPEELYNHVAEIIFNINWSKQYFLKBEQNFISANEIDNMVLIMPTATRRVTAVTGDT 3600  
Db 3541 NNVEPEELYNHVAEIIFNINWSKQYFLKBEQNFISANEIDNMVLIMPTATRRVTAVTGDT 3600  
Qy 3601 PQGGKKKKKRDKKRDKEVQASLMVACLKRLLPVGLNLPAGREQLVHCKDRFLKK 3660  
Db 3601 PQGGKKKKKRDKKRDKEVQASLMVACLKRLLPVGLNLPAGREQLVHCKDRFLKK 3660  
Qy 3661 MSEODVAEFAKTQTLTLPDKIDPADMSWOHYLSKLSKSNITVETAEKAKIIDTV 3720  
Db 3661 MSEODVAEFAKTQTLTLPDKIDPADMSWOHYLSKLSKSNITVETAEKAKIIDTV 3720  
Qy 3721 ERIVAMSKVLFGHMDHPQMSKNVRSVSIQRKRAVIACFRQTSLSLSPRHRACNIF 3780  
Db 3721 ERIVAMSKVLFGHMDHPQMSKNVRSVSIQRKRAVIACFRQTSLSLSPRHRACNIF 3780  
Qy 3781 ARTTYELWLEBENTGOEVMIEDLTQSFEDABLKSDVVVEGEKDPDLTQLVTTFCRGAMT 3840  
Db 3781 ARTTYELWLEBENTGOEVMIEDLTQSFEDABLKSDVVVEGEKDPDLTQLVTTFCRGAMT 3840  
Qy 3841 ERSALQEDPLMYSVAHIIAKSCGEEBEGGEEGGEAEABDEGRASITHEQEMEKQK 3900  
Db 3841 ERSALQEDPLMYSVAHIIAKSCGEEBEGGEEGGEAEABDEGRASITHEQEMEKQK 3900  
Qy 3901 LLFHOARLADRGVAEMVLLHISASKGLPSEMVMKTLQLGISILRGGNIDIQMGMLNHLKD 3960  
Db 3901 LLFHOARLADRGVAEMVLLHISASKGLPSEMVMKTLQLGISILRGGNIDIQMGMLNHLKD 3960  
Qy 3961 KQDVGFPTSITAGLMNSCSVLDDAFERNTKAELGVGLEGAABEKQNMHDAFTCALPRFI 4020  
Db 3961 KQDVGFPTSITAGLMNSCSVLDDAFERNTKAELGVGLEGAABEKQNMHDAFTCALPRFI 4020  
Qy 4021 QLTCEGNLDWQNYLRTQAGNTTNNVICTVDYLLRLOESIMDFYHYSKELIDPAGK 4080  
Db 4021 QLTCEGNLDWQNYLRTQAGNTTNNVICTVDYLLRLOESIMDFYHYSKELIDPAGK 4080  
Qy 4081 ANFFKALGVASQVNTLTVEIQGCTQNOQALAHSLRMDAVGGFLFLFSHMQDKLSKSHS 4140  
Db 4081 ANFFKALGVASQVNTLTVEIQGCTQNOQALAHSLRMDAVGGFLFLFSHMQDKLSKSHS 4140  
Qy 4141 QVDLLKELLNLQKDMI PMMLSMLEGNVNGTIGQMVDTLVESASNVBELILKYFDMFLKL 4200  
Db 4141 QVDLLKELLNLQKDMI PMMLSMLEGNVNGTIGQMVDTLVESASNVBELILKYFDMFLKL 4200  
Qy 4201 KDLTSSASFQBI DANNDGWLPDPFKEMEQOKSYTPEEIEFLLACCTNHDGKLDYIGF 4260  
Db 4201 KDLTSSASFQBI DANNDGWLPDPFKEMEQOKSYTPEEIEFLLACCTNHDGKLDYIGF 4260  
Qy 4261 CDRFHEPAKEIGFNLAVLLTNLSHMPNEPRLARFLETAGSVLNYFEPLGRIEIMGSK 4320  
Db 4261 CDRFHEPAKEIGFNLAVLLTNLSHMPNEPRLARFLETAGSVLNYFEPLGRIEIMGSK 4320  
Qy 4321 RIERVYFEIKESNIEQWEKPOIKESKRAFFYSIVTEGGDKLEAFVNFCEDAIFEMTHA 4380  
Db 4321 RIERVYFEIKESNIEQWEKPOIKESKRAFFYSIVTEGGDKLEAFVNFCEDAIFEMTHA 4380  
Qy 4381 SGLMAAESVESVGGTKNREASWYMGDDDDERAGKDPFRRLGQSVKDGATAFSSLSPSNI 4440  
Db 4381 SGLMAAESVESVGGTKNREASWYMGDDDDERAGKDPFRRLGQSVKDGATAFSSLSPSNI 4440  
Qy 4441 KAKTADMOQMPAPAEIAGVFFKMFVLYLGVGLVVRVYIFGVLLGLMRGPQTDPEPPE 4500  
Db 4441 KAKTADMOQMPAPAEIAGVFFKMFVLYLGVGLVVRVYIFGVLLGLMRGPQTDPEPPE 4500  
Qy 4501 PTEBEKIGQLRHRLLIATQSSRHLPALPPADDTGQMVSAFGLDITKEDNGOIQVKPHESP 4560  
Db 4501 PTEBEKIGQLRHRLLIATQSSRHLPALPPADDTGQMVSAFGLDITKEDNGOIQVKPHESP 4560  
Qy 4561 STPTSSGEEAEVSPDESADHTEQRPPSLIDLIGGEQAKKQQAQERMEAAQQAAMGAI 4620  
Db 4561 STPTSSGEEAEVSPDESADHTEQRPPSLIDLIGGEQAKKQQAQERMEAAQQAAMGAI 4620







Qy	1141	SGNTSEFKOWAVGDVGVFLDLIDKTI	SFSLNGELLMDALGGTTTADVQGDNFVPACT	1200	
Db	1141	SGNTSEFKOWAVGDVGVFLDLIDKTI	SFSLNGELLMDALGGTTTADVQGDNFVPACT	1200	
Qy	1201	LGVGQKARLTGYQDVNTLKYFTTTCGLQBGYPFCVNMKRDVTHWYTKDQPIFENTDEMID	1260		
Db	1201	LGVGQKARLTGYQDVNTLKYFTTTCGLQBGYPFCVNMKRDVTHWYTKDQPIFENTDEMID	1260		
Qy	1261	TRIDVTRIPAGSDTPPCLKI	SHNTFETMEKANWFLRLSLPVI	CHNEFIDEAEKARWVE	1320
Db	1261	TRIDVTRIPAGSDTPPCLKI	SHNTFETMEKANWFLRLSLPVI	CHNEFIDEAEKARWVE	1320
Qy	1321	IKDRQQILMKAEVAQMPAHIDQIMRSGFTWMDIKGLHYEDNQBELPSSKMRLPSRPPR	1380		
Db	1321	IKDRQQILMKAEVAQMPAHIDQIMRSGFTWMDIKGLHYEDNQBELPSSKMRLPSRPPR	1380		
Qy	1381	KGSMTRGVTIQNYNNLQPGVNGMHRSTSEAEAKYDILGAQGLTPDDKDKRGSRPFFKFF	1440		
Db	1381	KGSMTRGVTIQNYNNLQPGVNGMHRSTSEAEAKYDILGAQGLTPDDKDKRGSRPFFKFF	1440		
Qy	1441	RSKRGESSDRAKSRKSTPDPFSDTEVSPERGARRPNQIKVSOANQRYNGMARPSTN	1500		
Db	1441	RSKRGESSDRAKSRKSTPDPFSDTEVSPERGARRPNQIKVSOANQRYNGMARPSTN	1500		
Qy	1501	LYGSQVGLNMATPTQDRKQMTTSTLQAQATETVGNIEIFDAECLKLINIEFYGVRIYQGD	1560		
Db	1501	LYGSQVGLNMATPTQDRKQMTTSTLQAQATETVGNIEIFDAECLKLINIEFYGVRIYQGD	1560		
Qy	1561	PTHYVIGWVTTQYHLHSDKFNQSKVTKSSVITDDYDRVVENVNRQSCYMRADLEYNEV	1620		
Db	1561	PTHYVIGWVTTQYHLHSDKFNQSKVTKSSVITDDYDRVVENVNRQSCYMRADLEYNEV	1620		
Qy	1621	MAEATAKASQGMFTGCSVDSTSGVSPTCSGKOTSFYKMEPETKLPPIAFVEATSKEI	1680		
Db	1621	MAEATAKASQGMFTGCSVDSTSGVSPTCSGKOTSFYKMEPETKLPPIAFVEATSKEI	1680		
Qy	1681	LOIELGRATSILPISAAVLPSDKHVIPOFPRLKVQCLKPHQWARVFNQSLQVHALKLS	1740		
Db	1681	LOIELGRATSILPISAAVLPSDKHVIPOFPRLKVQCLKPHQWARVFNQSLQVHALKLS	1740		
Qy	1741	DIRGSMICEBDAVSMALHIPEEDRCIDILBPIEMDKLLSFHSHTLTILYAALCYQSNYRA	1800		
Db	1741	DIRGSMICEBDAVSMALHIPEEDRCIDILBPIEMDKLLSFHSHTLTILYAALCYQSNYRA	1800		
Qy	1801	AHALCTHVQDKQLLYAIQSYMSGPLRQGFYDILLIALHLESHATTMEACKNEFVIPLGPE	1860		
Db	1801	AHALCTHVQDKQLLYAIQSYMSGPLRQGFYDILLIALHLESHATTMEACKNEFVIPLGPE	1860		
Qy	1861	LKALYEEPDGMGHSLSLOTESVRPOMKMTDIAESITEISNLYSPYFPLEVAREFVMOALA	1920		
Db	1861	LKALYEEPDGMGHSLSLOTESVRPOMKMTDIAESITEISNLYSPYFPLEVAREFVMOALA	1920		
Qy	1921	EAVETNOVHNRDPVGGSNENILPLILKLVDRLLLVGMMDDEVEKLLIMTNPETWDPSPD	1980		
Db	1921	EAVETNOVHNRDPVGGSNENILPLILKLVDRLLLVGMMDDEVEKLLIMTNPETWDPSPD	1980		
Qy	1981	KEGKDEHRKGLLHMKQVAGAKLQMCYLLQHLNDIOLRHRVRAI	IAPAHDFVGDLOTQDLR	2040	
Db	1981	KEGKDEHRKGLLHMKQVAGAKLQMCYLLQHLNDIOLRHRVRAI	IAPAHDFVGDLOTQDLR	2040	
Qy	2041	RYTEIKQSDLPASAAKKTREFCPPREOMNAILSPKHLBEDKENCPCGBELIARMNEF	2100		
Db	2041	RYTEIKQSDLPASAAKKTREFCPPREOMNAILSPKHLBEDKENCPCGBELIARMNEF	2100		
Qy	2101	HDTLMAHVSLLHALQBPDAENQOEPAKPCAFGKLYNIINTVKELBEEAKAIEEPPKKTPE	2160		
Db	2101	HDTLMAHVSLLHALQBPDAENQOEPAKPCAFGKLYNIINTVKELBEEAKAIEEPPKKTPE	2160		
Qy	2161	EKFRKVLQITIYNVAAESQIETPKLVREMFSLLVRYQDAVGELIPALEKTYVINAKTKLD	2220		
Db	2161	EKFRKVLQITIYNVAAESQIETPKLVREMFSLLVRYQDAVGELIPALEKTYVINAKTKLD	2220		
Qy	2221	VAEMWVGLSQIRALLPVQMSQEBEELMRKRLWKLNNHTTFFQHPDLIRLIRLVHENVMAVM	2280		
Db	2221	VAGMWVGLSQIRALLPVQMSQEBEELMRKRLWKLNNHTTFFQHPDLIRLIRLVHENVMAVM	2280		
Qy	2281	MNTLGRRAQQAQSDAQPSSQPVAEADSKEDTSHEMVWVACCRFLCYFCFCTGRQNOKAMPDHF	2340		
Db	2281	MNTLGRRAQQAQSDAQPSSQPVAEADSKEDTSHEMVWVACCRFLCYFCFCTGRQNOKAMPDHF	2340		
Qy	2341	DFLLENSNILLSPRLSGSTPLDVAYSSLMENTELALALREHYLEKIAVLIRLRRPCLGALRGE	2400		
Db	2341	DFLLENSNILLSPRLSGSTPLDVAYSSLMENTELALALREHYLEKIAVLIRLRRPCLGALRGE	2400		
Qy	2401	ELVEKGYDPLGWDPVEGERYLDLFLRCVWNGESVEENANLIVIRLLIRRPCLGALRGE	2460		
Db	2401	ELVEKGYDPLGWDPVEGERYLDLFLRCVWNGESVEENANLIVIRLLIRRPCLGALRGE	2460		
Qy	2461	GEGLLKAIIVDANKMSERIAADRKLREMEQGDVNFHPLPESDEDEYIDTGAAILNFCY	2520		
Db	2461	GEGLLKAIIVDANKMSERIAADRKLREMEQGDVNFHPLPESDEDEYIDTGAAILNFCY	2520		
Qy	2521	TLVDLLGRCAPDAGVIALGKNESLRARAILRSLVPLEDLOGLVLSLRTLNPPAAAGEERP	2580		
Db	2521	TLVDLLGRCAPDAGVIALGKNESLRARAILRSLVPLEDLOGLVLSLRTLNPPAAAGEERP	2580		
Qy	2581	SDMPGSLIPGHKQSVGLFLERVYGIETQELFYKLLEBAFLPDLRAAATMLDRNDGCESDMA	2640		
Db	2581	SDMPGSLIPGHKQSVGLFLERVYGIETQELFYKLLEBAFLPDLRAAATMLDRNDGCESDMA	2640		
Qy	2641	LSMNRYTGNISILPLLIKHAYFYNEAENYASLLDATTHTVYRLSKVRMLTKGOREAVSDFL	2700		
Db	2641	LSMNRYTGNISILPLLIKHAYFYNEAENYASLLDATTHTVYRLSKVRMLTKGOREAVSDFL	2700		
Qy	2701	VALTSAMQPSMLLKLRLKLTVDVSKLSEYTTVALRLTLHYERCAYKYGSTGACQAGFA	2760		
Db	2701	VALTSAMQPSMLLKLRLKLTVDVSKLSEYTTVALRLTLHYERCAYKYGSTGACQAGFA	2760		
Qy	2761	SSDEEKLTMWLFNSIFDLSKMDYEPFLFGKALPCLIAIGCALPPYDYSKNDDEPYG	2820		
Db	2761	SSDEEKLTMWLFNSIFDLSKMDYEPFLFGKALPCLIAIGCALPPYDYSKNDDEPYG	2820		
Qy	2821	KEQAAGDLNDPQYDQPIINTSSVALNNDLNTIVQKFSHYHDHAWASRKIENGWYGEQWS	2880		
Db	2821	KEQAAGDLNDPQYDQPIINTSSVALNNDLNTIVQKFSHYHDHAWASRKIENGWYGEQWS	2880		
Qy	2881	DSQKTHPRLPKYNMNDYKERYKEPVRESILKALLAIGWSVEHSEVDI	PSNNRSMRRQS	2940	
Db	2881	DSQKTHPRLPKYNMNDYKERYKEPVRESILKALLAIGWSVEHSEVDI	PSNNRSMRRQS	2940	
Qy	2941	KSGGRPPEIV--TDSATPFDYNPHVPDMTNTLSREMOMNABERLADNAHDIWAKKKEELV	3000		
Db	2941	KSGGRPPEIV--TDSATPFDYNPHVPDMTNTLSREMOMNABERLADNAHDIWAKKKEELV	3000		
Qy	3000	TNGGGIHPQLVPYDILLTDKEKKKDRERSQBELKYLOQYKYLHRPSKAPQSDTQTTGV	3059		
Db	3001	TNGGGIHPQLVPYDILLTDKEKKKDRERSQBELKYLOQYKYLHRPSKAPQSDTQTTGV	3060		
Qy	3060	AIELRFAYSLEKLIQYIDRATINMKLLKPSSTTFESRSSPKTSTRDIFKFSKAVLPLMEK	3119		
Db	3061	AIELRFAYSLEKLIQYIDRATINMKLLKPSSTTFESRSSPKTSTRDIFKFSKAVLPLMEK	3120		
Qy	3120	YFSTHRNYFIAVATATNNVGAASLKEKEMVAALFCKLASLRLSRLAALFPGDVRITVRCQ	3179		
Db	3121	YFSTHRNYFIAVATATNNVGAASLKEKEMVAALFCKLASLRLSRLAALFPGDVRITVRCQ	3180		
Qy	3180	VLVKGIDAKSLVKQCPERTSMLTFFNNVADDVGHITIMNODGYAHLRGTHLKTSTSL	3239		
Db	3181	VLVKGIDAKSLVKQCPERTSMLTFFNNVADDVGHITIMNODGYAHLRGTHLKTSTSL	3240		
Qy	3240	GYINGVLLPILITAKFDHLANCEYCADLLDDEIQVASYKMLGSLVALGTDAISLTHDRKYLK	3299		
Db	3241	GYINGVLLPILITAKFDHLANCEYCADLLDDEIQVASYKMLGSLVALGTDAISLTHDRKYLK	3300		
Qy	3300	TEIRHHPALGSCGLGAFSSTPPVAFLEPHLNKRNQFSLNRIADHSLEAODIMQMEQCM	3359		

Db 3301 TEIERHPALGSCJGAFSTSPVAFLEPHLNKNQFSLNRIADHSLEAQDIMQMEQCM 3360  
Qy 3360 PTLTETIGEVDQFVESDKTYNEAPHIIDVVLPLLCVLPFWMAQPDNVTPTGNGHVTMV 3419  
Db 3361 PTLTETIGEVDQFVESDKTYNEAPHIIDVVLPLLCVLPFWMAQPDNVTPTGNGHVTMV 3420  
Qy 3420 TAEHNNQLKNVLKIKKIGNENAPWMTRTATYTQOIIINSSEELLRDSFLPLAERVRK 3479  
Db 3421 TAEHNNQLKNVLKIKKIGNENAPWMTRTATYTQOIIINSSEELLRDSFLPLAERVRK 3480  
Qy 3480 RTDNMFKEESLRGFIKSDTDDTQVESQIOEDQOLLVRDIYSYFPLLIKYVDLQRNHWL 3539  
Db 3481 RTDNMFKEESLRGFIKSDTDDTQVESQIOEDQOLLVRDIYSYFPLLIKYVDLQRNHWL 3540  
Qy 3540 RNNVPEAEELYNHVAEIPNIWSKYFLKEQNFISANEIDNMVYLIMPTATRRVTAVTDG 3599  
Db 3541 RNNVPEAEELYNHVAEIPNIWSKYFLKEQNFISANEIDNMVYLIMPTATRRVTAVTDG 3600  
Qy 3600 TPQGGGKKKKHRDKRDKDKEVOASLMVACLKELLVGLNLFAGREQLVQHCKDRP-- 3657  
Db 3601 TPQGGGKKKKHRDKRDKDKEVOASLMVACLKELLVGLNLFAGREQLVQHCKDRFLK 3660  
Qy 3658 ---LKKMSEQDVAEFAKTQLTLPDKIDPADMSMWHYLSKLSKSKSNITVETAENKAK 3714  
Db 3661 VGTLLKKMSEQDVAEFAKTQLTLPDKIDPADMSMWHYLSKLSKSKSNITVETAENKAK 3720  
Qy 3715 IIDTVERIVAMSKVLFGLMHIDHPQMSKNVRSVVSQIKRAVIACFRQTSLSHSLPRH 3774  
Db 3721 IIDTVERIVAMSKVLFGLMHIDHPQMSKNVRSVVSQIKRAVIACFRQTSLSHSLPRH 3780  
Qy 3775 RACHIFARTYVELWLEBENIQOEVIEDLTOSTPEDAELKSDVVEGEKDPDLTQLVTTF 3834  
Db 3781 RACHIFARTYVELWLEBENIQOEVIEDLTOSTPEDAELKSDVVEGEKDPDLTQLVTTF 3840  
Qy 3835 CRGAMTERSGALQBDPLMYSAHIIAKSCGEEBEGGEEBEGGEEBAEDEGRASITHEQ 3894  
Db 3841 CRGAMTERSGALQBDPLMYSAHIIAKSCGEEBEGGEEBEGGEEBAEDEGRASITHEQ 3900  
Qy 3895 EMEKQKLLFHOARLADRGVAEMVLLHISAKGLSPSEMMVMTLQGISILRGNNIDIQMG 3954  
Db 3901 EMEKQKLLFHOARLADRGVAEMVLLHISAKGLSPSEMMVMTLQGISILRGNNIDIQMG 3960  
Qy 3955 LNHLKDKDVGFFTSIAGLMNCSVLDDDAFERNTKAEGLVGLEGAAGEKNMHDAEFTC 4014  
Db 3961 LNHLKDKDVGFFTSIAGLMNCSVLDDDAFERNTKAEGLVGLEGAAGEKNMHDAEFTC 4020  
Qy 4015 ALPRFIQLTCEGHNLDWQNYLRTQAGNTTIVNVVICTVDYLLRLQESIMDFYWHYSKEL 4074  
Db 4021 ALPRFIQLTCEGHNLDWQNYLRTQAGNTTIVNVVICTVDYLLRLQESIMDFYWHYSKEL 4080  
Qy 4075 IDPAGKANFFKAIQVAGSVFNTLFEVIQGPCTQOQALHSRLWDVAGGFLFLPSHMODK 4134  
Db 4081 IDPAGKANFFKAIQVAGSVFNTLFEVIQGPCTQOQALHSRLWDVAGGFLFLPSHMODK 4140  
Qy 4135 LSKUSSQVDDLKELLNLQKDMIPMLSMLEGNVNGTIGQMVDTLVESASNVELLILKYF 4194  
Db 4141 LSKUSSQVDDLKELLNLQKDMIPMLSMLEGNVNGTIGQMVDTLVESASNVELLILKYF 4200  
Qy 4195 DMFLKLKDLTSSASFOEIDANNQDWLPKDPKEKMEQKSYTPPEIEBFLACCTNHDGK 4254  
Db 4201 DMFLKLKDLTSSASFOEIDANNQDWLPKDPKEKMEQKSYTPPEIEBFLACCTNHDGK 4260  
Qy 4255 LDYIGFCDRPHEPAKEIGFNLAVALLTNLSEHMPNEPRLARFLETAGSVLNYFEPFLGRIE 4314  
Db 4261 LDYIGFCDRPHEPAKEIGFNLAVALLTNLSEHMPNEPRLARFLETAGSVLNYFEPFLGRIE 4320  
Qy 4315 IMGSKRIERYVFIKESNITQWEKPKQIKESKRAFFYSIVTEGGDKLEAFVNFCEDAI 4374  
Db 4321 IMGSKRIERYVFIKESNITQWEKPKQIKESKRAFFYSIVTEGGDKLEAFVNFCEDAI 4380  
Qy 4375 FEMTHASGLMAASESVGGTKNREASVYMGDDDDDERAGKDPFRRLGLQSVKDGCVATAFSS 4434

Db 4381 FEMTHASGLMAASESVGGTKNREASVYMGDDDDDERAGKDPFRRLGLQSVKDGCVATAFSS 4440  
Qy 4435 LSPSNTIKAKIADNQMPPAELAVGFFKMPPEYLYGCGVLVVVRVYIFGVLLGLMRGPQT 4494  
Db 4441 LSPSNTIKAKIADNQMPPAELAVGFFKMPPEYLYGCGVLVVVRVYIFGVLLGLMRGPQT 4500  
Qy 4495 DEPPPEPTTEEEKIGQLRHRLLATQSSRHLPALPADDTGOMQVSAFGLDITTKEDNGQIQV 4554  
Db 4501 DEPPPEPTTEEEKIGQLRHRLLATQSSRHLPALPADDTGOMQVSAFGLDITTKEDNGQIQV 4560  
Qy 4555 KPHEPSTSTPSSGEEBAEVSPPDESADHTEBQRPPSLIDLGGEOAKKQAKQERMEAAQAAQ 4614  
Db 4561 KPHEPSTSTPSSGEEBAEVSPPDESADHTEBQRPPSLIDLGGEOAKKQAKQERMEAAQAAQ 4620  
Qy 4615 AANSAIEASKXAVQGPAPALSQVDLSQYTRAVSFLARNFYNLKYVALVLAFICINFVL 4674  
Db 4621 AANSAIEASKXAVQGPAPALSQVDLSQYTRAVSFLARNFYNLKYVALVLAFICINFVL 4680  
Qy 4675 LFYKVSTLDGEGGEGGGLGDI IAGGSGSGAGSGSGSGSGSGEDDDDALEVVHIDEFFY 4734  
Db 4681 LFYKVSTLDGEGGEGGGLGDI IAGGSGSGAGSGSGSGSGSGEDDDDALEVVHIDEFFY 4740  
Qy 4735 MEHVIKMAAVLHSIVSLAILIYGYHLKVPLAIFKREKEIARKLEFFDGLYTAEQPEDDDLK 4794  
Db 4741 MEHVIKMAAVLHSIVSLAILIYGYHLKVPLAIFKREKEIARKLEFFDGLYTAEQPEDDDLK 4800  
Qy 4795 SHWDLKVISAKSPVNVWDKFVKKVKRKYSETYDFDSISNMLGMEKTSFSAQEEEGSKG 4854  
Db 4801 SHWDLKVISAKSPVNVWDKFVKKVKRKYSETYDFDSISNMLGMEKTSFSAQEEEGSKG 4860  
Qy 4855 LIHYIINIDWRYQVWKAGVTITDNSFLYSLSWYFSFVMGNFNNFFFAAHLILDVAVGPKTL 4914  
Db 4861 LIHYIINIDWRYQVWKAGVTITDNSFLYSLSWYFSFVMGNFNNFFFAAHLILDVAVGPKTL 4920  
Qy 4915 RTILQSVTHNGKQLVLTVMLLTIIVYITVIAFNFRKFFYVQBEDDEVNRNCHDMLTCFV 4974  
Db 4921 RTILQSVTHNGKQLVLTVMLLTIIVYITVIAFNFRKFFYVQBEDDEVNRNCHDMLTCFV 4980  
Qy 4975 FNLKYGVRAGGGIGDELEPPDGDSEVYRIIFDISFFFIIVILLATLOGLIIDAFCGLR 5034  
Db 4981 FNLKYGVRAGGGIGDELEPPDGDSEVYRIIFDISFFFIIVILLATLOGLIIDAFCGLR 5040  
Qy 5035 DQLESVKEDMESNCFICGINKDYFDKVPHGFDTHVQREHNLANYMFFLMHLINKPDTTEY 5094  
Db 5041 DQLESVKEDMESNCFICGINKDYFDKVPHGFDTHVQREHNLANYMFFLMHLINKPDTTEY 5100  
Qy 5095 GQSTYVNMNYTORCWDFFPFGVDCFRKQYEDLMGE 5128  
Db 5101 GQSTYVNMNYTORCWDFFPFGVDCFRKQYEDLMGE 5134

## RESULT 3

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; Sequence 144, Application US/10668767  
; Publication No. US20040171114A1  
; GENERAL INFORMATION:  
; APPLICANT: Caspar, Timothy  
; APPLICANT: Cordova, Daniel  
; APPLICANT: Guttridge, Steven  
; APPLICANT: Rauh, James  
; APPLICANT: Smith, Rejane  
; APPLICANT: Tao, Yong  
; APPLICANT: Wu, Lihong  
; TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors  
; FILE REFERENCE: BB1533 US NA  
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; SOFTWARE: Patentin version 3.1

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; LENGTH: 5142									
; TYPE: PRT									
; ORGANISM: Heliothis virescens									
; FEATURE:									
; OTHER INFORMATION: pXL-Hv3									
US-10-668-767-144									
Query Match 99.4%; Score 26644; DB 4; Length 5142;									
Best Local Similarity 99.3%; Pred. No. 0;									
Matches 5107; Conservative 6; Mismatches 15; Indels 14; Gaps 3;									
Qy	1	MAEAGGASEQDDVSLRTEDMVCISCTATGERVCLAAEGFGRHCFLENIAADKNIIPDL	60						
Db	1	MAEAGGASEQDDVSLRTEDMVCISCTATGERVCLAAEGFGRHCFLENIAADKNIIPDL	60						
Qy	61	SOQVFIQALSVRALQELVTAAGSET-----GKGTGSGHRTLLYGNAILRHLSNDWYL	115						
Db	61	SOQVFIQALSVRALQELVTAAGSETGKENGKGTGSGHRTLLYGNAILRHLSNDWYL	120						
Qy	116	ACLSTSSSQDKLAFDVGILQOHSQGEACWMTLHPASKORSEGEKVRVGDDLLILSVATERY	175						
Db	121	ACLSTSSSQDKLAFDVGILQOHSQGEACWMTLHPASKORSEGEKVRVGDDLLILSVATERY	180						
Qy	176	LHTTKENEVSIVNASFHVTHWSVQPYGTGIGSRMKVGVYVFGDVLRFPHGGDECLTIPST	235						
Db	181	LHTTKENEVSIVNASFHVTHWSVQPYGTGIGSRMKVGVYVFGDVLRFPHGGDECLTIPST	240						
Qy	236	WTKGGQNI VVYEGGSVMSQARSWLRLBARTKWAAGFINNYHPMRIRHITGTRYLGVD	295						
Db	241	WTKGGQNI VVYEGGSVMSQARSWLRLBARTKWAAGFINNYHPMRIRHITGTRYLGVD	300						
Qy	296	QNELYLVSREATTASCACFLROEKDQKQVLEKDLKLEVI GAPIIKYGDSTVI VOHSETG	355						
Db	301	QNELYLVSREATTASCACFLROEKDQKQVLEKDLKLEVI GAPIIKYGDSTVI VOHSETG	360						
Qy	356	LWLSKSYETKKGVKVEEKQAILHEBGKMDGLDFRSQEEESRTARVIRKCSSLFTK	415						
Db	361	LWLSKSYETKKGVKVEEKQAILHEBGKMDGLDFRSQEEESRTARVIRKCSSLFTK	420						
Qy	416	FINGLETIQENRRHSMFFASVNLGEMVMCLEDLINYFAQPEDMBHEEKQNKFRALNRQ	475						
Db	421	FINGLETIQENRRHSMFFASVNLGEMVMCLEDLINYFAQPEDMBHEEKQNKFRALNRQ	480						
Qy	476	DLFQEGILNLLLEAIDKINVTISQGLAGFLAGDESGSHWEMISGYLYOLLAALIKGNH	535						
Db	481	DLFQEGILNLLLEAIVKINVTISQGLAGFLAGDESGSHWEMISGYLYOLLAALIKGNH	540						
Qy	536	TNCAQFANSNRLNWLFSRLGSAQSGEGTGMLDVHLHCVLIDSPEALNMMDHEIKVILSL	595						
Db	541	TNCAQFANSNRLNWLFSRLGSAQSGEGTGMLDVHLHCVLIDSPEALNMMDHEIKVILSL	600						
Qy	596	EKHGRDPKVDLVCISLCVGNVAVRSSQNNICDYLLPGKNLLQOTALVDHVSSVRPNIFV	655						
Db	601	EKHGRDPKVDLVCISLCVGNVAVRSSQNNICDYLLPGKNLLQOTALVDHVSSVRPNIFV	660						
Qy	656	GRVEGSAVTRKWKYFEVTMDHIEKTHMPHLRIGHANTTGYVPYGGGKGWGVGDDL	715						
Db	661	GRVEGSAVTRKWKYFEVTMDHIEKTHMPHLRIGHANTTGYVPYGGGKGWGVGDDL	720						
Qy	716	YSYFGDGYLWSGGRTPNVRTHAEPYIRKGDVGICALDLTPVIINFNFNGVRVTGSFT	775						
Db	721	YSYFGDGYLWSGGRTPNVRTHAEPYIRKGDVGICALDLTPVIINFNFNGVRVTGSFT	780						
Qy	776	NFNLEGMFPFVISCSSKLSCRFLGGEHGRRLRYAAPEGYSPLVESILLPQOILSLSPCFYF	835						
Db	781	NFNLEGMFPFVISCSSKLSCRFLGGEHGRRLRYAAPEGYSPLVESILLPQOILSLSPCFYF	840						
Qy	836	GNLSKRALAGPPLVQDDTAFVPTVDTLQITLPTVVEQIRDKLAENIHEMWMANKIEAGW	895						
Db	841	GNLSKRALAGPPLVQDDTAFVPTVDTLQITLPTVVEQIRDKLAENIHEMWMANKIEAGW	900						
Qy	896	MYGDQREDLHKIHPCLVPPERLPPAEKRYDIQLAVQTLKTLILALGYIISIDKPPAIRNV	955						
Db	901	MYGDQREDLHKIHPCLVPPERLPPAEKRYDIQLAVQTLKTLILALGYIISIDKPPAIRNV	960						
Qy	956	RLPNEPFMQSGYKPAPLDLSAVTLTPKMDDELVDQLAENTHNLWARERIQQGWTYGLNED	1015						
Db	961	RLPNEPFMQSGYKPAPLDLSAVTLTPKMDDELVDQLAENTHNLWARERIQQGWTYGLNED	1020						
Qy	1016	SDMHRSPHLYPYPKVDDAIKKANRD TASETVRTLLVYGYMLDPPGTGQHALLLEASKQK	1075						
Db	1021	SDMHRSPHLYPYPKVDDAIKKANRD TASETVRTLLVYGYMLDPPGTGQHALLLEASKQK	1080						
Qy	1076	QADPRTYRAEKNAVSSGKWFPEFEILLTAGPMRVGAHADWAPGMMLGQDENSWAFDGYN	1135						
Db	1081	QADPRTYRAEKNAVSSGKWFPEFEILLTAGPMRVGAHADWAPGMMLGQDENSWAFDGYN	1140						
Qy	1136	BEKYVSGNTSFGKQAVGVDVGVFLDLIDKTIISFSLNGELLMDALGETTFFADVQGDNF	1195						
Db	1141	BEKYVSGNTSFGKQAVGVDVGVFLDLIDKTIISFSLNGELLMDALGETTFFADVQGDNF	1200						
Qy	1196	VPACTLGVGQKARLTYYQDVNTLKYFTTCGLQEGYBFCVNMKRDVTHWYTKDQPIFENT	1255						
Db	1201	VPACTLGVGQKARLTYYQDVNTLKYFTTCGLQEGYBFCVNMKRDVTHWYTKDQPIFENT	1260						
Qy	1256	DEMIDTRIDVTRIPAGSDTTPPCLKISHTPTMEKANWELRLSLPVICHNEFIDEAEKA	1315						
Db	1261	DEMIDTRIDVTRIPAGSDTTPPCLKISHTPTMEKANWELRLSLPVICHNEFIDEAEKA	1320						
Qy	1316	RRWVEIKDROQILMKEAVEAQMPAHIQIMRSFGTMDIKGLHYEDNQEELPSSMKRLP	1375						
Db	1321	RRWVEIKDROQILMKEAVEAQMPAHIQIMRSFGTMDIKGLHYEDNQEELPSSMKRLP	1380						
Qy	1376	SRPPRKSGMTRGVTIIONYNNLQPCQVNGMHRSTSEAEKAYDLGAQGLTPDDKKDKGRS	1435						
Db	1381	SRPPRKSGMTRGVTIIONYNNLQPCQVNGMHRSTSEAEKAYDLGAQGLTPDDKKDKGRS	1440						
Qy	1436	PFKFRKRSGESSDRAKSRKSTPPDPSDTEVSPERGARRNPQIKVSOANQRYNGMAR	1495						
Db	1441	PFKFRKRSGESSDRAKSRKSTPPDPSDTEVSPERGARRNPQIKVSOANQRYNGMAR	1500						
Qy	1496	PSRNLVYGSQVGLN----MATPTQDRKQMTTSTLQAQATETVGNIEIPDAECLKLINEFY	1551						
Db	1501	PSRNLVYGSQVGLNQAQATETVGNIEIPDAECLKLINEFY	1560						
Qy	1552	GVRYPGQDPHTVYIGWVTTQYHLHSDFNQSKVTSVITDDYDRVVENVNQSCYVW	1611						
Db	1561	GVRYPGQDPHTVYIGWVTTQYHLHSDFNQSKVTSVITDDYDRVVENVNQSCYVW	1620						
Qy	1612	RADELYNEVMAEATAKASQGMFICGSVDTSVTSFCEGKDTSFKFMPEPTKLPFAI	1671						
Db	1621	RADELYNEVMAEATAKASQGMFICGSVDTSVTSFCEGKDTSFKFMPEPTKLPFAI	1680						
Qy	1672	FVEATSKELIQLIGRSATSLPSAVALPTSDKHVIPPRLKVCQKLPHQWARVPNQS	1731						
Db	1681	FVEATSKELIQLIGRSATSLPSAVALPTSDKHVIPPRLKVCQKLPHQWARVPNQS	1740						
Qy	1732	LOVHALKLSDIRGSMCLCEDAVSMLALHIPBEDRCIDILEPIEMDKLSFHSHTLTLYAA	1791						
Db	1741	LOVHALKLSDIRGSMCLCEDAVSMLALHIPBEDRCIDILEPIEMDKLSFHSHTLTLYAA	1800						
Qy	1792	LCYQSNYRAAAHALCTHVDQKOLLYAIQSYQMSGPLRQGFYDILLIALHLESHATWEACKN	1851						
Db	1801	LCYQSNYRAAAHALCTHVDQKOLLYAIQSYQMSGPLRQGFYDILLIALHLESHATWEACKN	1860						
Qy	1852	BFVPLGPBELLKALYEEPDMGHSLRSLQTESVVRPOMKMTDIAESITEISNLSPYFPLEVA	1911						
Db	1861	BFVPLGPBELLKALYEEPDMGHSLRSLQTESVVRPOMKMTDIAESITEISNLSPYFPLEVA	1920						
Qy	1912	REFVWQALAEAVETNQVHNRPVGGSNENLFLPLIKLVDRLLLVGMRDEDEVEKLLIMTN	1971						
Db	1921	REFVWQALAEAVETNQVHNRPVGGSNENLFLPLIKLVDRLLLVGMRDEDEVEKLLIMTN	1980						
Qy	1972	PETWDPSFDKGBKDEHRKGLLHMKAEGAKQMCYLLQHLNDIQLRHVRVEAIIAFAHPV	2031						

Db 1981 PETWDPFDKGGKDEHRRKGLLHMKWAGAKLQMCYLLQHLNDIQLRHRVEAIIAFAHDFV 2040  
Qy 2032 GDLOTDLRRYTEIKQSDLPASAAKKTREPRCPREOMNAILSFKHLEBEDKENCPCGE 2091  
Db 2041 GDLOTDLRRYTEIKQSDLPASAAKKTREPRCPREOMNAILSFKHLEBEDKENCPCGE 2100  
Qy 2092 ELIARMNEFHDTLMAHVSLSHALQSPDAENQEPKAPGAFKGLNYIINTVKELBEEAKAI 2151  
Db 2101 ELIARMNEFHDTLMAHVSLSHALQSPDAENQEPKAPGAFKGLNYIINTVKELBEEAKAI 2160  
Qy 2152 EEPKPKTPEEKFRKVLQIOTIYNVMAEESQIETPKLVREMFSLVRQYDAVGELIRALEKTY 2211  
Db 2161 EEPKPKTPEEKFRKVLQIOTIYNVMAEESQIETPKLVREMFSLVRQYDAVGELIRALEKTY 2220  
Qy 2212 VINAKTKLDVAMVMVGLSQIRALLPVQMSQBEELMRKRMLWKLNNHTFFQHPDLIRVLR 2271  
Db 2221 VINAKTKLDVAMVMVGLSQIRALLPVQMSQBEELMRKRMLWKLNNHTFFQHPDLIRVLR 2280  
Qy 2272 VHENVMAVMNMNTLGRRAQAQSDAPSSQOPVAEDSKEDTSHVMVACRFLCYFCRTGRQ 2331  
Db 2281 VHENVMAVMNMNTLGRRAQAQSDAPSSQOPVAEDSKEDTSHVMVACRFLCYFCRTGRQ 2340  
Qy 2332 NOKAMFHFDFLENSNILLRSPSLRGSTPLDVAYSISLMENTELALRHEHYLEKIAVYL 2391  
Db 2341 NOKAMFHFDFLENSNILLRSPSLRGSTPLDVAYSISLMENTELALRHEHYLEKIAVYL 2400  
Qy 2392 SRCGLQNSSELVEKGYPDGLGWDVPEGERYLDFLFCVWVNGESVEENANLIRLIRPE 2451  
Db 2401 SRCGLQNSSELVEKGYPDGLGWDVPEGERYLDFLFCVWVNGESVEENANLIRLIRPE 2460  
Qy 2452 CLGPAALRGEGLLKAIVDANKMSERTADRKLREMEQEGDVNFHPLPESDEDEDYIDT 2511  
Db 2461 CLGPAALRGEGLLKAIVDANKMSERTADRKLREMEQEGDVNFHPLPESDEDEDYIDT 2520  
Qy 2512 GAAILNFYCTLVLDLGRCAPDAGVIALGKNESLRARAILSLVPLEDLQGVLSLRFTLNN 2571  
Db 2521 GAAILNFYCTLVLDLGRCAPDAGVIALGKNESLRARAILSLVPLEDLQGVLSLRFTLNN 2580  
Qy 2572 PAAGEERPKDMPGSLIPGHKQSVGLFLERVYGIETQELFYKLEBEEAFLPDLRAATWMLDR 2631  
Db 2581 PAAGEERPKDMPGSLIPGHKQSVGLFLERVYGIETQELFYKLEBEEAFLPDLRAATWMLDR 2640  
Qy 2632 NDCGESDWMALSMNRYIIGNSILPLIKHAYFYNEAENYASLLDATHVTYRLSKRMMLTKG 2691  
Db 2641 NDCGESDWMALSMNRYIIGNSILPLIKHAYFYNEAENYASLLDATHVTYRLSKRMMLTKG 2700  
Qy 2692 QREAVSDPLVALTSAMQPSMLLKLRKLTVDVSKLSEYTTVALRLLTLHYERCAKYYGST 2751  
Db 2701 QREAVSDPLVALTSAMQPSMLLKLRKLTVDVSKLSEYTTVALRLLTLHYERCAKYYGST 2760  
Qy 2752 GAGQAGFASGSDEEKRLTMMLFSNIFDSLKSMDYEPPELFGKALPCLIAIGCALPPDYSL 2811  
Db 2761 GAGQAGFASGSDEEKRLTMMLFSNIFDSLKSMDYEPPELFGKALPCLIAIGCALPPDYSL 2820  
Qy 2812 KNYDDFVYCKEQAAAGDLNPQYDQPIINTSSVALNDLNTIIVQFSEHYHDAMASRKIEN 2871  
Db 2821 KNYDGEFYCKEQAAAGDLNPQYDQPIINTSSVALNDLNTIIVQFSEHYHDAMASRKIEN 2880  
Qy 2872 GWVYGEHWSDSQKTHPRLLKPNMNLNDYKERYKEPVPRESLKALLAIGWSVEHSDVIPS 2931  
Db 2881 GWVYGEHWSDSQKTHPRLLKPNMNLNDYKERYKEPVPRESLKALLAIGWSVEHSDVIPS 2940  
Qy 2932 NRSSMRQSGSGGRPPEIVTDSATPFDFYNPHFVDMTNTLTLRSREMNMAERLADNAHDIWA 2991  
Db 2941 NRSSMRQSGSGGRPPEIVTDSATPFDFYNPHFVDMTNTLTLRSREMNMAERLADNAHDIWA 3000  
Qy 2992 KKKKEELVTNGGGTHPQLVPYDILLTDKEKKDRERSQEBFLKYLOQYQYKHLRPSKAPQSD 3051  
Db 3001 KKKKEELVTNGGGTHPQLVPYDILLTDKEKKDRERSQEBFLKYLOQYQYKHLRPSKAPQSD 3060  
Qy 3052 TEQTTTGVAIERFAYSILLEKLIQYIDRATINMKLLKPSFTTFSRRSFKTSTRDIKFPFSK 3111  
Db 3061 TEQTTTGVAIERFAYSILLEKLIQYIDRATINMKLLKPSFTTFSRRSFKTSTRDIKFPFSK 3120

Qy 3112 AVLPLAMEKYFSTHRNYFIAVATATNNVGAASLAKEMVAAALFCKLASLRSRLAAFGPDV 3171  
Db 3121 VVLPLAMEKYFSTHRNYFIAVATATNNVGAASLAKEMVAAALFCKLASLRSRLAAFGPDV 3180  
Qy 3172 RITVRCLQVLVKGIDAKSLVKNCPEFIRTSMLTFFNNVADDVGHITMNLQDGKYAHLRGT 3231  
Db 3181 RITVRCLQVLVKGIDAKSLVKNCPEFIRTSMLTFFNNVADDVGHITMNLQDGKYAHLRGT 3240  
Qy 3232 HLKTSLSGLVINGVILLPILTAKPDLHANCYEGADLLDELQVASYKMLGSLYALGTDA 3291  
Db 3241 HLKTSLSGLVINGVILLPILTAKPDLHANCYEGADLLDELQVASYKMLGSLYALGTDA 3300  
Qy 3292 THDRKYLKTEIERHKHALGSCGAFSSTFPVAFLEPHLKNHNOFSLNLRADHSLEAQDI 3351  
Db 3301 THDRKYLKTEIERHKHALGSCGAFSSTFPVAFLEPHLKNHNOFSLNLRADHSLEAQDI 3360  
Qy 3352 MQKMEQCMPTLETILGEVQDFVESDKTYNEAPHIIDVPLPCLLSYLPFWMAQGPNDVTPT 3411  
Db 3361 MQKMEQCMPTLETILGEVQDFVESDKTYNEAPHIIDVPLPCLLSYLPFWMAQGPNDVTPT 3420  
Qy 3412 GGNHVTMTVAEHNQQLLKNVCLKIKNIGNENAPMWTRIATYTTQIIINSSEBLRDSFL 3471  
Db 3421 GGNHVTMTVAEHNQQLLKNVCLKIKNIGNENAPMWTRIATYTTQIIINSSEBLRDSFL 3480  
Qy 3472 PLAERYRKRTDNMFHKEESLRGFIKSTDDTDSQVESQIOEDWOLLVRDIYSFVPLLIKYV 3531  
Db 3481 PLAERYRKRTDNMFHKEESLRGFIKSTDDTDSQVESQIOEDWOLLVRDIYSFVPLLIKYV 3540  
Qy 3532 DLQRNHLRNVPBEALYNHVAEINFNIWSKSYFLKEEQNFISANEIDNMVLIIMPTATR 3591  
Db 3541 DLQRNHLRNVPBEALYNHVAEINFNIWSKSYFLKEEQNFISANEIDNMVLIIMPTATR 3600  
Qy 3592 RVTAVTDGTPQGCGKKKKKXHRDKKDKXEVQASLWVACLRLPLPVGLNLPAGREQBLVQ 3651  
Db 3601 RVTAVTDGTPQGCGKKKKKXHRDKKDKXEVQASLWVACLRLPLPVGLNLPAGREQBLVQ 3660  
Qy 3652 HCKDRF-----LKKMSEQDVAEFAKTQTLTPDKIDPADEMSWOHYLYSKLSGSKSNITV 3706  
Db 3661 HCKDRFLVGTCLKMSEQDVAEFAKTQTLTPDKIDPADEMSWOHYLYSKLSGSKSNITV 3720  
Qy 3707 ETAENKAKIIDDTVERIVAMSKVLFGLMIDHPQOMSKNYRSVSVISQIRKRAVIACPRQT 3766  
Db 3721 ETAENKAKIIDDTVERIVAMSKVLFGLMIDHPQOMSKNYRSVSVISQIRKRAVIACPRQT 3780  
Qy 3767 SLHSLPRHRACNIFARTYYELWLEENIIGQEVMIEDLTQSFEDAECLKSDVVEEGEKPD 3826  
Db 3781 SLHSLPRHRACNIFARTYYELWLEENIIGQEVMIEDLTQSFEDAECLKSDVVEEGEKPD 3840  
Qy 3827 LTOLVTTFCRGAMTERSGALQEDPLVMSVAHIIIAKSCGEEBEGGEGGEGGEGGEGGEGG 3886  
Db 3841 LTOLVTTFCRGAMTERSGALQEDPLVMSVAHIIIAKSCGEEBEGGEGGEGGEGGEGGEGG 3900  
Qy 3887 GRASIIHQEMEKOKLIFHOARLADRGVAEMVLLIHSASKGLPSEMVMKTLQLGSIILRGG 3946  
Db 3901 GRASIIHQEMEKOKLIFHOARLADRGVAEMVLLIHSASKGLPSEMVMKTLQLGSIILRGG 3960  
Qy 3947 NIDIQMGMLNHLKDKXDVGFFTSIAGLMNSCSVLDLDAFERNTKAEGLGVGLSGAAGEKN 4006  
Db 3961 NIDIQMGMLNHLKDKXDVGFFTSIAGLMNSCSVLDLDAFERNTKAEGLGVGLSGAAGEKN 4020  
Qy 4007 MHDAEFTCALFRFIQLTCEGHNDLWQNYLRTQAGNTTNNVITCTVDYLRLQESIMDFY 4066  
Db 4021 MHDAEFTCALFRFIQLTCEGHNDLWQNYLRTQAGNTTNNVITCTVDYLRLQESIMDFY 4080  
Qy 4067 WHYSSKELIDPAGKANFFKAIQVAVSOVFNLTETVIQGPCTQNOQALAHSLRDLAVGGLF 4126  
Db 4081 WHYSSKELIDPAGKANFFKAIQVAVSOVFNLTETVIQGPCTQNOQALAHSLRDLAVGGLF 4140  
Qy 4127 LFSHMQDKLSKHSQVDLLKELLNLQKDMIPMLSMLEGNVNGTIGKQWVDTLVESA 4186  
Db 4141 LFSHMQDKLSKHSQVDLLKELLNLQKDMIPMLSMLEGNVNGTIGKQWVDTLVESA 4200

QY 4187 VELILKYFDMFLKLDLSSASFQIBDANNQWVLPKDFKEMEQKQSYTPEEIEFFLIAC 4246  
Db VELILKYFDMFLKLDLSSASFQIBDANNQWVLPKDFKEMEQKQSYTPEEIEFFLIAC 4260  
QY 4247 CETNHDGKLDYGFCDRPHFAKETGPNLAVLLTNLSEHMPNEPLARFLETAGSVLNYF 4306  
Db CETNHDGKLDYGFCDRPHFAKETGPNLAVLLTNLSEHMPNEPLARFLETAGSVLNYF 4320  
QY 4307 EPFLGRIEIMGSKRIERYVEIKESTNIEQEKPOIKESKKAFFYSIVTEGGDKKLEAF 4366  
Db EPFLGRIEIMGSKRIERYVEIKESTNIEQEKPOIKESKKAFFYSIVTEGGDKKLEAF 4380  
QY 4367 VNFCEDAIFEMTHASGLMAASEESVGGTKNREASYMYGDDDDERAGKDPFRRLGQSVD 4426  
Db VNFCEDAIFEMTHASGLMAASEESVGGTKNREASYMYGDDDDERAGKDPFRRLGQSVD 4440  
QY 4427 GVATAFSSLSPSNIAKADMQMPAPALAVGFQKMPFYLFFYLGYGVLVVRVIFGVLL 4486  
Db GVATAFSSLSPSNIAKADMQMPAPALAVGFQKMPFYLFFYLGYGVLVVRVIFGVLL 4500  
QY 4487 GLMRGPQDEPPPEPEBEKIGQLRHLLATQSSRHLPALPPADDTGOMQVSAGFLDITK 4546  
Db GLMRGPQDEPPPEPEBEKIGQLRHLLATQSSRHLPALPPADDTGOMQVSAGFLDITK 4560  
QY 4547 EDNGQIQVKPHESPSTSPSSGEEAEVSPDESADHTEBQRPSPSLDILLGGEQAKKQAOER 4606  
Db EDNGQIQVKPHESPSTSPSSGEEAEVSPDESADHTEBQRPSPSLDILLGGEQAKKQAOER 4620  
QY 4607 MEAQAAQQAAMSAIEAESKAVQGPAPALSQVLSQVTRRAVSPLARFVNLKVVALVL 4666  
Db MEAQAAQQAAMSAIEAESKAVQGPAPALSQVLSQVTRRAVSPLARFVNLKVVALVL 4680  
QY 4667 AFCINFVLLFYKVTLDGEGGSGGLDIIAGGSGSGAGSGSGSGSGEDDDALEV 4726  
Db AFCINFVLLFYKVTLDGEGGSGGLDIIAGGSGSGAGSGSGSGSGEDDDALEV 4740  
QY 4727 HIDEFFYMEHVIKMAAHLHSIVSLAIIIGYHLKVLPLAIFKREKEIARKLEFDGLYIAE 4786  
Db HIDEFFYMEHVIKMAAHLHSIVSLAIIIGYHLKVLPLAIFKREKEIARKLEFDGLYIAE 4800  
QY 4787 QPEDDDLKSHWDKLVISAKSPFNWYDKFVKKKVRAKYSYTFDPSISNMLGMEKTSFSA 4846  
Db QPEDDDLKSHWDKLVISAKSPFNWYDKFVKKKVRAKYSYTFDPSISNMLGMEKTSFSA 4860  
QY 4847 QEEEGSKGLIHYIINDRYQWKAGVITDINSFLYSLWYSFSGVMGNFNFFFAAHLLD 4906  
Db QEEEGSKGLIHYIINDRYQWKAGVITDINSFLYSLWYSFSGVMGNFNFFFAAHLLD 4920  
QY 4907 VAVGPKTLRTILOQSVTHNGKQLVLTVMLLTIIVYITVIAFNFFKFFVQBEDDEVNRNC 4966  
Db VAVGPKTLRTILOQSVTHNGKQLVLTVMLLTIIVYITVIAFNFFKFFVQBEDDEVNRNC 4980  
QY 4967 HDMLTCFVFNLYKVRAGGIGDELEPPDGDSEVYRIIFDISFFFFIIVILLALOGLI 5026  
Db HDMLTCFVFNLYKVRAGGIGDELEPPDGDSEVYRIIFDISFFFFIIVILLALOGLI 5040  
QY 5027 IDAFGLRLDQLESVKEDMESNCFICGINKDYDPKPHGPDTHVQBEHLNANYMFFLMHLI 5086  
Db IDAFGLRLDQLESVKEDMESNCFICGINKDYDPKPHGPDTHVQBEHLNANYMFFLMHLI 5100  
QY 5087 NKPDTEYTGQETVYVNMVITQRCWDFPFGDCFRKQYEDLMGE 5128  
Db NKPDTEYTGQETVYVNMVITQRCWDFPFGDCFRKQYEDLMGE 5142

RESULT 4

US-10-668-767-146  
; Sequence 146, Application US/10668767  
; Publication No. US2004017114A1  
; GENERAL INFORMATION:  
; APPLICANT: Caspar, Timothy  
; APPLICANT: Cordova, Daniel  
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; APPLICANT: Smith, Rejane  
; APPLICANT: Tao, Yong  
; APPLICANT: Wu, Lihong  
; TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors  
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; CURRENT APPLICATION NUMBER: US/10/668,767  
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; SOFTWARE: PatentIn version 3.1  
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; LENGTH: 5100  
; TYPE: PRT  
; ORGANISM: Heliothis virescens  
; FEATURE:  
; OTHER INFORMATION: pXL-Hv6  
US-10-668-767-146

Query Match 98.9%; Score 26506; DB 4; Length 5100;

Best Local Similarity 99.0%; Pred. No. 0;  
Matches 5082; Conservative 5; Mismatches 8; Indels 38; Gaps 3;

QY 1 MAEAGGASEODDVSFLRTEDMVCLSTCTATGERVCLAAEGFNHCFLENIAADKNIPDDL 60  
Db 1 MAEAGGASEODDVSFLRTEDMVCLSTCTATGERVCLAAEGFNHCFLENIAADKNIPDDL 60  
QY 61 SQCVFVIEQALSVALQELVTAAGSET-----GKGTGSGHRTLLYGNAILLRHLSNDMYL 115  
Db 61 SQCVFVIEQALSVALQELVTAAGSETKENLKGTSGHRTLLYGNAILLRHLSNDMYL 120  
QY 116 ACLSTSSQDKLAFDVGLOHSGQSEACWWTLHPASKORSEGEKVRVGDDLLVSVATERY 175  
Db 121 ACLSTSSQDKLAFDVGLOHSGQSEACWWTLHPASKORSEGEKVRVGDDLLVSVATERY 180  
QY 176 LHHTKENEVSIVNASFHVTHWSVOPYGTGIRSMKYVGVFGDVLRFPHGGDECLTIPST 235  
Db 181 LHHTKENEVSIVNASFHVTHWSVOPYGTGIRSMKYVGVFGDVLRFPHGGDECLTIPST 240  
QY 236 WTKDGGQNI VYVEGGSVMSQARSRLWRLRLARTKWAGGFINWYHPMRIRHITTGRLGVND 295  
Db 241 WTKDGGQNI VYVEGGSVMSQARSRLWRLRLARTKWAGGFINWYHPMRIRHITTGRLGVND 300  
QY 296 QNELYLVSRBATTATACAFCLRQSKDDOKQVLEKDLVIGAPIIKYGDSTVIQHSSETG 355  
Db 301 QNELYLVSRBATTATACAFCLRQSKDDOKQVLEKDLVIGAPIIKYGDSTVIQHSSETG 360  
QY 356 LMLSYKSVETKKGVKVEEKQAILHBEKGMDGLDFSRSQEESRTARVIRKCSSLFTK 415  
Db 361 LMLSYKSVETKKGVKVEEKQAILHBEKGMDGLDFSRSQEESRTARVIRKCSSLFTK 420  
QY 416 FINGLETIQENRRHSMFPFASVNLGEMVNCLEDLINYPADQDEMEHEEKQKFRALNRQ 475  
Db 421 FINGLETIQENRRHSMFPFASVNLGEMVNCLEDLINYPADQDEMEHEEKQKFRALNRQ 480  
QY 476 DLFOEGEILNLIILBAIDKINIVITSGQFLAGLAGESQSWEMISGYLYQLLAAIKGNH 535  
Db 481 DLFOEGEILNLIILBAIDKINIVITSGQFLAGLAGESQSWEMISGYLYQLLAAIKGNH 540  
QY 536 TNCAQAFANSRLNMLFSLGSAQSGEGTGMLDVHLCHVLIDSPALNMNRDEHIKVIISLL 595  
Db 541 TNCAQAFANSRLNMLFSLGSAQSGEGTGMLDVHLCHVLIDSPALNMNRDEHIKVIISLL 600  
QY 596 EKHGRDPKVLVDLCSLCVNGVAVRSSQNNICDYLLPGKNLLQTLVHDVHSSVRPNIFV 655  
Db 601 EKHGRDPKVLVDLCSLCVNGVAVRSSQNNICDYLLPGKNLLQTLVHDVHSSVRPNIFV 660  
QY 656 GRVEGSAVYRKWYFEVMTMDHIETKTHMPHLIRIGWANTGVYPPGGGKGGVGGDDL 715  
Db 661 GRVEGSAVYRKWYFEVMTMDHIETKTHMPHLIRIGWANTGVYPPGGGKGGVGGDDL 720

Qy 716 YSYGFDGAYLWSGGRKTPVNRTHAEBPYIRKGDVIGCALDLTVPIINFMFNGVRVTSFT 775  
Db 721 YSYGLDGAYLWSGGRKTPVNRTHAEBPYIRKGDVIGCALDLTVPIINFMFNGVRVTSFT 780  
Qy 776 NFNLEGMFFPVISSSKSLSCRFPLGGHGRLYAAPGYSPLVESLLPQOILSLPFCFYF 835  
Db 781 NFNLEGMFFPVISSSKSLSCRFPLGGHGRLYAAPGYSPLVESLLPQOILSLPFCFYF 840  
Qy 836 GNLSKRALAGPPLVQDDTAFVPTVDTLQITLPTFYVEIQIRDKLAENIHEMWMNKIEAGW 895  
Db 841 GNLSKRALAGPPLVQDDTAFVPTVDTLQITLPTFYVEIQIRDKLAENIHEMWMNKIEAGW 900  
Qy 896 MYGDQREDLHKIPLCLVPFERLPAPAEKRYDIQLAVQTLKTLIALGYYSISLDKPPARIRNV 955  
Db 901 MYGDQREDLHKIPLCLVPFERLPAPAEKRYDIQLAVQTLKTLIALGYYSISLDKPPARIRNV 960  
Qy 956 RLPNEPFMQSNGYKPAFLDLSAVTLTPKMDELVDOLAEHTNHLWARERIIOGWTYGLNED 1015  
Db 961 RLPNEPFMQSNGYKPAFLDLSAVTLTPKMDELVDOLAEHTNHLWARERIIOGWTYGLNED 1020  
Qy 1016 SDMHSRPHLVPYPKVDDAIKANKRDTASETVRTLTVGYMLDPTTGGHEALLLEASKQK 1075  
Db 1021 SDMHSRPHLVPYPKVDDAIKANKRDTASETVRTLTVGYMLDPTTGGHEALLLEASKQK 1080  
Qy 1076 QADFRTYRAEKNYAVSSGKMYFEFEILITAGPMRVGMAHADMAPGMMLQGDENSWAFDGYN 1135  
Db 1081 QADFRTYRAEKNYAVSSGKMYFEFEILITAGPMRVGMAHADMAPGMMLQGDENSWAFDGYN 1140  
Qy 1136 BEKYVSGNTESFGQWAGVGVFLDLIDKTIISFSLNGELLMALGETTFADVQGDNF 1195  
Db 1141 BEKYVSGNTESFGQWAGVGVFLDLIDKTIISFSLNGELLMALGETTFADVQGDNF 1200  
Qy 1196 VPACTLGVGQKARLTLYGQDVNTLYKFTTCGLQEGYEPEFCVMKRDVTHWTYKQDPIFENT 1255  
Db 1201 VPACTLGVGQKARLTLYGQDVNTLYKFTTCGLQEGYEPEFCVMKRDVTHWTYKQDPIFENT 1260  
Qy 1256 DEMIDTRIDVTRIIPAGSDTPPCLKISHNTPTMEKANWFEURLSLPVICHNEFIDEAEKA 1315  
Db 1261 DEMIDTRIDVTRIIPAGSDTPPCLKISHNTPTMEKANWFEURLSLPVICHNEFIDEAEKA 1320  
Qy 1316 RRWVEIKDRQOILMKEAVEAQAHPAHIDQIMRSGFTMNDIKGLHYEDNQEBELPSSKMRLP 1375  
Db 1321 RRWVEIKDRQOILMKEAVEAQAHPAHIDQIMRSGFTMNDIKGLHYEDNQEBELPSSKMRLP 1380  
Qy 1376 SRPPRKSGMTRGVTIIONYNLQPGQVNGMRHSTSEAEWAKYDLGAQGLTPDDKDKRGRS 1435  
Db 1381 SRPPRKSGMTR-----QOVNGMHRSTSEAEWAKYDLGAQGLTPDDKDKRGRS 1428  
Qy 1436 PFKEFRSKRGESSDRAKSRKSTPDPSDTEVSPERGARRNPQIKVSPANQRYNGMWAR 1495  
Db 1429 PFKEFRSKRGESSDRAKSRKSTPDPSDTEVSPERGARRNPQIKVSPANQRYNGMWAR 1481  
Qy 1496 PSRTNLYGSQVGLMNAPTQDRKQMTTSLAQSATETVGNIEIPAECLKLINEFYGVRI 1555  
Db 1482 -----MATPTQDRKQMTTSLAQSATETVGNIEIPAECLKLINEFYGVRI 1527  
Qy 1556 YPGQDPHTHYIGWTTQVHLHSKDPNOSKVTKSSVITDDYDRVVENNRQSCVMVRADE 1615  
Db 1528 YPGQDPHTHYIGWTTQVHLHSKDPNOSKVTKSSVITDDYDRVVENNRQSCVMVRADE 1587  
Qy 1616 LYNEVMAEATAKGASQGMFICGSVDSTSGSVSFTCEGKDTSFKFKMEPETKLPFAIFVEA 1675  
Db 1588 LYNEVMAEATAKGASQGMFICGSVDSTSGSVSFTCEGKDTSFKFKMEPETKLPFAIFVEA 1647  
Qy 1676 TSKEILQIELGRSATSPLSAVLPTSDKHVIPOPPRPLKVQCLKPHQWARPVNSQLOVH 1735  
Db 1648 TSKEILQIELGRSATSPLSAVLPTSDKHVIPOPPRPLKVQCLKPHQWARPVNSQLOVH 1707  
Qy 1736 AKLSDIRGWSMLCEDAVSMLALHIPEDRCIDILEPTIEMDKLSFHSHTLTLVAALCYQ 1795  
Db 1708 AKLSDIRGWSMLCEDAVSMLALHIPEDRCIDILEPTIEMDKLSFHSHTLTLVAALCYQ 1767

Qy 1796 SNYRAAHALCTHVQDKOLLYAIQOSQYMSGPLRQGFYDLLIALHLESHATTMEACKNEFVI 1855  
Db 1768 SNYRAAHALCTHVQDKOLLYAIQOSQYMSGPLRQGFYDLLIALHLESHATTMEACKNEFVI 1827  
Qy 1856 PLQPELKALYEEBDMGHSLRSLOTESVRPQMKMTDIAESITEISNLYSPYFPLEVAREFV 1915  
Db 1828 PLQPELKALYEEBDMGHSLRSLOTESVRPQMKMTDIAESITEISNLYSPYFPLEVAREFV 1887  
Qy 1916 MQALAEAVETNQVHNRDPVGGSGNENFLPLIKLVDRLLLVGMNRDDEVEKLLIMTNPETW 1975  
Db 1888 MQALAEAVETNQVHNRDPVGGSGNENFLPLIKLVDRLLLVGMNRDDEVEKLLIMTNPETW 1947  
Qy 1976 DPSDFDEGDEHRRKGLLHKMAEGAKLQMCYLLQHLNDIQLRHRVAI IAFADHDFVGDLO 2035  
Db 1948 DPSDFDEGDEHRRKGLLHKMAEGAKLQMCYLLQHLNDIQLRHRVAI IAFADHDFVGDLO 2007  
Qy 2036 TDQLRRYTEIKQSDLPASVAAAKKTRFRCPPRQMNAILSFKHLEEDKENCPCGEBLIA 2095  
Db 2008 TDQLRRYTEIKQSDLPASVAAAKKTRFRCPPRQMNAILSFKHLEEDKENCPCGEBLIA 2067  
Qy 2096 RMNEFHTTLMAHVSLSHALQEPDAAENQEPBAKPGAFGLYNIINTVKELBEEBAKAI BEPP 2155  
Db 2068 RMNEFHTTLMAHVSLSHALQEPDAAENQEPBAKPGAFGLYNIINTVKELBEEBAKAI BEPP 2127  
Qy 2156 KKTPEEKFRKVLQITIVNMAEESQIETPKLVRMFSLVRQYDAVGELIRALEKTYVINA 2215  
Db 2128 KKTPEEKFRKVLQITIVNMAEESQIETPKLVRMFSLVRQYDAVGELIRALEKTYVINA 2187  
Qy 2216 KTKLDVAEMVMVGLSQRALLPVQMSQEBEELMRKMLKVLNNHTFFQHPDLIRVLRVHEN 2275  
Db 2188 KTKLDVAEMVMVGLSQRALLPVQMSQEBEELMRKMLKVLNNHTFFQHPDLIRVLRVHEN 2247  
Qy 2276 VMAVMNMTLGRRAQAQSDAQSPQVAEDSKEDTSHEMVVAACRFICYPCRTGRQNOKA 2335  
Db 2248 VMAVMNMTLGRRAQAQSDAQSPQVAEDSKEDTSHEMVVAACRFICYPCRTGRQNOKA 2307  
Qy 2336 MPDHPDPLLENSNILLSRPSLRGSTPLDVAYSSIMMENTELALAREHLYBKIAVYLSRCG 2395  
Db 2308 MPDHPDPLLENSNILLSRPSLRGSTPLDVAYSSIMMENTELALAREHLYBKIAVYLSRCG 2367  
Qy 2396 LQNSSELVEKGYDGLGWDPEGERYLDFLRFVVMNGESVEENANLVRILLIRREPECLGP 2455  
Db 2368 LQNSSELVEKGYDGLGWDPEGERYLDFLRFVVMNGESVEENANLVRILLIRREPECLGP 2427  
Qy 2456 ALRGEGBGLLKATVDANKMSERIADRRKUREMOBQGVNPSHPLPESDEDEDYDTGAAI 2515  
Db 2428 ALRGEGBGLLKATVDANKMSERIADRRKUREMOBQGVNPSHPLPESDEDEDYDTGAAI 2487  
Qy 2516 LNFYCTLVDLGRCAPDAGVIALGKNESLRARAILRSLVPLEDLOGLVLSLRFTLNPAAG 2575  
Db 2488 LNFYCTLVDLGRCAPDAGVIALGKNESLRARAILRSLVPLEDLOGLVLSLRFTLNPAAG 2547  
Qy 2576 EERPCKSDMPGSLIPGHKQSVGLFERYGIEETOELFYKLEEAFLPDLRAATMLDRNDGC 2635  
Db 2548 EERPCKSDMPGSLIPGHKQSVGLFERYGIEETOELFYKLEEAFLPDLRAATMLDRNDGC 2607  
Qy 2636 ESDWALSMNRYIGNSILPLLIKHAYFYNEAENYASLLDATLHTVYRLSKNRMLTKGOREA 2695  
Db 2608 ESDWALSMNRYIGNSILPLLIKHAYFYNEAENYASLLDATLHTVYRLSKNRMLTKGOREA 2667  
Qy 2696 VSDFLVALTSAMQPSMLLKLRLKLTVDVSKLSEVTTVALRLLTLHYERCAKYGSTCAGO 2755  
Db 2668 VSDFLVALTSAMQPSMLLKLRLKLTVDVSKLSEVTTVALRLLTLHYERCAKYGSTCAGO 2727  
Qy 2756 GAFGASSDEBKRLTMMLFNSIFDSLKMDYEPFLFGKALPCLIAIGCALPPDYSLSKNYD 2815  
Db 2728 GAFGASSDEBKRLTMMLFNSIFDSLKMDYEPFLFGKALPCLIAIGCALPPDYSLSKNYD 2787  
Qy 2816 DEFYKGQAAAGDLNPOYDQPPINTSSVALNNDLNTIVQKFSFSEHYHDAMASRKIENGWY 2875  
Db 2788 DEFYKGQAAAGDLNPOYDQPPINTSSVALNNDLNTIVQKFSFSEHYHDAMASRKIENGWY 2847  
Qy 2876 GEGWSUSQKTHPRLKPNYMLNDYKERYKEPVRRESLKALLAIGWSVEHSEVDIPSNRRSS 2935



Db 2848 GEGWSDSQKTHPRLKPYNNLNDYEKERYKEPVRESLKALLAIGVSEHSEVDIPSNNRSS 2907  
Qy 2936 MRRQSKSGRPEIIVTDSATFDPYNPHVDVMTNLTLSREMQMAERLADNAHD1WAKKK 2995  
Db 2908 MRRQSKSGRPEIIVTDSATFPNYPHPVDVMTNLTLSREMQMAERLADNAHD1WAKKK 2967  
Qy 2996 EELVTNGGCIHPQLVPYDILLTDKEKKDRERSQEFKYLQYQGKYLHRPSKAPQSDTEQT 3055  
Db 2968 EELVTNGGCIHPQLVPYDILLTDKEKKDRERSQEFKYLQYQGKYLHRPSKAPQSDTEQT 3027  
Qy 3056 TTGVAIELRFPAYSLEKLIQVIDRATINMKLLKPSSTFRRSSPKTSTRDIKFFSKAVLP 3115  
Db 3028 TTGVAIELRFPAYSLEKLIQVIDRATINMKLLKPSSTFRRSSPKTSTRDIKFFSKVLP 3087  
Qy 3116 LMEKYFSTRNYFIAVATATNNVGAASLKEKEMVAALFCKLASLLRSLAFAFGPDVRTV 3175  
Db 3088 LMEKYFSTRNYFIAVATATNNVGAASLKEKEMVAALFCKLASLLRSLAFAFGPDVRTV 3147  
Qy 3176 RCLQVLKVIDAKSLVKNCPEFIRTSMLTFFNNVADDVGHTIMNLQDGKYAHLRGTHLKT 3235  
Db 3148 RCLQVLKVIDAKSLVKNCPEFIRTSMLTFFNNVADDVGHTIMNLQDGKYAHLRGTHLKT 3207  
Qy 3236 STSLGYINGVLLPILITAKFDHLANCEYGADLLLDIEIQVASYKMLGSLVALGTDAASLTHDR 3295  
Db 3208 STSLGYINGVLLPILITAKFDHLANCEYGADLLLDIEIQVASYKMLGSLVALGTDAASLTHDR 3267  
Qy 3296 KYLKTEIERHPKALGSCLGAFSSPPVAFLEPHLNKHNQFSLNRIADHSLEBAQDIOQM 3355  
Db 3268 KYLKTEIERHPKALGSCLGAFSSPPVAFLEPHLNKHNQFSLNRIADHSLEBAQDIOQM 3327  
Qy 3356 EQCMPTLETILGEVDQFVESDKTYNEAPHIIDVLPPLCSVLPFWMAOGPDNVTPTGNH 3415  
Db 3328 EQCMPTLETILGEVDQFVESDKTYNEAPHIIDVLPPLCSVLPFWMAOGPDNVTPTGNH 3387  
Qy 3416 VTMVTAEHMQLKNVLLKIKKIGNENAPWMTRIATYTOQIIINSSEELRDSFPLPAE 3475  
Db 3388 VTMVTAEHMQLKNVLLKIKKIGNENAPWMTRIATYTOQIIINSSEELRDSFPLPAE 3447  
Qy 3476 RVRKRTDNMFKEESLRGFIKSTDDTSQVRSQIOEDWQLLVRIYSPYLLIKYVDLQR 3535  
Db 3448 RVRKRTDNMFKEESLRGFIKSTDDTSQVRSQIOEDWQLLVRIYSPYLLIKYVDLQR 3507  
Qy 3536 NHWLRNNVPEABELNHNVAEIPNIWSKOYFLKEQNFISANEIDNMVLIIMPTATRRVTA 3595  
Db 3508 NHWLRNNVPEABELNHNVAEIPNIWSKOYFLKEQNFISANEIDNMVLIIMPTATRRVTA 3567  
Qy 3596 VTDGTPQGGKKKKHDKRDKDKEVQASLMVACLKRLLPVGLNLFAGREQELVQHCKD 3655  
Db 3568 VTDGTPQGGKKKKHDKRDKDKEVQASLMVACLKRLLPVGLNLFAGREQELVQHCKD 3627  
Qy 3656 RFLKMSQSDVAEFAKTQTLTDPDKIDPADENSWOHLYSKLGSKSKSNIITVETAENKAKI 3715  
Db 3628 RFLKMSQSDVAEFAKTQTLTDPDKIDPADENSWOHLYSKLGSKSKSNIITVETAENKAKI 3687  
Qy 3716 IDDTVERIVAMSKVLPGLHMDHPQMSKNVRSVVSIOQRKAVTACFROTSLHSLPRHR 3775  
Db 3688 IDDTVERIVAMSKVLPGLHMDHPQMSKNVRSVVSIOQRKAVTACFROTSLHSLPRHR 3747  
Qy 3776 ACNIFARTYELWLBEENIGQWMLIEDLTQSPEDAELKSDVVEGEKPDPLTQLVTTFFC 3835  
Db 3748 ACNIFARTYELWLBEENIGQWMLIEDLTQSPEDAELKSDVVEGEKPDPLTQLVTTFFC 3807  
Qy 3836 RGAMTERSGALQEDPLYMSYAHIIAKSCGEEBEGGEEGGGABAEDEGRASIHQOE 3895  
Db 3808 RGAMTERSGALQEDPLYMSYAHIIAKSCGEEBEGGEEGGGABAEDEGRASIHQOE 3867  
Qy 3896 MEKQKLLFHOARLARGVAEMVLLHISASKGIPSEMWKTLQGLSILRGGNIDIQMGWL 3955  
Db 3868 MEKQKLLFHOARLARGVAEMVLLHISASKGIPSEMWKTLQGLSILRGGNIDIQMGWL 3927  
Qy 3956 NHLKDKKDVGFFTSIAGLMNCSVLDDAFERNTKAEGLVGLEGAAGEKNMHDAEFTCA 4015

Db 3928 NHLKDKKDVGFFTSIAGLMNCSVLDDAFERNTKAEGLVGLEGAAGEKNMHDAEFTCA 3987  
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Qy 4136 SKISSQVDDLKELLNLQKDMI PWMLSMLEGNVNGTIGKQWVDTLVESASNVLELILKYFD 4195  
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Qy 4196 MFLKLDLTSSASFOEIDANNMGVLPKDPKEKMEQKSYTPEIEBIFLLACCETHHDGKL 4255  
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Qy 4256 DYIGFCDRFHEPAKEIGFNLAVALLTNLSEHMPNEPRLARFLETAGSVLNTPEPFLGRIEI 4315  
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Qy 4316 MGSKRTERVYFEIKESNIEQWEKPOIKESKRAFFYSIVTEGGDKEXLEAFVNFCEDAIF 4375  
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Qy 4376 EMTHASGLMAASEBSVGCTKNREASYMYMGDDDDERAGKOPFRRLGLOSKVGATAFSSL 4435  
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Qy 4436 SPSNIKAKIADMQOMPAPLAELAVGFFKMFYLYLYGYGVLVVRYIIFGVLLGLMRGPOTD 4495  
Db 4408 SPSNIKAKIADMQOMPAPLAELAVGFFKMFYLYLYGYGVLVVRYIIFGVLLGLMRGPOTD 4467  
Qy 4496 EPPPEPTEEBEKIGOLRHLLATQSSRHLPALPPADDTGOMQVSAFGDITKEDNGQIOVK 4555  
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Qy 4616 AMSAIEAESKKAQVGPAPSALSQVDLSQYTRRAVSFLARNFYNLKYVALVLAFCINFVLL 4675  
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Db 4708 EHVIKMAAVLHSIVSLATILIGYHLKVPLAIFKREKEIARKLEPDGLYIAEQPEDDDLLKS 4767  
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Qy 4856 IHYIINIDWRVQVWKAGVTITDNSFLYSWTFSVSMGNFNFPFAAHLLDVAVGFKTLR 4915  
Db 4828 IHYIINIDWRVQVWKAGVTITDNSFLYSWTFSVSMGNFNFPFAAHLLDVAVGFKTLR 4887  
Qy 4916 TILOSVTHNGKQLVLTWMLLTIIIVYITVIAFNFRKFPYVOEEDDEVNRNCHMDLTCFVF 4975  
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RESULT 5

US-10-668-767-2  
; Sequence 2, Application US/10668767  
; Publication No. US20040171114A1  
; GENERAL INFORMATION:  
; APPLICANT: Caspar, Timothy  
; APPLICANT: Cordova, Daniel  
; APPLICANT: Gutteridge, Steven  
; APPLICANT: Rauh, James  
; APPLICANT: Smith, Rejane  
; APPLICANT: Tao, Yong  
; APPLICANT: Wu, Lihong  
; TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors  
; FILE REFERENCE: BBI533 US NA  
; CURRENT APPLICATION NUMBER: US/10/668.767  
; CURRENT FILING DATE: 2003-09-23  
; PRIOR APPLICATION NUMBER: 60/412,795  
; PRIOR FILING DATE: 2002-09-23  
; PRIOR APPLICATION NUMBER: 60/427,324  
; PRIOR FILING DATE: 2002-11-18  
; NUMBER OF SEQ ID NOS: 149  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 5142  
; TYPE: PRT  
; ORGANISM: Heliothis virescens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1755)..(1755)  
; OTHER INFORMATION: Xaa = Ser  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (4250)..(4250)  
; OTHER INFORMATION: Xaa = Thr  
US-10-668-767-2

Query Match 98.8%; Score 26469; DB 4; Length 5142;  
Best Local Similarity 98.7%; Pred. No. 0;  
Matches 5074; Conservative 18; Mismatches 36; Indels 14; Gaps 3;  
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Db 1 MAEAGGASEDDVSILRTEDMVCISCTATGERVCLAAEGGLGRHCFLENADKNIPDL 60  
Qy 61 SQCVFVIEQALSVRALQELVTAAGSET-----GKGTGSGHRTLTYGNAILLRHLNSDMYL 115  
Db 61 SQCVFVIEQALSVRALQELVTAAGSETGKENGKGTSGGYRTLTYGNAILLRHLNSDMYL 120  
Qy 116 ACLTSSSQDKLAFDVLGLOQHSQGEACWWTLHPASQORSEGEKVRVGGDLILSVATERY 175  
Db 121 ACLTSSSQDKLAFDVLGLOQHSQGEACWWTLHPASQORSEGEKVRVGGDLILSVATERY 180  
Qy 176 LHTTKENEVSIVNASFVHTWSVOPYGTGIRMKYGVVFGGDVLRFPFHGGDECLTIPST 235  
Db 181 LHTTKENEVSIVNASFVHTWSVOPYGTGIRMKYGVVFGGDVLRFPFHGGDECLTIPST 240  
Qy 236 WTKDGGQNI VYVEGGSVMSQARSRLRLRLATKWKAGGFINWYHPMRIRHITTGRLYGND 295  
Db 241 WTKDGGQNI VYKGSVMSQARSRLRLRLATKWKAGGFINWYHPMRIRHITTGRLYGND 300  
Qy 296 QNELYLVSREBATTASCAFLRQEKDQKQVLEBKDLEVI GAPIIKYGDSTVI VQHSETG 355  
Db 301 QNELYLVSREBPTTASCAFLRQEKDQKQVLEBKDLEVI GAPIIKYGDSTVI VQHSETG 360  
Qy 356 LWLSYKSYETKKGVKVEEQAILHBECKMDDGLDFRSQEEBSRTARVIRKCSSLFTK 415  
Db 361 LWLSYKSYETKKGVKVEEQAILHBECKMDDGLDLRSQEEBSMTARVIRKCSSLFTK 420

Qy 416 FINGLETLOENRRHSMPFASVNLGEMVMCLIEDLINYPAQDDEMEHEEKONKFRALNRQ 475  
Db 421 FINGLETLOENRRHSMPFASVNLGEMVMCLIEDLTNYPAQDDEMEHEEKONKFRALNRQ 480  
Qy 476 DLFOEBGILNLILEADKINVITSQGFAGFLAGDESQGSWEMISGYLYQLLAAIKGNH 535  
Db 481 DLFOEBGILNLILEADKINVITSQGFAGFLAGDESQGSWEMISGYLYQLLAAIKGNH 540  
Qy 536 TNCAQFANSNRLNWLFSRLGSQASGEGTGMLDVLHCVLIDSPEALNMRRDEHIKVIISLL 595  
Db 541 TNCAQFANSNRFNLFSRLGSQASGEGTGMLDVLHCVLIDSPEALNMRRDEHIKVIISLL 600  
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Db 601 EKGRDPKVL DVLCSLCVGNVAVRSQNNICDYLPGKNLILQ TALVDHVSVRPNI FV 660  
Qy 656 GRVEGSAVYRKWYFEVTMDHIEKTHMPHLRIGWANTTGYVPYGGGCKWGGNGVGGDL 715  
Db 661 GRVEGSAVYRKWYFEVTMDHIEKTHMPHLRIGWANTTGYVPYGGGCKWGGNGVGGDL 720  
Qy 716 YSYGFDGAYLWSGGRKTPVNRTHAEPYIRKGDVIGCALDLTVPIINFMFNGVRVTSFT 775  
Db 721 YSYGFDGAYLWSGGRKTPVNRTHAEPYIRKGDVIGCALDLTVPIINFMFNGVRVTSFT 780  
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Db 781 NFNLEGMFPFVISCSSKLSRFLGGEHGLRYAAPEGYSPLVESLLPQOILSLEPCFYF 840  
Qy 836 GNLKRALAGPPLVQDDTAFVPTPVDLTQITLTYVEQIRDKLAENIHEMWNMKIEAGW 895  
Db 841 GNLKRALAGPPLVQDDTAFVPTPVDLTQITLTYVEQIRDKLAENIHEMWNMKIEAGW 900  
Qy 896 MYGDQREDLHKIHPCLVPPFERLPPAEKRYDIO LAVOTLKITLALGYVISLDKPPARINV 955  
Db 901 MYGDQREDLHKIHPCLVPPFERLPPAEKRYDIO LAVOTLKITLALGYVISLDKPPARINV 960  
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Db 1081 QADFRTYRAEKNYAVSSGKWYFEFEILLTAGPMRVGWAHADMAFGMMLGQDENSWAFPGYN 1140  
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Db 1321 RRWVEIKDRQOILMKEAVEAQMPAHIDQIMRSFTWMDIKGLHYEDNQEBLPSSMKRLP 1380  
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Qy 1436 PFKFRSKRGESSDRAKSRKSTPDPSPDTEVSPERGARPNIQIVKVSQANQRVNGNAR 1495  
Db 1441 PFKFRSKRGESSDRAKSRKSTPDPSPDTEVSPERGARPNIQIVKVSQANQRVNGNAR 1500



1496 PSRTNLYGSQVGLN----MATPTQDRKQMTTSTLAQSAATETVGNIEFPAECLKLINEFY 1551  
1501 PSRTNLYGSQVGLNSNAQWATPTQDRKQMTTSTLAQSAATETVGNIEFPAECLKLINEFY 1560  
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1561 GVR IYPGQDPHVIYIGWTTQYHLHSKDPNOSKVTKSSVITDDYDRVVENVNRQSCVMV 1620  
1612 RADELYNEWMAEATAKAGSQGMFICGSVDYTGVSFTCEGKDTSFKEKMBETKLPFAI 1671  
1621 RADELYNEWMAEATAKAGSQGMFICGSVDYTGVSFTCEGKDTSFKEKMBETKLPFAI 1680  
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1681 SVEATSKELIQELGRSATSPLSAVLPTSDKHVIPPRLKVCQKLPHQWARVPNQS 1740  
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1741 LQVHALKSGIRGWSMLCEDAVSMALHIPEEDRCIDILEPIEMDKLLSFHSHITLYAA 1800  
1792 LCYQSNYRAAHALCTHVQKOLLYAIQSYMSGPLRQGFYDLIALHLESHATTMEACKN 1851  
1801 LCYQSNYRAAHALCASHADOKOLLYAIQSYMSGPLRQGFYDLIALHLESHATTMEACKN 1860  
1852 EFVIFLGPPELKALYEEDPDGHSLSRLQTESVPRQPMKMTDIAESITEISNLYSPYPLEVA 1911  
1861 EFVIFLGPPELKALYEEDPDGHSLSRLQTESVPRQPMKMTDIAESITEISNLYSPYPLEVV 1920  
1912 REFVMOALAEAVETNVQHNDRPVGGSNENLFLPLIKLVDRLLVGMWDEDEVEKLLIMTN 1971  
1921 REFVMOALAEAVETNVQHNDRPVGGSNENLFLPLIKLVDRLLVGMWDEDEVEKLLIMTN 1980  
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2281 VHENVMAVMNMTLGRRAQAQSDAQSSQPVASDNKEKDTSHEMVACCRFLCYFCRTGRQ 2340  
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2701 QREAVSDFLVALTSAMQPSMLLKLRLKTVDVSKLSYTTVALRLLTLHYBRCAKYGST 2760  
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2872 GWYTGEGWSDSQKTHPRLPKYNMMLNDYKERYKEPVRESLKALLAIGWSVEHSEVDIPSN 2931  
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2932 NRSSMRQSKSGRPPPEIVTDSATPPDYNPHVPDNTMLTSLREMNMAERLADNAHDIA 2991  
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3472 PLABRVRKRTDNMFHKEESLGRGFIKSSTDDTSQVESQIOEDWQLLVROIYFYPLLIKYV 3531  
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3532 DLQRNHWLRNNVPEABELYNHVAEIFNIWSKQYFLKEEQNFISANEIDNMVLIIMPATR 3591  
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Qy 4067 WHYSKELIDPAGKANPFKATGVASQVNTLTETVIOGPCTOQOALAHSLRWDVAGGFLF 4126  
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Qy 4247 CETNHDGKLDYIGCDRPHPEPAKEIGFNVLAVLLTNLSHMNPNRPLARFLETAGSVLYNF 4306  
Db 4261 CETNHDGKLDYIGCDRPHPEPAKEIGFNVLAVLLTNLSHMNPNRPLARFLETAGSVLYNF 4320  
Qy 4307 EPPFLGRIBMGSKRIERYVEIEKESNIEQWEKQIKESKRAFFYSIVTEGGDKLEAF 4366  
Db 4321 EPPFLGRIBMGSKRIERYVEIEKESNIEQWEKQIKESKRAFFYSIVTEGGDKLEAF 4380  
Qy 4367 VNFCEDAIFEMTHASGLMAASEESVGGTKNREASVYMGDDDDBRAGKDPFRRLQSVKD 4426  
Db 4381 VNFCEDAIFEMTHASGLMAASEESVGGTKNREASVYMGDDDBRAGKDPFRRLQSVKD 4440  
Qy 4427 GVATAFSSLSPSNIAKADIADQMPAPBLAVGPFKMPFYLPIYLYGYGLVWVRYIFGVLL 4486  
Db 4441 GVATAFSSLSPSNIAKADIADQMPAPBLAVGPFKMPFYPPIYLYGYGLVWVRYIFGVLL 4500  
Qy 4487 GLMRGPOTDEPPPEEIEKIGQLRHRLATQSSRHLPALPADDTGQMVSAGFLDITK 4546  
Db 4501 GLMRGPOTDEPPPEEIEKIGQLRHRLATQSSRHLPALPADDTGQMVSAGFLDITK 4560  
Qy 4547 EDNGQIQVKPHESPSTSPSSGGEAEVSPDSADHTEQRPSPSIDLLIGGEQAQKQOER 4606  
Db 4561 EDNGQIQVKPHESPSTSPSSGGEAEVSPDSADHTEQRPSPSIDLLIGGEQAQKQOER 4620  
Qy 4607 MEAQAAQAAVSAIEAESKAVQGPAPSAQSQVDSLQYTRRAVSFLARNFNLYKVALVL 4666  
Db 4621 MEAQAAQAAVSAIEAESKAVQGPAPSAQSQVDSLQYTRRAVSFLARNFNLYKVALVL 4680  
Qy 4667 AFCINFVLLFYKYSTLDGEGGSGGLDIIAGGSGGAGSGSGDGGESGEDDALEVV 4726  
Db 4681 AFCINFVLLFYKYSTLDGEGGSGGLDIIAGGSGGAGSGSGDGGESGEDDALEVV 4740  
Qy 4727 HIDEFFYMEHVIKMAAVLHISVLSAILIYGYHLKVPLAIFKREKEIARKLEFDGLYIAE 4786  
Db 4741 HIDEFFYMEHVIKMAAVLHISVLSAILIYGYHLKVPLAIFKREKEIARKLEFDGLYIAE 4800

Qy 4787 QPEDDDDLKSHWDKLVISAKSFPVNYWDKFVKKVKRAKYSYTDYDFDSISNMLGMEKTSFSA 4846  
Db 4801 QPEDDDDLKSHWDKLVISAKSFPVNYWDKFVKKVKRAKYSYTDYDFDSISNMLGMEKTSFSA 4860  
Qy 4847 QEESGSKGLHYIINIDRWYQVWKAGVTITDNSFLYSLSLWYFSVMGNFNPNFFFAAHLDD 4906  
Db 4861 QEESGSKGLHYIINIDRWYQVWKAGVTITDNSFLYSLSLWYFSVMGNFNPNFFFAAHLDD 4920  
Qy 4907 VAVGFKTLRTILQSVTHNGKQLVLTVMLLTIIUYIYTVIAFNPRKPYVQEEDEVNRNC 4966  
Db 4921 VAVGFKTLRTILQSVTHNGKQLVLTVMLLTIIUYIYTVIAFNPRKPYVQEEDEVNRNC 4980  
Qy 4967 HDMLTCFVFNLYKVGKAGGIGDELBPDDGDSSEVYRIIFDISFFFFIIIVILLAILQGLI 5026  
Db 4981 HDMLTCFVFNLYKVGKAGGIGDELBPDDGDSSEVYRIIFDISFFFFIIIVILLAILQGLI 5040  
Qy 5027 IDAFBELRDQLESVKEDMESNCFICGINKDYFDKVPHPGFDTHVQREHNLANYNMFFLMHLI 5086  
Db 5041 IDAFBELRDQLESVKEDMESNCFICGINKDYFDKVPHPGFDTHVQREHNLANYNMFFLMHLI 5100  
Qy 5087 NKPDTEYTGQETTVNNMYTORCWDFFPVGDCFRKQYEDLMGE 5128  
Db 5101 NKPDTEYTGQETTVNNMYTORCWDFFPVGDCFRKQYEDLMGE 5142

RESULT 6  
US-10-668-767-8  
; Sequence 8, Application US/10668767  
; Publication No. US20040171114A1  
; GENERAL INFORMATION:  
; APPLICANT: Caspar, Timothy  
; APPLICANT: Cordova, Daniel  
; APPLICANT: Gutteridge, Steven  
; APPLICANT: Rauh, James  
; APPLICANT: Smith, Rejane  
; APPLICANT: Tao, Yong  
; APPLICANT: Wu, Lihong  
; TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors  
; FILE REFERENCE: BB1533 US NA  
; CURRENT APPLICATION NUMBER: US/10/668,767  
; CURRENT FILING DATE: 2003-09-23  
; PRIOR APPLICATION NUMBER: 60/412,795  
; PRIOR FILING DATE: 2002-09-23  
; PRIOR APPLICATION NUMBER: 60/427,324  
; PRIOR FILING DATE: 2002-11-18  
; NUMBER OF SEQ ID NOS: 149  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 8  
; LENGTH: 5127  
; TYPE: PRT  
; ORGANISM: Peregrinus maidis  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (416)..(416)  
; OTHER INFORMATION: Xaa = Ile  
US-10-668-767-8

Query Match 80.7%; Score 21630; DB 4; Length 5127;  
Best Local Similarity 80.3%; Pred. No. 0;  
Matches 4174; Conservative 396; Mismatches 484; Indels 142; Gaps 46;

Qy 1 MAEAGGASQDDVSEFLRTEDMVCLSCTATGERVCLAAEGFGRHCFLENIAADKNIPDDL 60  
Db 1 MADSEGG-SEQDDVSEFLRTEDMVCLSCTATGERVCLAAEGFGRHCFLENIAADKNIPDDL 59  
Qy 61 SQCVFVIEQALSVRALQELVTAAGSETGKGTGSHRTRLLYCNAILLRHLNSDMYLACLS 120  
Db 60 STCVFVIEQALSVRALQELVTAAGSEEGKGTGSHRTRLLYGNAILLRHNSDMYLACSS 119  
Qy 121 SSSQDLAFDVGLOQHSQSGACWMTLHPASKQSEGEKVRGDDLLILSVATERYLHTTK 180  
Db 120 SSSNDKLSFDVGLQEHSGQACWMTVHPASKQSEGEKVRGDDLLILSVATERYLHTTK 179



Db 2309 HEMWACCRLVCPCRTSRQKAMFHPAFLLENSNILSRSLRGSTPDLVAYSIME 2368  
Qy 2372 NTELALALRHYLEKIAVYLSRCGLQNSBLVEKGYDPLGWDVPVEGRYDLFLRFCVWVN 2431  
Db 2369 NTELALALRHYLEKIAIYLSRCGLQNSBLIEKGYDPLGWDVPVEGRYDLFLRFCVWVN 2428  
Qy 2432 GESVEENANLIRILLIRPECLGPALRGEBGLLKAIVDANKMSERTADRRKLREMEQBG 2491  
Db 2429 GESVEENANLIRILLIRPPCLGPALRGEBGLLRAIVDANKMSERTADRRKVMDE-EPEG 2487  
Qy 2492 D---VNFESHPLPESEDDEYDITGAAILNFYCTLVLDLILGRCAPDAGVIALGKQESLRARA 2548  
Db 2488 TTVMWHFEHPLPESEDDEYDITGAAILAFYCTLVLDLILGRCAPDSVSIAGKQESLRARA 2547  
Qy 2549 ILRSLVPLEDLQGVLSLRFTLNNPAAGEERPKSDMPGSLIPGHKQSVGLFLERYGIETQ 2608  
Db 2548 ILRSLVPLEDLQGVLSLKFTLQNPAAAGEERPKSDMPGSLIPGHKQSVVLFLERYGIETQ 2607  
Qy 2609 ELFYKLLIEEAPLPDLRAATMLDRNDGCESDMALSMRYIIGNSILPLLIKHAYFNEAENY 2668  
Db 2608 ELFPRLLEEAFPLDRAATMLDRNDGSESDMALAMNRYIIGNSILPLLIHSHKIFYNEADNY 2667  
Qy 2669 ASLLDATLHTVYRLSKNRMLTKGOREAVSDFLVALTSAMOPSMLLKLLKLTVDVSKLSE 2728  
Db 2668 ASLLDATLHTVYRLSKNRMLTKGOREAVSDFLVALTSMPQSMMLKULKLTVDVSKLSE 2727  
Qy 2729 YTTVALRLTLHYERCAKYGSTGAGOGAFGASDEEKRLTMMFLFSNIFDSLSKMDYEPE 2788  
Db 2728 YTTVALRLTLHYDRCAKYGSTG-GOGLYGSSDEEKRLTMMFLFSNIFDSLSKMDYDPE 2786  
Qy 2789 LFGKALPCLIAIGCALPPDYSLSKNYDDEFVG-KEQAAGDLNDPQYDPOPIINTSSVALNN 2847  
Db 2787 LFGKALPCLIAIGCALPPDYSLSKNYDDELYGARDSQAPSDGP-YNPQPIINTSHSVVLLN 2845  
Qy 2848 DLNTIVOKFSEHYHDWASRKIENGWYGEWSDSQKTHPRLKPYNNLNDY----BKER 2902  
Db 2846 DLNTIVOKFSEHYHDWASRKLENGWYGDQMSQKTHPRLKPYNNLNDYVEPSIERER 2905  
Qy 2903 YKEPVRESLKALLAIGSVSEHVIDIPSNRSMRRQSKSGRPPETVDSATPFDYNPH 2962  
Db 2906 YKEPVRESIKALLAIGTWVEHSEADVPLTSGRSIRRSQK----PNAMVDSSTFPNVHPN 2960  
Qy 2963 PVDMTNLTLSREMOMNAERLAADNAHDIAWKKKEBELVTNGGIIHPQLVPYDILLTDKSKKK 3022  
Db 2961 PIDMTNLTLSREMOMNAERLAENAHDIWAKKKBELITCGGIIHPQLVPYDILLTDKSKKK 3020  
Qy 3023 DRERSQBELKYLQYGGYKLRHPSK-APQSDTEQTTTGVATLREAYSLLEKLIQYIDRAT 3081  
Db 3021 DRERSQBELKYLQYGGYKLRHPSRTGPFSESEQLAAQATGELRFAYSLLEKLIQYIDRAS 3080  
Qy 3082 INMKLLKPSFTFRRSGFKTSTROIKPFKSAVLPIMKEYFSTHRNYFIATATANNYGAA 3141  
Db 3081 INMKLLKPSFTFRRSGFKTCTROIKPFKSVLPLVEKYFSTHRNYFIATATANNIGAA 3140  
Qy 3142 SLKEKEMVAALFCKLASLRSRLAAGFDVNRITVRCQLVVKIGDAKSLVKNCPEFIRTS 3201  
Db 3141 SLKEKEMVASLFCKANLLRSRLAAGFADVARISVKQLVVKIGDAKSLVKNCPEFIRTS 3200  
Qy 3202 MLTFENNVADDVGHITIMNLQDKYAHLRGHTLKTSTSLGYINGVLLPLTAKDPHLANCE 3261  
Db 3201 MLTFENNTADDLGHITQNLQEGKYSHLRGAHLKTSTSLFYINDVILPVLTAAMPDHLAACE 3260  
Qy 3262 YGADLLDEIOVASYKMLGSLYALGTDASTLHDKRLKLTETIERHKPALGSCLGAFSSTFP 3321  
Db 3261 YGSDLVLEIOVASYKMLGSLYITIGIDVLTLDHDKRYLKTEDRHRPQLGRCLGAYASTFP 3320  
Qy 3322 VAFLEPHLNKHNQFSLNRIADHLSLEAQDIMOKMEQCMTLETILGEVDQFVESDKTYNE 3381  
Db 3321 VAFLEPHLNKHNQFSLVNRIADHLSLEAQDILSRMESTMPTLDNILSELVESDKTND 3380  
Qy 3382 APHIDVVLPLLCYLPFWAQGPNDVPTCGNHVMTVTAENHQLLKNVLLKIKKNIGN 3441  
Db 3382 APHIDVVLPLLCYLPFWAQGPNDVPTCGNHVMTVTAENHQLLKNVLLKIKKNIGN 3441

Db 3381 APHIDVIMPMCLCSYLPVWMOQPDNVALTAGNAVTTVTSEHMQNQLLKNVLLKIKKNIGN 3440  
Qy 3442 ENAPWMTTRATYTOQIIINSSEBELLSDSFLPLAERYKRTDNNPHKEESLRGFTKSSTDD 3501  
Db 3441 ESAPWMTTRIAAYTOQIIINSSEBELLKDPFLPLAERYKRTDAMPHKEESLRGFTKSASDD 3500  
Qy 3502 TSQVESQIOEDWOLLVRDIYSFYPLLIKYVDLQRNHWRNNVPEABEYLHNHVAEIFNIWS 3561  
Db 3501 TSQIEAQIOEDWOLLVRDIYSFYPLLIKYVDLQRNHWRNNISEAEDLYNHVAEIFNTWS 3560  
Qy 3562 KSQYFLKEBQNFISANEIDNMVLIMPTARRVTAVDGT--POGGGKKKKKHRRDKGDKD 3619  
Db 3561 KSQYFLKEBQNFISANEIDNMVLIMPTARRSAVSDSAAPPGSGSGKKKKKREKKDKD 3620  
Qy 3620 KEVQASLWACLKRLLPVGLNLPAGREOELVQCKRFLKMKSEQDVAAEFKTLTLPDK 3679  
Db 3621 KELQASLWACLKRLLPVGLNLPAGREOELVQCKRFLKMKQDYEIFEFAKLTLPDK 3680  
Qy 3680 IDPADMSWQHYLYSKLGSKSKSNITVETAENKAKIIDDTVERIVAMSKVLFGLHMTDHP 3739  
Db 3681 LDPGDEMSWQHYLYSTLGSKKEI-----TEGGKPEQIDAVVDRIVAMAKVLFGLHMTDHP 3735  
Qy 3740 QOMSKNIVRSVVSIOKRRAVIACFRQTSLSHSLPRHRACNIFARTYVELWLEEBENIGQVM 3799  
Db 3736 QLQSKASYRSVVSQTKRAVIACFRQLSLHALPRKAINIFARSYVELWLTETENVGTEVL 3795  
Qy 3800 IEDLTQSFEADAEUKKSD-VVEGEKDPDLTQIYTTFCRGANTERSGALQSDPLYMSYAH 3858  
Db 3796 IEDLTQSFEADAEUKKTDDEYDEG-KSDPLTQIYTTFCRGANTERSGALQSDPLYMSYAEI 3854  
Qy 3859 IAKSCGEEBEEGEGEAEABDEGRASIEHQBEMEKQLLHQARLADRGVABMVL 3918  
Db 3855 AAKSCGEEBEE--GDEBEEG--EGBEQG--ASIEHQBEMEKQLLHQARLANRGVABMVL 3909  
Qy 3919 LHISASGLPSEVMKTLQIGISILRGGNIDIQMGMLNHLKDKKQVGFSTSIAGLMNSCS 3978  
Db 3910 LHISACGVPSDMVEKTLQIGISILRGGNIDIQMGMLNHLKDKKQVGFSTSIAGLMNSCS 3969  
Qy 3979 VLDLDAFERNTKAEGLVGLEGAAGEKNMDAFTCALFRFIOLTCGHNLDMQNYLRTQ 4038  
Db 3970 VLDLDAFERNTKAEGLVGSDGAAGEKNMDAFTCTLFRFIOLTCGHNLDMQNYLRTQ 4029  
Qy 4039 AGNTTNNVVICVVDYLLRLOESIMDPYHYSKELIDPAGKANFFKAIGVASQVFNTLT 4098  
Db 4030 AGNTTNNVVICVVDYLLRLOESIMDPYHYSKELIDPAGKANFFKAIGVASQVFNTLS 4089  
Qy 4099 EVIQGCTQNOQALAHSLMDAVGGFLFLFSHMQDKLSKISSQVDLLKELNLQKDMIPM 4158  
Db 4090 EVIQGACTQNOQALAHSLMDAVGGFLFLFSHMQDKLSKISSQVDLLKELNLQKDMITM 4149  
Qy 4159 MLSMLEGNVNGTIGKQWDTLVESASNVLELILKYFDMFLKLDLTSSAQFQETDANNDG 4218  
Db 4150 MLSMLEGNVNGTIGKQWDTLVESASNVLELILKYFDMFLKLDMTAPFLEIDPNHGD 4209  
Qy 4219 WVLPKDFKEMEQKSVTPPEIEBFLACCTNHDGKLDYIGFCDFRHEPAKEIGFNLAVL 4278  
Db 4210 WVLPKDFKEMEQKSVTTEIEISFMLQCCCTNHDGKVDYIGFVDRFHEPSKEIGFNLAVL 4269  
Qy 4279 LTNLSEHMPNEPRLARFLETAGSVLNYFEPFLGRIEIMGSKRIERYVEIKEISNIBOWE 4338  
Db 4270 LTNLSEHMPNEPRLARFLETAGSVLNYFEPFLGRIEIMGSKRIERYVEIKEISNIBOWE 4329  
Qy 4339 KPQIKESKRAFFYSIVTEGGDKLEAFVNFCEDAIFEMTHASGLMAASESVGKTNRE 4398  
Db 4330 KPQIKESKRAFFYSIVTEGGDKLEAFVNFCEDAIFEMTHASGLMVDVDDSGG--GGK 4387  
Qy 4399 ASYWMGDDDERAGDKPERRGLQSVKDGAVATAPSSLSPSNIAKADMOQMPAEALAVG 4458  
Db 4388 AAYTISEDEEKNAPDIRRTQAFKDAIYFILTMLSPNICKINEMQMSVPELVVG 4447  
Qy 4459 FFKMFFLYVLGYVLVVVRYIFGVLLGLMRGQTDPPPEPTEBEKI-GOLRHRLLAT 4517  
Db 4448 FFKIFFYFYSGFSVSVLRYFGRILMTLMRGQTPEPVAEVKKEDEIMGPI-----4500

QY	4518	QSSRHLPALPPADDTGQMVSAFGDLITKDNGOIQVPHESPET-STPSSGEE-----	4570
Db	4501	---RALP--PPPDNKKEASSS-----AKDDSG--QAKPADGGATLALTASGEHKEGGA	4548
QY	4571	----AUVSPDESADITEORPPSLIDLILGGQAKQOQERNEAQAQAAMSALEAESKK	4626
Db	4549	TEBEAGDGAKEGAEATTETGTTMTLADLILGGGAARKEAVARAEEVAEQQA VNAEAEAKH	4608
QY	4627	AVQGPAPSALSQVDLSQVTRAVSFLARNFYNLKYVALVLAFCINFVLLFKYKSTL----	4682
Db	4609	EVUS-EPNSFQIDNRRYTHRAVSFLARNFYNLKYVALVLAFCINFVLLFKYKSTL----	4667
QY	4683	-DGEUGE-GSGLGDII-----AGGSGG-SGAGSGSGDGGEGGED-----DAALEVHVIDED	4731
Db	4668	DDGSGGELGGLAEADLLEELGGSGEGGGLSGGSGGSGEDSGEGEEDPIELVHVNED	4727
QY	4732	FYMEHVKMAAVLHSHSVSLAILLIGYHLYKVLPAIFKREKEIARKLFPDGLYTAEOPEDD	4791
Db	4728	FFYMAHVKMAAHLHSLVSLAMLIAIYHLYKVLPAIFKREKEIARKLFPDGLYTAEOPEDD	4787
QY	4792	DLKSHWDKLVIAKSPFPVNYWDKFKVKVRAKYSETYDFDSISNMLGWKETSFSQAQEEG	4851
Db	4788	DLKSHWDKLVIAKSPFPVNYWDKFKVKVRAKYSETYDFDSISNMLGWKETSFSQAQEEG	4847
QY	4852	SKGLIHYIINIDWRVQVWKAGVTITDNGSFLXSLWYFSPVNGFNFFFAHLLDVAVG	4911
Db	4848	GTGIIINFILNIDWRVQVWKAGVTITDNGSFLXSLWYFSPVNGFNFFFAHLLDVAVG	4907
QY	4912	KTLRTILQSVTHNGKOLVLTVMMLTIIVYIYTVIAFNFRFPYQOEDEDEVRNCHDMLT	4971
Db	4908	KTLRTILQSVTHNGKOLVLTVMMLTIIVYIYTVIAFNFRFPYQOEDEDEVDKCKCHDMLT	4967
QY	4972	CFVFNLYKGVRAAGGTGDELEPPDGDSDSVRIIPDISFFFTVIVILLAIQGLIIDAFG	5031
Db	4968	CFVFNLYKGVRAAGGTGDELEPPDGDSDSVRIIPDISFFFTVIVILLAIQGLIIDAFG	5027
QY	5032	ELRDQLESVKEDMESNCFICGINKNDYFDKVPHPGPDTHVQREHNLANYMFFILMHLINKPDT	5091
Db	5028	ELRDQLESVKEDMESNCFICGINKNDYFDKVPHPGPDTHVQREHNLANYMFFILMHLINKPDT	5087
QY	5092	EYTGQTYVNNYTORCWDFFPVPGDCFRKQYEDLMG	5127
Db	5088	EYTGQTYVNNYTORCWDFFPVPGDCFRKQYEDLMG	5123
RESULT 7			
US-10-668-767-122			
; Sequence 122, Application US/10668767			
; Publication No. US2004017114A1			
; GENERAL INFORMATION:			
; APPLICANT: Caspar, Timothy			
; APPLICANT: Cordova, Daniel			
; APPLICANT: Guttridge, Steven			
; APPLICANT: Rauh, James			
; APPLICANT: Smith, Rejane			
; APPLICANT: Tao, Yong			
; APPLICANT: Wu, Lihong			
; TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors			
; FILE REFERENCE: BB1533 US NA			
; CURRENT APPLICATION NUMBER: US/10/668,767			
; CURRENT FILING DATE: 2003-09-23			
; PRIOR APPLICATION NUMBER: 60/412,795			
; PRIOR FILING DATE: 2002-09-23			
; PRIOR APPLICATION NUMBER: 60/427,324			
; PRIOR FILING DATE: 2002-11-18			
; NUMBER OF SEQ ID NOS: 149			
; SOFTWARE: PatentIn version 3.1			
; SEQ ID NO 122			
; LENGTH: 5127			
; TYPE: PRT			
; ORGANISM: Drosophila melanogaster			
; FEATURE:			

Db 960 IFMQNGYKPAPLDLASVTLTPKLEELVDQLAENTHNLWARERIQOGWTYGLNBDSENHR 1019  
Qy 1021 SPHLVPYKVDADATKKANRDASTVTRTLIVYGWLDPPPTGEOHEALLLEASKOKQADFR 1080  
Db 1020 SPHLVPYAKVDEATKKANRDASTVTRTLIVYGWLDPPPTGEGTEALLAEARLUKFAGR 1079  
Qy 1081 TYRAEKYAVSSGKWYFEFEILTAPMRVGHADMAFGMMLGODENSWAFDGYNEEKVY 1140  
Db 1080 TYRVERNAYVTSKWYFEFEVLTSOPMRVGHARADCYPGMLGSEDTSWAFDGHNEEKVY 1139  
Qy 1141 SGNTESEKQWAVGVGVFLDLIDKITSFSLNGELLMALDGGTTTFADV--QGDNFVPA 1198  
Db 1140 GGVSESEKQCGPDIIVGVFLDLADHTISFSLNGELLMALDGGTTTFADVTAEGVFPVA 1199  
Qy 1199 CTLGVGOKARLYQGDVNTLYKYFTTCGLOGBYEPFCVNMKRDVTHWTKOPIFENTDEM 1258  
Db 1200 CTLGVGOKARLYQGDVNTLYKYFTTCGLOGBYEPFCVNMKRDVTHWTKOPIFENTDEM 1259  
Qy 1259 IDTRIDVTRIPAGSDTPPCLKISHNTPETMEKANWFLRLSLPVICHNEFTIDEAEKARRW 1318  
Db 1260 PDCRIDVTRIPAGSDTPPCLKISHNTPETMEKANWFLRLSLPVTMCGEFISEQEKARRW 1319  
Qy 1319 VEIKDRQOILMKEA-VEAQM-----PAHIDQIMRSGFTMNDIKGLHYE-DNQEELPSSKM 1371  
Db 1320 DEIKNRQVRLMREAIEIAAQMVQTOAAHMDHMLKGGFNMDIKGLTRNFDEHADAEADHM 1379  
Qy 1372 KRLFSRPPRKSMTRGVTIQNNYLQGOVNGMRSTSEABMAKYDLAGOGLTPDDKKDK 1431  
Db 1380 MRGNRPFRKSGLSRNTIT---FETDMSAALDEMQRSTS-----VLDMNGLGEEMDDKK-K 1430  
Qy 1432 RGRSPFKFRSKRGESSDRAKSRKTPDPSPDTEVSPERGARRPNQIKVSOANQRYNG 1491  
Db 1431 RGRSPFKFRF-SKSRDQSGREK-MGARTLDTLSLRNTVHAHRNVVNOQMTTRAPTRLNN 1488  
Qy 1492 MNARPSRNLVYGSQVGLNMAFTQDRKQMTTSTLQAQATETVGNIEIFDAECLKLINEFY 1551  
Db 1489 AEIPLSPV-----PQPKQLSGSLNGQOPVETSGDEMFDACELKLINEFY 1534  
Qy 1552 GVRYPGQDPHVYIGWTTQYHLHSDKFNOSKYTKSGSVITDDYDRVVENVNROSICYMV 1611  
Db 1535 GVRIFPGQDPHVYIGWTTQYHLHSDKFNOSKYTKSGSVITDDYDRVVENVNROSICYMV 1594  
Qy 1612 RADELYNEVMAEATAKASQSMFTGCSVDSTGVSFTCEGKDTSPFKMEPETKLPAPAI 1671  
Db 1595 RADELFEVTDQAGKASQSMFTGCSVDSTGVSFTCEGKDTSPFKMEPETKLPAPAI 1654  
Qy 1672 FVEATSKELIQELGRSATSPLSAAVLPTSDKHVIFQFPPLKXVQCLKPHQWARVENQS 1731  
Db 1655 FVEATSKELIQELGRTPPTLPLSAAVLPTSDKHINPQSPPLKXVQCLRPHQWARVENTA 1714  
Qy 1732 LQVHALKLSDIRGWSMLCEDAVSMALHIPEEDRCIDIPIEMDKLLSHSHSTLTLYAA 1791  
Db 1715 LQVHALKLSDIRGWSMLCEDAVSMALHIPEEDRCIDIPIEMDKLLSHSHSTLTLYAA 1774  
Qy 1792 LCYQSNVRAAHALCTHVDOKLLVAISOVMSGPLRGFGFYDLLLALHLESHATTMEACKN 1851  
Db 1775 LCYQSNVRAAHALCOHVQKOLLVAIRSEYMSGPLRGFGFYDLLLALHLESHATTMEACKN 1834  
Qy 1852 EFVPLPLGPELKALYEEPMDSHLSLQTESVRPQMKMTDI-----AESITE 1897  
Db 1835 EYITPLGNALKELYSDEEMQHSLSLVTESVRPQLRMTETITPPVIATSSMPSVSSEPIPD 1894  
Qy 1898 ISNLYSPFPLEVAREFVQALABAVETNOVHNRDPVGGSNENIFLPLIKLVDRLLLVGM 1957  
Db 1895 IDQLYSPKFFLEVVRQFVMEALKDAVEINQVHNRDPIGWNTENIFLPLIKLVDRLLLVGV 1954  
Qy 1958 MRDEDEKLLTWTNPETWDPDFDEKDEHKGILLHMKMAEGAKLQWCYLLQHLNDQLR 2017  
Db 1955 LTDEBQRLLVNIDPETWQDAFEREGKDEHKGILLHMKMAEGAKLQWCYLLHUYDTQLR 2014  
Qy 2018 HRVEAITAFADHFDVGDQLQTLQRYTEIKQSDPLSAAAKKTRFCRPPRQMNAILSFK 2077  
Db 2015 HRVESITAFSHDFVGDQLQTLQRYTEIKQSDPLSAAAKKTRFCRPPRQMNAILCFK 2074

Qy 2078 HLEEDKENCPCGEELIARMNEFHDTLMAHVSLSLHALQEPDAAENQOE-PEAKPGAFGKLYN 2136  
Db 2075 NLEPDDQDNCTCGLELRGLRGLDHFHDSLMQKVSINALQEPDGVGTAIEEVKTKPITKIYN 2134  
Qy 2137 IINTVKELBEEAKAIEBPPKKTPEEKFRKVLITQIVNVWABESQIETPKLVREMFSLVRQ 2196  
Db 2135 FINTVKEEESGPKEVEPEKKTPEEVFRKVLITKIVSWABESQIENPKLVREMFSLLRQ 2194  
Qy 2197 YDAVGELIRALEKTYVINAKTLDVAMVMVGLSQIRALLPVQMSOEBEELMRKELWLVN 2256  
Db 2195 YDTVGLSRALEKTYVINRARDVAMVMVGLSQIRALLPVQMSOEBEELMRKELWLVN 2254  
Qy 2257 NHTFFFOHPPDLIRVLRVHENVMAVMNTLGRRAQAQSDAOPSSQPVAB--DSKEKDTSHEM 2314  
Db 2255 NATFFFOHPPDLIRVLRVHENVMAVMNTLGRRAQAQSDA-PTQSEVAEGASKEKDTSHEM 2313  
Qy 2315 VVACCRFLCYFCRTGRQNKQKAMFDHFDLLENSNILLRSLRGSTPLDVAYSLSMENTE 2374  
Db 2314 VVACCRFLCYFCRTGRQNKQKAMFDHFDLLENSNILLRSLRGSTPLDVAYSLSMENTE 2373  
Qy 2375 LALALREHYLEKTAIVLSRCGLQSNSELVEKGYPDLDGWDVVEGERYLDLFRFCVWNGES 2434  
Db 2374 LALALREHYLEKTAIVLSRCGLQSNSELVEKGYPDLDGWDVVEGERYLDLFRFCVWNGES 2433  
Qy 2435 VEENANLVIRLLRRRPECIGPALRGEGGLLKAIVDANKMSERIAADRKLREMEQEGDV- 2493  
Db 2434 VEENANLVIRLLRRRPECIGPALRGEGGLFRAIVEANRMSERISDRCKWQD-EAEGTIA 2492  
Qy 2494 --NFSHPLPESDEDEYIDTGAAILNFYCTLDLLGRCAPDAGVIALGKNESIRARAILR 2551  
Db 2493 GLNFTHPLPEGEDEYIDTGAAILNFYCTLDLLGRCAPDASVIEQKNESIRARAILR 2552  
Qy 2552 SLVPLBEDLQGLVLSRLTLPANPAAGEBERPKSDMPSGLIPGHKQSVGLFLEHYVIGETQLF 2611  
Db 2553 SLVPLBEDLQGLVLSRLTLPANPAAGEBERPKSDMPSGLIPGHKQSVGLFLEHYVIGETQLF 2612  
Qy 2612 YKLEBAFIPDLRAAATMLDRNDCESDMALSMNRYIGNSILPLLIKHAYFNAENYASL 2671  
Db 2613 YRLUEDAFIPDLRAAATMLDRNDCESDMALSMNRYIGNSILPLLIKHAYFNAENYASL 2672  
Qy 2672 LDATLHTVYRLSKNRMMLTKQREAVSDFLVALTSAMQPSMMLLKLRLKLVDSKLSYTT 2731  
Db 2673 LDATLHTVYRLSKNRMMLTKQREAVSDFLVALTSAMQPSMMLLKLRLKLVDSKLSYTT 2732  
Qy 2732 VALRLTLHYERCAKYGTGACQAGAFGASSDEBEKLTMMLFPSNIPDSLSKMDYEPFLFG 2791  
Db 2733 VALRLTLHYERCAKYGTGACQAGAFGASSDEBEKLTMMLFPSNIPDSLSKMDYEPFLFG 2791  
Qy 2792 KALPCLIAIGCALPPDYSLSKNYDDDFYKGEQAAGDLDPQYDPOPIINTSSVALNNDLNT 2851  
Db 2792 KALPCLIAIGCALPPDYSLSKNYDDDFYKGEQAAGDLDPQYDPOPIINTSSVALNNDLNT 2849  
Qy 2852 IVQKFSHYHDAWASARKIENGWYVYEGWSDSQKTHPRKLPYNNMLNDEYKERYKEPVRESL 2911  
Db 2850 LVQKFSHYHDAWASARKIENGWYVYEGWSDSQKTHPRKLPYNNMLNDEYKERYKEPVRESL 2909  
Qy 2912 KALLATGWSVEHSEVDIPSNRSMRQSKSGRPEI--VTDSATPFDPNPHVDMTNL 2969  
Db 2910 KGLLAIGWTVEHSEVEVALNHRGSTRQSK-----FQINSEFQNEGSPFNYPHPVDMNSL 2964  
Qy 2970 TLSREMNMAERLADNAHDIIWAKKKEELVTNCGGHPOLVPYDILLTDEKKKDRERSQE 3029  
Db 2965 TLSREMNMAERLADNAHDIIWAKKKEELVTNCGGHPOLVPYDILLTDEKKKDRERSQE 3024  
Qy 3030 FLXYLOVQGYKLRHSPKAPQSDTEQTTTGVVAIELRFAYSLLEKLIOYIDRATINMCLKP 3089  
Db 3025 FLXYLOVQGYKLRHSPKAPQSDTEQTTTGVVAIELRFAYSLLEKLIOYIDRATINMCLKP 3083  
Qy 3090 STTFSRRSSPKTATROIKFFSKVPLMEKYFTHRNYFIATATATNNVGAASIKEMV 3149  
Db 3084 STTFSRRSSPKTATROIKFFSKVPLMEKYFTHRNYFIATATATNNVGAASIKEMV 3143





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Qy	1	MAEAGGASEDDVSFLRTEDMVLCTATGERTVCLAAEGFGRHCFLENIADKNIIPDDL	60
Db	1	MAEAGG-SEQDDVSFLRTEDMVLCTATGERTVCLAAEGFGRHCFLENIADKNIIPDDL	59
Qy	61	SQCVPVLEQALSVALQELVTAAGSETCKGSGHRTLLYGNALLRHNSDMYLACLS	120
Db	60	SQCVPVLEQALSVALQELVTAAGSETCKGSGHRTLLYGNALLRHNSDMYLACLS	119
Qy	121	SSSQDLAFDVLGLOHSGOGEACWTLHPASKQRSEGEKVRVGGDILLVSVATERYLHTTK	180
Db	120	SSSDKLSFDVLGLOHSGOGEACWTLHPASKQRSEGEKVRVGGDILLVSVATERYLHTTK	179
Qy	181	ENEVSIVNASPHVTHWSVQPTGTSIRMKYGVYVFGDVLFPFHGGDECLTIPSTWYKDG	240
Db	180	ENEQSIVNASPHVTHWSVQPTGTSIRMKYGVYVFGDVLFPFHGGDECLTIPSTWGRE	239
Qy	241	GQNTVVYEGGSMQASRLWLELARTKMGAGFTNWHVPMIRHITTCRYLGVNDQNELY	300
Db	240	GQNTVIVYEGGVMAQASRLWLELARTKMGFTNWHVPMIRHITTCRYLGVNDNSNELI	299
Qy	301	LVSREEATTASCAFLROEKDDQVLEDKDLEVIGAPIIKYGDSTVIVQHSETGLWLSY	360
Db	300	LVKKEASIAITTCFLROEKDEKKVLEDKDLEVIGSPIIKYGDTVIVQHSETGLWLSY	359
Qy	361	KSYETKKGVGVBEKQAILHEBGMDDGLDFRSQBESESTARVIRKCSLSLFTKFLINGL	420
Db	360	KSYETKKGVGVBEKQAILHEEGKMDCLDFRSQBESESTARVIRKCSLSLFTQFITAL	419
Qy	421	ETLQENRRHSFPAASVNLGEMVCLLEDLINYFAOPDEDEHEEKONKFRALRNQDLFOE	480
Db	420	ETLQSNRRHSIFFOKNVNLNEMVCLLEDLINYFQPEDDEHEEKONKFRALRNQDLFOE	479
Qy	481	EGILNLILEADKINVTISQGLAGDSGQSWEMISGYLQLLAAIIKGNHTNCAQ	540
Db	480	EGVLNLILEADKINITSQGLASFLASFLAGDTGQSWDLISYLYQLLAAIIKGNHTNCAQ	539
Qy	541	FANSNRLNWLFSRLGSAQSGEGTGMVLVHCVLIDSPEALNMMDDEHIKVIISLLEKHGR	600
Db	540	FANSNRLNWLFSRLGSAQSSGSGMVLVHCVLIDSPEALNMMDDEHIKVIISLLEKHGR	599
Qy	601	DPKVLVLCSLCVGVNGVAVRSQNNICDYLLPGKNLLQTLVLDHVSVRNIEFVGVEG	660
Db	600	DPKVLVLCSLCVGVNGVAVRSQNNICDFLLPGKNLLQTLVLDHVASIRNIEFVGVDG	659
Qy	661	SAVYRKWYFEVTMDHIEQTHMPLHRIGWANTTGYVPYPGGGEKVGNGVGGDLYSYGF	720
Db	660	SSMYQKWYFEVTMDHIEQTHMPLHRIGWANTSGYVPYPGGGEKVGNGVGGDLYSYGFG	719
Qy	721	DGAYLWSGGRKTPVNRTHAEEPIYIRKGDVIGCALDLTVPIINEMENGVRVTGSGFTNFLE	780
Db	720	DGAFLWTGGKRTLVVDALPEEPFIRKGDVIGVAIDLSVPIITFTFNGVKVGRGFRDNLD	779
Qy	781	GMEFFPVISCSSKLSRFLGGEHGRLYAAPEGYSPLVESLLPQQLISLSPCFYFGLSK	840
Db	780	GMEFFPVMSCSSKLSRFLFGDHRLLKAPPMPGFSALVQCLMPQQLISLSPCFYFGLAK	839
Qy	841	RALAGPPLVODDTAFVPTPVDTLQITLPTVYEQIRDKLAENIHEMMANMKIEAGWYGDQ	900
Db	840	NVLAGPWLIEDDTAFVPKPVDTTGVTLPSSVDQIKELAEINHEMMALNKIEAGWSGEH	899
Qy	901	REDLHKHPCLVPFERLPAAEKRYDQLAVQTLTKTILALGYISLDKPPARIINVRLPNE	960
Db	900	RDDYHRIHPCLTHFEKLPAAEKRYDQLAVQTLTKTISLGYYITMDKPPARIIPVRLPNE	959
Qy	961	PFMQSNGYKPAPLDLSAVTLTPKMDBELVDQLAENTHNLWARERIQQGWTYGLNEDSDMR	1020
Db	960	IFMQSNGYKPAPLDLSAVTLTPKLEBELVDQLAENTHNLWARERIQQGWTYGLNEDSENHR	1019
Qy	1021	SPHLVPYKVDDAIKKANRDTSSETVRTLIVGYMLDPPPTGEOHEALLLEASKQKQADFR	1080
Db	1020	SPHLVPYAKYDEAIKKANRDTSSETVRTLIVGYVLDPPPTGEGTEALLAQAOLKFAGR	1079
Qy	1081	TYBAEKYAVSSCKWYFEFEILTAGPMRVGMAHADMAPGMMLGQDENSWAFDGVNEBKVY	1140
Db	1080	TYVERNYAVTSKWKYFEFEVLTSGPMRVGMAARADCVPGAMLGSEDTSWAFDGHVNTXMH	1139
Qy	1141	SGNTSEFGQKQWAGDVGVVFLDLIDKTIISFLNGELIMDALGETTTFADY--GQDNFVPA	1198
Db	1140	AGSIEHFVRYEAGDVIGCFIDVKEQTIISFLNGELIMDALGETTTFADVTAEGVGPVA	1199
Qy	1199	CTLGVQOKARLTQGVQDNTLYKYETTCGLQSGYFPFCVNMKRDVTHWTKQOPIFENTDEM	1258
Db	1200	CTLGVQOKARLIYQGVQDVSLEKFTTCGLQSGYFPFCVNMERPVTWYTKQOPIFENTDEM	1259
Qy	1259	IDTRIDVTRIPAGSDTPPCLKISHNTFETMEKANWEFLRLSLPVIChNEFIDBAEKARRW	1318
Db	1260	PDCRIDVTRIPGGADTPPHLKI SHNTFETMEKANWEFLRLSLPVTGCEFIISQEKARRW	1319
Qy	1319	VEIKDRQIILMKEA-VEAQW-----PAHIDQIMRSGFTMNDIKGLHYE-DNQBELPSSKM	1371
Db	1320	DEIKNRQYRLMREAEIAAQVQVQAAHMDHMLKGGFNMDIKGLTRNFDHADAADHM	1379
Qy	1372	KRLPSRPPRKSGMTRGVITQNYNNLQPGQVNGHMRSTSEAMAKYDLGAQGLPDDDKDK	1431
Db	1380	MRGNRPPRKSGSLTRNIT---FETDMSAALDEMQRSTS-----VLDNMNGLGEEMDDKK-K	1430
Qy	1432	RGRSPKFPKRSKRGESSDRAKSRKSTPDPFSDTEVSPERGARRPNPQIKVSOANORYNG	1491
Db	1431	RGRSPKFPF-SKRSRQSRK-MGARTLDTSLERRNTVAHGRNVNVNQOMTTAPTLEANN	1488
Qy	1492	MNARSPRTNLGYSQVGLNMAATPQDRKQMTTSLAQSATETVGNIEPDAECLKLINIFY	1551
Db	1489	AEIPSPV-----PQPKQLSGSLNQGPVETSGDGMFPAECLKLINIFY	1534
Qy	1552	GVIYFGQDPDTHYVIGWTTQYHLHSHKDFNQSKVTSSVITDDYDRVENVNRQSCVMV	1611
Db	1535	GVIYFGQDPDTHYVYVWTTQYHLHSREFNKNKRRGSVYIEDDYENAIERIDRQSCVV	1594
Qy	1612	RADELNYEMAEATAGASOGMFIGSDVTSTGVSFTCEGKDTSPFKMKPEPTKLPFAI	1671
Db	1595	RADELNEVTDASGKASOGMFGVCPVDATGIIIRFTCEGKDTSHRWMEPTKLPFAI	1654
Qy	1672	FVEATSKELIQLIELGRTPPTLPLSAAVLPTSDKHVLPQFPPLKVCQLKPHQARVNPQS	1731
Db	1655	FVEATSKELIQLIELGRTPPTLPLSAAVLPTSDKHINPQSPPLKVCQLRPHQARVENTA	1714
Qy	1732	LQVHALKSLDIRGWSMLCEDAVSNLALHIPEEBCRDIDILEPMDKLLSHSHSLTLTYAA	1791
Db	1715	LQVHALKSLDIRGWSMLCEDFVSNLALHIPEEBCRDIDILEIEMDKLLSFAHSLTLTYAA	1774
Qy	1792	LCYQSNVRAAAHALCTHVQDKQLLYVAIQSYQWSGFLRQGFYDILLIALHLESHATTMEACKN	1851



Db	1775	LCVQSNRAAHALCQHVQKOLLYAIRSEYMSGPLRQGFYDLLIAHLHESHATTMEVCNK	1834	Db	2850	SRLEGQWTYGDIISDNDNRKHPRLKPKYNMLSEYERERYRDPVRRECLKGLLAIGTWVEHSE	2909
Qy	1852	ERVPIGLBPKALYBEPDMGHSLSRLOTESVRPQMKMTDIAESITEISNLSPYEPLEVA	1911	Qy	2926	VDIPSNRRSMRROSKSGGRPPEI--VTDSATPPDYNPHPVDMTNLTLSREMOMNAERLA	2983
Db	1835	EYITPLGAELELYSDEEMQHSLSRVTSVRPQURMTETIPEPIDOLYSKPPLEVV	1894	Db	2910	VEVALNHRGSTRROSK-----PQINEFQNEGSPENYNPHPVDMSNLTLISREMOMNAERLA	2964
Qy	1912	REFVMOALAEAVETQVHNRPDPVCGSNENLFLPLIKLVDRLLLVGMDEDEVEKLLIMTN	1971	Qy	2984	DNAHDIWAKKKBEELVTNGGIIHPQLVPYDILLTQKEKKKDBERSQEBFLKYLOYQYKILHR	3043
Db	1895	ROFVMEALKDAVEINQVHNRPDPVCGSNENLFLPLIKLVDRLLLVGMDEDEVEKLLIMTN	1954	Db	2965	ENSHDIWAKKKBEELVTNGGIIHPQLVPYDILLTQKEKKKDBERSQEBFLKYLOYQYKILHR	3024
Qy	1972	PETWPSDFDKEGDBHRKGLLHKWABGAKIOMCYLLOHLNDIQLRHRVEAIIAPAHDFV	2031	Qy	3044	PSKAPQSDTEQTTGVAIELERFAYSLLEKLIQYIDRATINMKLLKPSFTFRRRSFSTST	3103
Db	1955	PETWDOAFEREKDEHRKGLLTKMAEGAKIOMCYLLOHLNDIQLRHRVEAIIAPAHDFV	2014	Db	3025	PSKAGAVE--EGGATQAAVELRFSYSLLEKLIQYIDRATINMKLLKPSFTFRRRSFSTST	3083
Qy	2032	GLOLTDQRRRYTEIKOSDLPSSAVALKTEPRCPREOQNAITLSFKHLEEDKENCPCGE	2091	Qy	3104	RDIKFFSKAVLPLMEKFFSTHRNYFIAVATATNNVGAASLKEKEMVAALFCKLASLRSR	3163
Db	2015	GLOLTDQRRRYTEIKOSDLPSSAVALKTEPRCPREOQNAITLSFKHLEEDKENCPCGE	2074	Db	3084	RDIKFFSKAVLPLMEKFFSTHRNYFIAVATATNNVGAASLKEKEMVAALFCKLASLRSR	3143
Qy	2092	ELIARMNEFHDLTMAHVSJLHQLQEPDAENQOE--PEAKPCAFGLKLYNIINTVKELEEEAKA	2150	Qy	3164	LAAPGPDVRIIVRCLQVLVKGIDAKSLVQNCPEFIRTSMLTFFNNVADDVGHITMNLQDG	3223
Db	2075	ELRGLGDPHDSLMQKVSJLHQLQEPDAENQOE--PEAKPCAFGLKLYNIINTVKELEEEAKA	2134	Db	3144	LSAFGPDVRIIVRCLQVLVKGIDAKSLVQNCPEFIRTSMLTFFNNVADDVGHITMNLQDG	3203
Qy	2151	IEBPPKTPPEERKPKVLIQTIYVNWABESQIETPKLVREMFSLVRYDAVAGELIRALEKT	2210	Qy	3224	KYAHLRGTHLKTSTSLGYINGVLLPILTAKEFDHLANCEYAGADLLDEIQVASYKMLGSLY	3283
Db	2135	VEBEPKTPPEERKPKVLIQTIYVNWABESQIETPKLVREMFSLVRYDAVAGELIRALEKT	2194	Db	3204	KYSHLRGTHLKTSTSLGYINGVLLPILTAKEFDHLANCEYAGADLLDEIQVASYKMLGSLY	3263
Qy	2211	YVINAKTKLDVAMVWGLSQIRALLPVMQSQEBSBELMRKRLKLYNNHTFFQHPDLIRVL	2270	Qy	3284	ALGTDASLTHDRKYLKTEIERHKPALGCLGAFSTFPVAFLEPHLNKHQNFSLNRIAD	3343
Db	2195	YVINAKTKLDVAMVWGLSQIRALLPVMQSQEBSBELMRKRLKLYNNHTFFQHPDLIRVL	2254	Db	3264	HLGTDGTLTHDRKYLKTEIERHKPALGCLGAFSTFPVAFLEPHLNKHQNFSLNRIAD	3323
Qy	2271	RVENHNVAMMTNLGRRQAQSDAOPSSQPVABE--DSKEKDTSHMWVACCRFLCYFCRT	2328	Qy	3344	HSLEAQDIMQKMEQCMPTLETILGEVDQFVBSDKTYNEAPHI IDVVLPLLCYSYLPFWNAQ	3403
Db	2255	RVENHNVAMMTNLGRRQAQSDAOPSSQPVABE--DSKEKDTSHMWVACCRFLCYFCRT	2313	Db	3324	HSLEAQDIMQKMEQCMPTLETILGEVDQFVBSDKTYNEAPHI IDVVLPLLCYSYLPFWNAQ	3383
Qy	2329	GRQNKAMPDFHDFLLENSNILLRPSLRGSTPLDVAYSSLMENLTELALAREHYLEKIA	2388	Qy	3404	GPDNVTPGNGHVTMTVAEHNQILLKNVLLKLI KKNIGNENAPMWTIATYTOQIIINSE	3463
Db	2314	GRQNKAMPDFHDFLLENSNILLRPSLRGSTPLDVAYSSLMENLTELALAREHYLEKIA	2373	Db	3384	GPDNVTPGNGHVTMTVAEHNQILLKNVLLKLI KKNIGNENAPMWTIATYTOQIIINSE	3443
Qy	2389	VYLSRCGLQSNSELYKGPYDPLGMDPVEGERYLDPLFCVWNGSVENANLVRILLIR	2448	Qy	3464	ELLRDSPLPLAERVRKRTDNMFHKEESLRGFIKSTDDTSQVESQIQBDWQLLVDRDIYSF	3523
Db	2374	VYLSRCGLQSNSELYKGPYDPLGMDPVEGERYLDPLFCVWNGSVENANLVRILLIR	2433	Db	3444	ELLKDPFLPLAERVRKRTDNMFHKEESLRGFIKSTDDTSQVESQIQBDWQLLVDRDIYSF	3503
Qy	2449	RPECLGPAIRGEGGILLKAIIVANKMSERIDRRKLREMEQBGDV--NFSPHLPESDED	2505	Qy	3524	YPLLIKYVDLQNRNHLRNNVPEABEELYNHVAEIEFNIWSKQYFLKEEQNFISANEIDNNV	3583
Db	2434	RPECLGPAIRGEGGILLKAIIVANKMSERIDRRKLREMEQBGDV--NFSPHLPESDED	2492	Db	3504	YPLLIKYVDLQNRNHLRNNVPEABEELYNHVAEIEFNIWSKQYFLKEEQNFISANEIDNNV	3563
Qy	2506	EYIDTGAAILNFYCTVLDLLGRCAPDAGVIALGKNESLRARAILRSLVPLEDLQGVLSL	2565	Qy	3584	LIMPTATRRVAVTDGTPQGGG--KKKKHHRDKKDKDKEVQASLMVACLKLLPVGLNL	3641
Db	2493	EYIDTGAAILNFYCTVLDLLGRCAPDAGVIALGKNESLRARAILRSLVPLEDLQGVLSL	2552	Db	3564	LIMPTATRRVAVTDGTPQGGG--KKKKHHRDKKDKDKEVQASLMVACLKLLPVGLNL	3622
Qy	2566	RFTLNNPAAABRPKSDMPGSLIPGHQKQVGLFLERVYGIETQOELFYKLLBEAFIPDLRA	2625	Qy	3642	FAGREQLVQHCORFLKMSQEDVABEFAKTQTLTPDKIDPADENMSQWYLYSKLGSKS	3701
Db	2553	KFTLSQAPGEBKPKSDMPGSLIPGHQKQVGLFLERVYGIETQOELFYKLLBEAFIPDLRA	2612	Db	3623	FAGREQLVQHCORFLKMSQEDVABEFAKTQTLTPDKIDPADENMSQWYLYSKLGSKS	3681
Qy	2626	ATMLBNDQCESDMALSMNRYIGNSILPLLIIKHAYFNEAENYASILLDTLTHVYRLSKN	2685	Qy	3702	SNITVETAEAKAKI-----IDDTVERIVAMSKVLFGLHMDHPQMSKNVYRSVVS	3752
Db	2613	ATMLBNDQCESDMALSMNRYIGNSILPLLIIKHAYFNEAENYASILLDTLTHVYRLSKN	2672	Db	3682	BPVD--EQALEKXANVNSNEKGDKTQETVDRIVAMAKVLFGLHMDHPQMSKNVYRSVVS	3740
Qy	2686	RMLTKQREAVSDFVALTSAMQPSMLLKLRLKLVDSVSKLSEYITVALRLLTLHYERCA	2745	Qy	3753	IQRKAVIACFRQTSLSLPHRACNIIPARTYELWLLEENIGOEWMLEDLTQSFEDEL	3812
Db	2673	RMLTKQREAVSDFVALTSAMQPSMLLKLRLKLVDSVSKLSEYITVALRLLTLHYERCA	2732	Db	3741	IQRKAVIACFRQTSLSLPHRACNIIPARTYELWLLEENIGOEWMLEDLTQSFEDEL	3800
Qy	2746	KYVGSTGAGQAGASSDEKRLTMMLFSNI FDSLSKMDYBEPFLFKALPCLIIAGCALP	2805	Qy	3813	KKSDVVBEGEPDPLUTQVTTCRGAMTERSGALQEDPLYNMAYAHIIAKSCGEEBEEGGG	3872
Db	2733	KYVGSTGAGQAGASSDEKRLTMMLFSNI FDSLSKMDYBEPFLFKALPCLIIAGCALP	2791	Db	3801	SKKEGEEETSDPDPULUTQVTTCRGAMTERSGALQEDPLYNMAYAHIIAKSCGEEBEEGGG	3860
Qy	2806	PYLSLKNVDDDEYKQAGADLDNPOYDPOPIINTSSVVALNNDLNTIIVOKFSEHYHDWA	2865	Qy	3873	BEKEGGGAEAEDEGRASIEHEQEMEKQLLPHQARLADRGVAEMVLLHI SASKGIPSEMV	3932
Db	2792	PYLSLKNVDDDEYKQAGADLDNPOYDPOPIINTSSVVALNNDLNTIIVOKFSEHYHDWA	2849	Db	3861	BE--GGEGEGEGEG--TSIHEQEMEKQLLPHQARLADRGVAEMVLLHI SASKGIPSEMV	3916
Qy	2866	SRKIENGWYVGEWSDSQKTHPRKPKYNMLNDYKERYKEPVRESLAKALLAIGWSVEHSE	2925	Qy	3933	MKTLOLGSIIIRGGNIDITOMGMLNHLKOKKOVGFPTSITAGLMNSCSVLDDLDAFERNTKAE	3992
				Db	3917	MTTLNLGAILRGGNIDITOMGMLNHLKOKKOVGFPTSITAGLMNSCSVLDDLDAFERNTKAE	3976

Qy 3993 GLGVLEGAAGEKXNDHAEFTCALFRITQLTCEGHNDWQYLRTOAGNTTNNVVLCTV 4052  
Db 3977 GLGVSEGAAGEKXNDHAEFTCALFRITQLTCEGHNLWQYLRTOAGNTTNNVVLCTV 4036  
Qy 4053 DYLLRLOESIMDFYWHYSSKEIIPAGKANFFKAIGVASOVFNTLTVEIQGPCTQNOAL 4112  
Db 4037 DYLLRLOESIMDFYWHYSSKEIIPAGKANFFKAIGVASOVFNTLTVEIQGPCTQNOAL 4096  
Qy 4113 AHSRLWDAVGGFLFLFSHMQDKLSKSSQVDLLKELLNLQKDMIPMLSLMLBGNVNGTI 4172  
Db 4097 AHSRLWDAVGGFLFLFSHMQDKLSKSSQVDLLKELLNLQKDMITWMLSLMLBGNVNGTI 4156  
Qy 4173 GKQWDTLVESASNVELIKYFDMLPLKDLTSSASFOEDDANNDGWVLPKDFKKEWEO 4232  
Db 4157 GKQWDTLVESASNVELIKYFDMLPLKDLTSSASFOEDDANNDGWVLPKDFKKEWEO 4216  
Qy 4233 KSYTPERTFLACCEHNDKLDYIGCDRPFHPAKEIGFNLAVALTINLSEHMPNPR 4292  
Db 4217 KNYTPEEMDFLACCEHNDKLDYIGCDRPFHPAKEIGFNLAVALTINLSEHMPNPR 4276  
Qy 4293 ARFLETAGSVLNYPFPLGRIEIMGSKRIERVYFEIKESNIEQWKPQIKESKRAFFYS 4352  
Db 4277 ARFLETAGSVLNYPFPLGRIEIMGSKRIERVYFEIKESNIEQWKPQIKESKRAFFYS 4336  
Qy 4353 IVTEGGDKKLEAFNFCDEDAIFEMTHASGLMAAEEVSGTKNREASY-MYMGDDDDER 4411  
Db 4337 IVTEGGDKKLEAFNFCDEDAIFEMTHASGLMAAEEVSGTKNREASY-MYMGDDDDER 4394  
Qy 4412 AGKOPPRGLQSDGVATATSSISPSNIIKAKIADMOQMPAEIAGVFFKMFYLYLG 4471  
Db 4395 AARDPIRTITAVKEGLKFGVHMLSPANIKQIGVMQTKSIPELIVGFFKIIFYITG 4454  
Qy 4472 YGVLVWVRYIFGVLLGLMRGQTPDEPPPEPEEKEIGQLRHRLATOSSRHLPPALPAD 4531  
Db 4455 YAHFCVRYIFGILLNMRGAPAPQEBEPPVVEETFG-----RALPPLPLEEP 4502  
Qy 4532 TGQMVSAFGIDITKEDNGOIQVHPESPSTSTSSGEEAEVSPDESADHTEE----- 4584  
Db 4503 PGTVQ--AFGLDINKEENGMKVHVHESPANSSMEEGES--SPEDGAASGEIIVGEPEH 4558  
Qy 4585 QRPESLDLGEQAKQAQERMAQAQAQAQAQAQAQAQAQAQAQAQAQAQAQAQAQAQAQA 4643  
Db 4559 QEPISIVDLGGEAAKQAQERMAQAQAQAQAQAQAQAQAQAQAQAQAQAQAQAQAQAQAQA 4618  
Qy 4644 YTRAVSFLARNFYNLKYVALVLAFCINFLVLLFYKYSTLDGEGEGSGGLDIIAGGSGS 4703  
Db 4619 YTHRAVSFLARNFYNLKYVALVLAFCINFLVLLFYKYSTLDGEGEGSGGLDIIAGGSGS 4677  
Qy 4704 GA---GS---GSGDGSSEGE-DDDALEVVHIDBDFYMEHVIMAAVLHISIVSLAILIG 4756  
Db 4678 GADITGSGFGSGDGSSEGEDEIPELVHDEDFYMEHVIMAAVLHISIVSLAILIG 4737  
Qy 4757 YHLLKVPPLAIKREKEIARKEFGLYTAEOPEDDDLKSHWDKLVISAKSPVNVWDKFV 4816  
Db 4738 YHLLKVPPLAIKREKEIARKEFGLYTAEOPEDDDLKSHWDKLVISAKSPVNVWDKFV 4797  
Qy 4817 KKKVRAKYSEYDFDSISNMLGMEKTSFSAQEEGSKGLIHYINIDWRYQVWKAQVIT 4876  
Db 4798 KKKVRAKYSEYDFDSISNMLGMEKTSFSAQEEGSKGLIHYINIDWRYQVWKAQVIT 4856  
Qy 4877 DNSFLYSWYFSFSGVGNFNNFFFAAHLDDVAVGFKTLRTILQSVTHNGKOLVITVMLLT 4936  
Db 4857 DNAFLYSWYFSFSGVGNFNNFFFAAHLDDVAVGFKTLRTILQSVTHNGKOLVITVMLLT 4916  
Qy 4937 IIVYITVIAFNFRKFVQDEDEVNENCHDMLTCFVFNLYKGVRAAGGIGDELEPDG 4996  
Db 4917 IIVYITVIAFNFRKFVQDEDEVNENCHDMLTCFVFNLYKGVRAAGGIGDELEPDG 4976  
Qy 4997 DDSEYRIIFDISPFFFIIVILLATLOGLIIDAQFGLRDQLESVKEDMESNCFICGINK 5056  
Db 4977 DDSEYRIIFDISPFFFIIVILLATLOGLIIDAQFGLRDQLESVKEDMESNCFICGINK 5036

RESULT 9

US-10-668-767-120  
; Sequence 120, Application US/10668767  
; Publication No. US20040171114A1  
; GENERAL INFORMATION:  
; APPLICANT: Caspar, Timothy  
; APPLICANT: Cordova, Daniel  
; APPLICANT: Guttridge, Steven  
; APPLICANT: Rauh, James  
; APPLICANT: Smith, Rejane  
; APPLICANT: Tao, Yong  
; APPLICANT: Wu, Jihong  
; TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors  
; FILE REFERENCE: BB1533 US NA  
; CURRENT APPLICATION NUMBER: US/10/668,767  
; CURRENT FILING DATE: 2003-09-23  
; PRIOR APPLICATION NUMBER: 60/412,795  
; PRIOR FILING DATE: 2002-09-23  
; PRIOR APPLICATION NUMBER: 60/427,324  
; PRIOR FILING DATE: 2002-11-18  
; NUMBER OF SEQ ID NOS: 149  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 120  
; LENGTH: 5127  
; TYPE: PRT  
; ORGANISM: Drosophila melanogaster  
; FEATURE:  
; OTHER INFORMATION: gi 17352465  
US-10-668-767-120

Query Match 79.7%; Score 21360; DB 4; Length 5127;  
Best Local Similarity 78.9%; Pred. No. 0;  
Matches 4090; Conservative 448; Mismatches 522; Indels 122; Gaps 41;

Qy 1 MAEAGCASQDDVSFLRTEDMVCISCTATGERVCLAAEGFGRHCFLENIADKNIPDL 60  
Db 1 MAEAGG-SEQDDVSFLRTEDMVCISCTATGERVCLAAEGFGRHCFLENIADKNIPDL 59  
Qy 61 SQCVFVIEQALSVRALQELVTAAGSETGKGTGSHRTLLYGNAILLRHNSDMYLACLST 120  
Db 60 SQCVFVIEQALSVRALQELVTAAGSETGKGTGSHRTLLYGNAILLRHNSDMYLACLST 119  
Qy 121 SSSQDKLAFDVLGLOQHSQGEACWTLHPASKQSEGEKVRGDDLLVSVATERYLHTTK 180  
Db 120 SSSNDKLSFDVLGLOQHSQGEACWTLHPASKQSEGEKVRGDDLLVSVATERYLHTTK 179  
Qy 181 ENEQSIIVNASFHTHNSVQPYGTGISMKVGVYVFGDVLRFPHGGDECLTIPSTWTKG 240  
Db 180 ENEQSIIVNASFHTHNSVQPYGTGISMKVGVYVFGDVLRFPHGGDECLTIPSTWTKG 239  
Qy 241 GQNIIVYEGSVMSQARSRLRLARLTKWAGGFINWHPMRIRHITGRYLVGNVNDNELY 300  
Db 240 GQNIIVYEGSVMSQARSRLRLARLTKWAGGFINWHPMRIRHITGRYLVGNVNDNELY 299  
Qy 301 LVREEAATASCAPFLRQEKDDQKQVLEDKLEVGAPIIKYGDSTVVOHSETGLWLSY 360  
Db 300 LVKKEEASIAATTFCLRQEKDDQKQVLEDKLEVGAPIIKYGDSTVVOHSETGLWLSY 359  
Qy 361 KSVETKKKGKVEEKAQIILHEGKMDGDLDFSRQSEESRTARVIRKCSLFTKFTINGL 420  
Db 360 KSVETKKKGKVEEKAQIILHEGKMDGDLDFSRQSEESRTARVIRKCSLFTKFTINGL 419  
Qy 421 ETLQENRRHSMTFASVNLGEMVMCLEDLINYFAQPDDEMEHEEKQNKFRALRNQDLPQE 480

Db 420 ETLOGNRRHSIPFQKVNLMNVMCLDLINYPQPEDDWEHEEKQNRFRALNRQDLPOE 479  
Qy 481 EGILNLIIEADIKINIVTSQGLAGDESGOSWEMISGVLQOLLAIIKGNHNTCAQ 540  
Db 480 EGVNLIIIEADIKINIVTSQGLASFLAGDETGQSDWLLISTYLYQLLAAIIKGNHNTCAQ 539  
Qy 541 FANSNRLNWLFSRLGQSASGEGTGMDLVHLCVLDSPALNMNRDEHIKVIISLLEKHGR 600  
Db 540 FANSNRLNWLFSRLGQSASGEGSGLMDVHLCVLDSPALNMNRDEHIKVIISLLEKHGR 599  
Qy 601 DPKVLDTLCSLCVGVGAVRSSONNICDYLIPGKNLLLOLALVHVSVRPNIFVGRVEG 660  
Db 600 DPKVLDTLCSLCVGVGAVRSSONNICDYLIPGKNLLLOLALVHVSVRPNIFVGRVEG 659  
Qy 661 SAVYRKWFEVMTMDHIEKTHMPHLRGWANTTGYVYPGGEKWKGVGDDLYSYGF 720  
Db 660 SSMYQKWFEVMTMDHIEQTHMPHLRGWANTSGYVYPGGEKWKGVGDDLYSYGF 719  
Qy 721 DGAYLWSGGRKTPVNRTHAEPEYIRKGDVIGCALDLTVPIINFMEGVVRVTGSFTNFNLE 780  
Db 720 DGAFWTGGRKTLVVDALPEEPFIRKGDVIGVAILDSVPIITFTENGKVRGSPDFNLD 779  
Qy 781 GMFFPVISSCKSLSCRFLLGGHGLRYAAPGYSPLVESLLPOQILSLEPCFYFNGLSK 840  
Db 780 GMFFPVMSSCKSLSCRFLLGGHGLKFPAPMGFSALVQCLMPQOILSLDPCFYFNGLAK 839  
Qy 841 RALAGPPLVODDTAFVPTPVDTLQITLPTYVEQIRDKLAENIHENWANKIEAGHWYGDQ 900  
Db 840 NYLAGPWLIEDTAFVFPKVDVTGTVLPSSVDQIKEKLAENIHENWALNKIEAGWSGEH 899  
Qy 901 REDLHKIHPCLVFPFRLPAEKRYDIOQLAVQTLKTLALGYYSILDKPPARIRNRVLNE 960  
Db 900 RODYRHIHPCLTHFEKLPAAEKRYQNLAVQLTKIISLYYITWDKPPARIRPVLNE 959  
Qy 961 PFMQSGNGKPAPLDLASVTLTPKMBELVDQLAENTHNLWARERIQQGWTYGLNEDSDMR 1020  
Db 960 IFMQGNGKPAPLDLASVTLTPKLEELVDQLAENTHNLWARERIQQGWTYGLNEDSENHR 1019  
Qy 1021 SHPLVPYKVDIAIKANRDTASETVRTLLVGYMLDPTTGOHEALLLEASKQOQADPR 1080  
Db 1020 SHPLVPYAKVDEAIKANRDTASETVRTLLVGYVLDPTTGEGETALLAEAQRLAPFGR 1079  
Qy 1081 TYRAEKYAVSSGKWFPEEILTAGPMRVGAHADWAPGMMLGDBENSWAPDGYNEEKYV 1140  
Db 1080 TYRVERNYAVTSKGYFEEVLTSGPMRVGMARADCYPGMLGSEDTSWAFDGHVNTKWH 1139  
Qy 1141 SGNTESEFGQWAGVDVGVFLDLIDKTIISFSLNGELLMDALGETTFADV--QGDNFVPA 1198  
Db 1140 AGSIEHFVRYEAGDVIGCFIDVKEQTIISFSLNGELLMDALGETTFADVTAEGVGFVPA 1199  
Qy 1199 CTLGVGQKARLYGQDVNTLYFTTCGLQEGVEPFCVNMKRDVTHWYTKQDPIFENTDEM 1258  
Db 1200 CTLGVGQKARLYGQDVNTLSKFTTCGLQEGVEPFCVNMRRPVTHWYTKQDPIFENTDEM 1259  
Qy 1259 IDTRIDVTPIPAGSTPPCLKISHTNFTFMEXKANFEFLSLPVICHNEFIDEAEKARRW 1318  
Db 1260 PBCRIDVTPIPGADTPPHLKIISHTNFTFMEXKANFEFLSLSPVTCOMGEFISEQEKARRW 1319  
Qy 1319 VEIKORQOILMKEA-VEAQM-----PAHIDQIMRSQFTMNDIKGLHYE--DNQEEPLSSRM 1371  
Db 1320 DEIKROYRLMEAEATAAQOVQTAHNDHMLKGGFNMDIKGLTRNFDEHADAADHM 1379  
Qy 1372 KRLPSRPPRGSMTRGVITONYNLQPGVNGHMRSTSEAEWAKYDVLGAQGLTPDQDKDK 1431  
Db 1380 MRGPNRPPRGSLTRNIT---PETDMSAALDEMQRSTS-----VLDMNLGGEEMDDK-K 1430  
Qy 1432 RGRSPKFRSKGESSDRASKSKTTPDFSDTEVSPERGARRPNPQIKVQANQRYNG 1491  
Db 1431 RGRSPKFPF--SKKSRDQSRK-MGARTLDTSLERRNTVAHGRNVVNVNQMTTRAPTLRLNN 1488  
Qy 1492 MNAPSRNTLYGSQVGLNMATPTQDRKQMTTSTLAQSAETATVGNETIFDAECLKLINEFY 1551  
Db 1489 AEIPSPFV-----PQGPQLSGSGLGQOPVETSGDEMFAECLKLINEFY 1534

Qy 1552 GVRYPQDPTHVYIGWVTTQYHLHSKDFNQSKVTKSVIITDDYDRVVENVRQSCVMV 1611  
Db 1535 GVRIFPQDPTHVYIGWVTTQYHLHSREFKNKNVRRGVSIVIEDDYEMAIBRIDQSCVMV 1594  
Qy 1612 RADELYNEVMAEATAKASQGMFICGSVDSTSGSVSTCEGKDTSPFKKMEPEFKLPAL 1671  
Db 1595 RADELNEVTDASGKGSQGMFVGCFTATGIRFTCEGKDTSHRMMEPDTKLPAL 1654  
Qy 1672 FVEATSEIIOLEIELGRSATSLPLSAAVLPTSDKHVIOFPFRLKVQCLKPHOWARVPNOS 1731  
Db 1655 FVEATSEIIOLEIUGRPTTLLPLSAAVLPTSDKHINPQSPRLKVQCLRPHQWARPNTA 1714  
Qy 1732 LQVHALKLSIDIRGWSMLCEDAVSMALHIPEEDRCIDILEPIENDKILSPHSHTLTLYAA 1791  
Db 1715 LQVHALKLSIDIRGWSMLCEDAVSMALHIPEEDRCIDILEPIENDKILSPHSHTLTLYAA 1774  
Qy 1792 LCYQSNVRAAHALCTHVDQKOLLYAIOQYWSGRLPGFYDILLIALHLESHATWAEACN 1851  
Db 1775 LCYQSNVRAAHALCQHVDQKOLLYAIRSEVMSGRLQGFYDILLIALHLESHATWAEACN 1834  
Qy 1852 EFVITPLGPELKALYEEEDPMGHSLSLOTESVRPQMKMTDI-----AESITE 1897  
Db 1835 EYITPLGAELKELYSDEEMQHSLSLVTESVRPQLRMTEITPPVIAITSSMSVSEPIPD 1894  
Qy 1898 ISNLYSPVFPLEVAREFVMOALAEAVETNOVHNDRDPVGGSNENFLPLIKLVDRLLLYGM 1957  
Db 1895 IDQIYSPKFPLEVVRQFWEALKDAVEINQVHNDRDPVGGSNENFLPLIKLVDRLLLYGM 1954  
Qy 1958 MRDEVEKLLIMTNPETWDPSPFDEKGDHHRKGLLHMHMAAGAKLQMCYLLLOHLNDIOJR 2017  
Db 1955 LTDESDVQKLLVMDPETWQAFEREKGDHHRKGLLHMHMAAGAKLQMCYLLLOHLNDIOJR 2014  
Qy 2018 HRVEAITAFADHFDVGDLOTDLRYTEIKOSDLSAAVAAKKTREFRCPREPMQNAILSPK 2077  
Db 2015 HRVESIIAFSDHFDVGDLOTDLRYTEIKOSDLSAAVAAKKTREFRCPREPMQNAILSPK 2074  
Qy 2078 HLEBEDKENCPCGBELTARMNEFHTLMAHVSLSALQEPDAAENOE--PEAKPGAFGLYN 2136  
Db 2075 NLEPDDQONCTCGLRGLRGDFHDSLMQKVSINALQEPDGVGTAIEBVKTGPTIKIYN 2134  
Qy 2137 IINTVKELEEBEAKAIEEPPKKTPEEKFKVLIQITVNMWAEESQIETPKLVREMFSLLRQ 2196  
Db 2135 FINTVKELEEBEKEVEBEPEKKTPEEVFRKVLIKTIVSWAEESQIENPKLVREMFSLLRQ 2194  
Qy 2197 YDAVGEILRALIKTYVINAKTKLDAENWVGLSQIRALLPVQMSQEBEELMRKRLWKLVN 2256  
Db 2195 YDTVGEIVRALIKTYVINTRADDVAEMWVGLSQIRALLPVQMSQEBEELMRKRLWKLVN 2254  
Qy 2257 NHTPFQHPDLIRLVLRVHENVMAVMNMTLGRRAQASDAQSPSSQPVAE--DSKEKDTSHM 2314  
Db 2255 NATPFQHPDLIRLVLRVHENVMAVMNMTLGRRAQASDAQSPSSQPVAE--DSKEKDTSHM 2313  
Qy 2315 WVACCRFLCYFCRTGRQNKAMFDFHFLLENSNILLSRPSLRGSTPLDVAVSSSLMENTE 2374  
Db 2314 WVACCRFLCYFCRTGRQNKAMFDFHFLLENSNILLSRPSLRGSTPLDVAVSSSLMENTE 2373  
Qy 2375 LALALREHYLEKIAVILSRGLOSNSELVEKGYPDGLHNDPVEGERYLDLFLRCVWNGES 2434  
Db 2374 LALALREHYLEKIAVILSRGLOSNSELVEKGYPDGLHNDPVEGERYLDLFLRCVWNGES 2433  
Qy 2435 VEENANLVIRLLIRPECLGPALRGEGGLLKAIVDANKMSBRIADRRKLREMEQBGDV- 2493  
Db 2434 VEENANLVIRLLIRPECLGPALRGEGGLLKAIVDANKMSBRIADRRKLREMEQBGDV- 2492  
Qy 2494 --NFSHPLEPSEDEDEYIDTGAAILNFYCTLVDLGRCAPDAGVITALGNESLRARAILR 2551  
Db 2493 GLNFTHPLPGEDEDEYIDTGAAILNFYCTLVDLGRCAPDASVIEQGNESLRARAILR 2552  
Qy 2552 SILVPLEDIOGVLSURFTLNPAAGERPKNSDMPSGLIFGHKQSVGLFLERVYGIETOLF 2611  
Db 2553 SILVPLEDIOGVLSURFTLNPAAGERPKNSDMPSGLIFGHKQSVGLFLERVYGIETOLF 2612



Db 4738 ACLSHLSVLAHLIAYHLLKVLPLAIPKREKEIARRLEFEGLFIAEQPEDDDDFKSHWDKLV 4797  
Qy 4803 SAKSPVNVWDFKVKVKYAKYSEYDFDSISNMLGMEKTSFSQAEBEGSKGLIHYIINI 4862  
Db 4798 SAKSPVNVWDFKVKVKYQKYSYDFDSISNMLGMEKTSFAAQESB-ETGIKFIYINWI 4856  
Qy 4863 DWRYQVWKAGVTITDNSFLYSLSWYFSFSGMGNFNNFFFAAHLDDVAVGFKTLRTILQSVT 4922  
Db 4857 DWRYQVWKAGVTITDNLFLYSLSWYFSFSGMGNFNNFFFAAHLDDVAVGFKTLRTILQSVT 4916  
Qy 4923 HNGKQLVLTVMLLTIIIVYIVIAENFRKFFVQBEDDEVRNCHDMLTCFVFNLYKQVR 4982  
Db 4917 HNGKQLVLTVMLLTIIIVYIVIAENFRKFFVQBEDDEVRNCHDMLTCFVFNLYKQVR 4976  
Qy 4983 AGGGIGDELEPPDGDSDSEYRIIPDISPFFFTIIVALLIOGLIIDAFAEGLRDLQESVKE 5042  
Db 4977 AGGGIGDEIGDDGDGYEYRIIPDITFFFFVIIILLALIOGLIIDAFAEGLRDLQESVKE 5036  
Qy 5043 DMESNCFICGINKDYFDKVPYHGFDTTHVQREHNLANYMFFLMHLINKPDTYTGQTYVYN 5102  
Db 5037 NMESNCFICGKMGKDFDVPYHGFDTTHVQREHNLANYMFFLMHLINKPDTYTGQTYVYN 5096  
Qy 5103 MYQRCWDFPVPVGDGCFRQYED 5124  
Db 5097 MYQRCWDFPVPVGDGCFRQYED 5118

RESULT 10

US-10-668-767-10  
; Sequence 10, Application US/10668767  
; Publication No. US2004017114A1  
; GENERAL INFORMATION:  
; APPLICANT: Caspar, Timothy  
; APPLICANT: Cordova, Daniel  
; APPLICANT: Gutteridge, Steven  
; APPLICANT: Rauh, James  
; APPLICANT: Smith, Rejane  
; APPLICANT: Tao, Yong  
; APPLICANT: Wu, Lihong  
; TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors  
; FILE REFERENCE: BB1533 US NA  
; CURRENT APPLICATION NUMBER: US/10/668,767  
; CURRENT FILING DATE: 2003-09-23  
; PRIOR APPLICATION NUMBER: 60/412,795  
; PRIOR FILING DATE: 2002-09-23  
; PRIOR APPLICATION NUMBER: 60/427,324  
; PRIOR FILING DATE: 2002-11-18  
; NUMBER OF SEQ ID NOS: 149  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 10  
; LENGTH: 5109  
; TYPE: PRT  
; ORGANISM: Drosophila melanogaster  
US-10-668-767-10

Query Match 79.6%; Score 21326; DB 4; Length 5109;  
Best Local Similarity 79.0%; Pred. No. 0;  
Matches 4081; Conservative 450; Mismatches 527; Indels 108; Gaps 40;  
Qy 1 MAEAGGAGEQDDVSPFLRTEDMVCLISCTATGERVCLAAEGFNGRHCFLNIADKNIPDL 60  
Db 1 MAEAGG-SEQDDVSPFLRTEDMVLTCTATGERVCLAAEGFNGRHCFLNIADKNVPPDL 59  
Qy 61 SQCFVIEQALSVRALQELVLAAGSETGTGSGHRTLLYGNAILLRHNSMYLACLST 120  
Db 60 SQCFVIEQALSVRALQELVLAAGSETGTGSGHRTLLYGNAILLRHNSMYLACLST 119  
Qy 121 SSSQDKLAFDVLQHQSGEACWTLHPASKORSEGEKVRVGDGLILSVATERYLHTTK 180  
Db 120 SSSNDKLSFDVLQHQSGEACWTLHPASKORSEGEKVRVGDGLILSVATERYLHTTK 179  
Qy 181 ENEVSIVNASFHVTHWSVOPGTGSRMKYGVYFGDGLRFFHGGDECLTIPSTWTGKG 240  
Db : :

Db 180 ENEOSIVNASFHVTHWSVOPGTGSRMKYGVYFGDGLRFFHGGDECLTIPSTWGREA 239  
Qy 241 QONIVVYEGSVMSQARSRLARLELARTKWAGGFNNYTHPMRIRHITTGRVLGVNDQNELY 300  
Db 240 QONIVVYEGSVMSQARSRLARLELARTKWAGGFNNYTHPMRIRHITTGRVLGVNDQNELY 299  
Qy 301 LVSREERATTASCFLRQEKDDQKQVLEDKOLEVIGAPIIKYGDSTVIVQHSETGLWLSY 360  
Db 300 LVKKEEASIAITTTCLRQEKDDQKQVLEDKOLEVIGAPIIKYGDSTVIVQHSETGLWLSY 359  
Qy 361 KSVETKKKGVKVEKQAILHEEGKDDGLDFSRSQSEESTARVIRKCSLSLTKFJNGL 420  
Db 360 KSVETKKKGVKVEKQAILHEEGKDDGLDFSRSQSEESTARVIRKCSLSLTKFJNGL 419  
Qy 421 ETLQENRRHSFFASVNLGEMVMCLEDLINYFAQDEDEMEHEEKONFRALNRQDLFOE 480  
Db 420 ETLQENRRHSFFASVNLGEMVMCLEDLINYFAQDEDEMEHEEKONFRALNRQDLFOE 479  
Qy 481 EGIUNLILEAIDKINVTISQGLAGFLAGDESGOSWEMI SGYLLQLLAAIIKGHTNCAQ 540  
Db 480 EGIUNLILEAIDKINVTISQGLAGFLAGDESGOSWEMI SGYLLQLLAAIIKGHTNCAQ 539  
Qy 541 FANSNRLNWLFSRLGSGASGEGTGMLDVHLHCVLIDSPEALNMMRDEHIIKVIISLEKHGR 600  
Db 540 FANSNRLNWLFSRLGSGASGEGTGMLDVHLHCVLIDSPEALNMMRDEHIIKVIISLEKHGR 599  
Qy 601 DPKVLDVLCSLCVGNGVAVRSSQNNICDYLPGKNLLLTALVDHVSVRPNI FVGRVEG 660  
Db 600 DPKVLDVLCSLCVGNGVAVRSSQNNICDYLPGKNLLLTALVDHVSVRPNI FVGRVEG 659  
Qy 661 SAVYRKWYFEVTMDHIEKTHMHPHLRIGWANTTGYVPYGGGKMGNGVGGDLYSYGPF 720  
Db 660 SSMYQKWYFEVTMDHIEKTHMHPHLRIGWANTTGYVPYGGGKMGNGVGGDLYSYGPF 719  
Qy 721 DGAYLWSGGRKTPNVRTHABEPIYRKGDVIGCALDLTVPIINFMFNGVRVTSFNTNLE 780  
Db 720 DGAYLWSGGRKTPNVRTHABEPIYRKGDVIGCALDLTVPIINFMFNGVRVTSFNTNLE 779  
Qy 781 GMFFPVISSCSKLSRFLGGEHGRRLRYAAPEGSPVLESLLPQOILSLEPCFYFGLNLSK 840  
Db 780 GMFFPVISSCSKLSRFLGGEHGRRLRYAAPEGSPVLESLLPQOILSLEPCFYFGLNLSK 839  
Qy 841 RALAGPPLVQDDTAFVPPVDTLOITLPTVYEQIRDKLAENIHEMWAANKIEAGHWGDEQ 900  
Db 840 NVLAGPWLIEDDTAFVPPVDTLOITLPTVYEQIRDKLAENIHEMWAANKIEAGHWGDEQ 899  
Qy 901 REDLHKHPCLVPPERLPPAEKRYDIOAVOTLTKILALGYVVISLDEKPARIRNVRLENE 960  
Db 900 RDDYHRIHPCLTHFEKLPAAEKRYDIOAVOTLTKILALGYVVISLDEKPARIRNVRLENE 959  
Qy 961 PFMOSNGYKPAPLDLSAVTLTPKMDLVQDLAENHNLWABERIQOQWYTYGLNEDSDMHR 1020  
Db 960 PFMOSNGYKPAPLDLSAVTLTPKMDLVQDLAENHNLWABERIQOQWYTYGLNEDSDMHR 1019  
Qy 1021 SPHLVVPYKVDDAIKKANRDTSATVTRTLVYGYMLDPPTEGQHEALLLEASQKQADPR 1080  
Db 1020 SPHLVVPYKVDDEIKKANRDTSATVTRTLVYGYMLDPPTEGQHEALLLEASQKQADPR 1079  
Qy 1081 TYRAKNAVSSGKWFYFEFILLTAGPMRVGHADMAFGMLGODENSWAGDYNEKVVY 1140  
Db 1080 TYRVERNAVYSGKWFYFEFILLTAGPMRVGHADMAFGMLGODENSWAGDYNEKVVY 1139  
Qy 1141 SGNTESEKONAVGVDVGVFLDLTKTISFSLNGELLDALGGETTFADV--QGDNFVPA 1198  
Db 1140 SGNTESEKONAVGVDVGVFLDLTKTISFSLNGELLDALGGETTFADV--QGDNFVPA 1199  
Qy 1199 CTLGVGQKARLYGQDVNTLKYFTTCGLQEGYEPFCVMKRDVTHWYTKQDIPFNTDEM 1258  
Db 1200 CTLGVGQKARLYGQDVNTLKYFTTCGLQEGYEPFCVMKRDVTHWYTKQDIPFNTDEM 1259  
Qy 1259 IDTRIDVTRIPAGSDTTPCLKISHNTFETMEKANWFLRLSLPVI CHNEFTIDEAKARRW 1318  
Db 1260 PDCRIDVTRIPAGSDTTPCLKISHNTFETMEKANWFLRLSLPVI CHNEFTIDEAKARRW 1319





Db 3442 LKDPFLPLAERVKRTENMLHKEDSMRGFIKSATDDTSQVETQLQEDWNLLVRDIYSFVP 3501  
QY 3526 LLIKYVDLQRNHLNRNNPEAREELYNHVAEININWSQYFLKBEQNFISANEIDNMVLI 3585  
Db 3502 LLIKYVDLQRNHLNNDIPAEAREELYNHVAEININWSQYFLKBEQNFISANEIDNMALI 3561  
QY 3586 MPTATRRVTAVDGTPOGGG--KKKKHRDKKDKDKEVQASLMVACLRLLPVGNLNFA 3643  
Db 3562 MPTATRR-SAISEGAPAVGGVKKKKGNPKDKDKDKEVQASLMVACLRLLPVGNLNFA 3620  
QY 3644 GREQLVQHKCDRFLKCKMSEQDVAEPKATQTLPLPKIDPADMSQWYLYSKLGSKSN 3703  
Db 3621 GREQLVQHKCDRFLKCKMPEYDVEBFARNQLTLPDKLDPDSQWYLYSKLG-KTBE 3679  
QY 3704 IIVETAENKAKT-----IDDTVERIVAMSKVLFGHMTDHPQOQSKNRYRVSQ 3754  
Db 3680 VD-EQALEKANYNSNEKGDKTQETVDRIVAMAKVLFGHMTDHPQOQSKNRYRVSQ 3738  
QY 3755 RKRVIACPROTSLHSLPHRACNIFARTYVELWLBEENIGQEVMIEDLTQSFDAELKK 3814  
Db 3739 RKRVIACPROTSLHSLPHRACNIFARSYYQWLOEENVGQEVMIEDLTQSFDAELKK 3798  
QY 3815 SDVBEKEGKPDPLTQVLTTCRGAMTERSGALQEDPLYSYAHIIAKSCGEEBEGGDE 3874  
Db 3799 KSGEETDSKPDPLTQVLTTCRGAMTERSGALQEDPLYSYAHIIAKSCGEEBEGGDE 3858  
QY 3875 EGGGEAEABDGRASIHQEMEKOKLPHQARLADRGVAEMVLHIHISAKGLPSEMVMK 3934  
Db 3859 ---GGGGEAEABG-TSIIHQEMEKOKLPHQARLADRGVAEMVLHIHISAKGLPSEMVMK 3914  
QY 3935 TLQGLSILRGNDIQMGLMHLKDKDVGFTTSIAGLMNSCVLDLDAERNNTKAELG 3994  
Db 3915 TLNLGAILRGNDIQMGLMHLKDKDVGFTTSIAGLMNSCVLDLDAERNNTKAELG 3974  
QY 3995 GVGLEGAAGEKMHDAEFTCALFRITQTCGHNLDQWYLYRTOAGNTTNNVVICTVDY 4054  
Db 3975 GVGSEGAAGEKMHDAEFTCALFRITQTCGHNLDQWYLYRTOAGNTTNNVVICTVDY 4034  
QY 4055 LRLQESIMDFVHYSKELIDPAGKANPFAKIGVASQVNTLITEVIGQPCPTQNOQALAH 4114  
Db 4035 LRLQESIMDFVHYSKELIDPAGKANPFAKIGVASQVNTLITEVIGQPCPTQNOQALAH 4094  
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Db 4095 SRLWDAVGGFLFSLHMQDKLSHSSQVLLKELNLQKDMIPMLSMLEGNVNGTIGK 4154  
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Db 4155 QMVDTLVESASNVELLTKYDFMFLKLADLIESPSPHEVDMKNEGWTPKDFKEMEQOKS 4214  
QY 4235 YTPETIEFLACCTNHDGKLDYIGPCDRFHPKAEIGNLAVALTLNLSEHNPBPRLAR 4294  
Db 4215 YTPETIEFLACCTNHDGKLDYIGPCDRFHPKAEIGNLAVALTLNLSEHNPBPRLAR 4274  
QY 4295 FLETAGSVLNYEPFLGRITGMSKRIERVVFETKESNIEQWKPQIKESKRAFPYSIV 4354  
Db 4275 FLETAGSVLNYEPFLGRITGMSKRIERVVFETKESNIEQWKPQIKESKRAFPYSIV 4334  
QY 4355 TEGGDKKELEAFVNFCEDAIFEMTHASGLMAAASSESVGCTKNREASY-MYMGDDDDDERAG 4413  
Db 4335 TEGGDKKELEAFVNFCEDAIFEMTHASGLMATDDG--GGNVKRDATSYSSYMSSEBERAA 4392  
QY 4414 KDPFRGLQSVKGVATAFSSISPSNIIKAKIADMQMPAPBLAVGFFKMFYLYLVG 4473  
Db 4393 RDPRIITAVKEGLKFGVHMLSPANIKHIGVMTKSIPELIVGFFKLIIFYVYTGVA 4452  
QY 4474 VLWVRYIGVLLGIMRGQTOBPPPEPEEKEIGQLRHLLATQSSRLPALPADDTG 4533  
Db 4453 HFCVRYIFGILLNMRGPAQEPPEPVVEETFG-----RALPPLSLEPPG 4500  
QY 4534 QMVSAGFLDKEDNGQIQVPHSPSTSTPSSGEEAVSPDESADHTEE-----QR 4586

Db 4501 TVQ--AFGLDINKBEANGMYKVVVHSPANSMBEGGES--SPEDGAAASBELVEGEHQG 4556  
QY 4587 PPSLIDLLGBOAKQOERMEAOAQAQAASAEAEAKKAVQGPAPS-ALSOVDLSQYT 4645  
Db 4557 PISIVDLLGGBAKKAQERQEAQAQAANASAEAEAKKSSAPQETPAVHQIDFSQYT 4616  
QY 4646 RRAVSFLARNFYNLKYVALVAFNCINFLVLYKYVSTLDEGEGGSGGLGDIITAGGSGSGA 4705  
Db 4617 HRAVSFLARNFYNLKYVALVAFNINFLVLYKYVSTLDEGEGGSGGLGDIITAGGSGSGA 4675  
QY 4706 ---GS---GSDGSGEGSE--DDDALEVVHIDEDEFFMEHVIKMAVLHSIVSLATLIGYV 4758  
Db 4676 DITSGFGSGSGSGSGGDEMEIPELVHDEDEFFMEHVIKMAVLHSIVSLATLIGYV 4735  
QY 4759 HLKVPALATFKKEKEIARLEFDGLVIAEQPDDDLKSHWDKLVISAKSPVNYWMDKFKVK 4818  
Db 4736 HLKVPALATFKKEKEIARLEFDGLVIAEQPDDDLKSHWDKLVISAKSPVNYWMDKFKVK 4795  
QY 4819 KVRKYSITYDFDISINMLGMEKTSFSAQEEBEGSGKLIHYIINIDRWYQVWKAQVTITDN 4878  
Db 4796 KVRKYSITYDFDISINMLGMEKTSFSAQEEBEGSGKLIHYIINIDRWYQVWKAQVTITDN 4854  
QY 4879 SFLYSLVYFSPVSMGNFNNFFAAHLLDVAVGFKTLRTILOSVTHNGKQLVLTVMLLTII 4938  
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Db 4975 SEVRIIPIDISFFPFIIVILLAIQGLIIDAFGLRDQLESVKEDMESNCFICGINKDYF 5034  
QY 5059 DKVPHGPDTHVQREHNLANYPFLLMLINKDPTTGTQETVWNYTORCWDFFVGVGDF 5118  
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RESULT 11

US-11-097-143-22563  
; Sequence 22563, Application US/11097143  
; Publication No. US20050208558A1  
; GENERAL INFORMATION:  
; APPLICANT: Venter, J. Craig  
; APPLICANT: et al.  
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID  
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE  
; TITLE OF INVENTION: DROSOPHILA GENES.  
; FILE REFERENCE: CL000728  
; CURRENT APPLICATION NUMBER: US/11/097,143  
; CURRENT FILING DATE: 2005-04-04  
; PRIOR APPLICATION NUMBER: 60/157,832  
; PRIOR FILING DATE: 1999-10-05  
; PRIOR APPLICATION NUMBER: 60/160,191  
; PRIOR FILING DATE: 1999-10-19  
; PRIOR APPLICATION NUMBER: 60/161,932  
; PRIOR FILING DATE: 1999-10-28  
; PRIOR APPLICATION NUMBER: 60/164,769  
; PRIOR FILING DATE: 1999-11-12  
; PRIOR APPLICATION NUMBER: 60/173,383  
; PRIOR FILING DATE: 1999-12-28  
; PRIOR APPLICATION NUMBER: 60/175,693  
; PRIOR FILING DATE: 2000-01-12  
; PRIOR APPLICATION NUMBER: 60/184,831  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: 60/191,637  
; PRIOR FILING DATE: 2000-03-23  
; NUMBER OF SEQ ID NOS: 43008

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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22563
; LENGTH: 5107
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-22563

Query Match      79.4%; Score 21270.5; DB 6; Length 5107;
Best Local Similarity 78.9%; Pred. No. 0;
Matches 4070; Conservative 448; Mismatches 522; Indels 121; Gaps 40;

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Db 1 MVTLSCTATGRRVCLAAAGFGNRHCFLENIADKNVPDLSOCVVFIEQALSVRALQELVT 60
Qy 82 AAGSETGKTGSGHRTLLYGNAILLRHLSNMYLACLSTSSSQDKLAFDVGLOQHSQGEA 141
Db 61 AAGSETGKTGSGHRTLLYGNAILLRHNSDMYLACLSTSSSNDKLSFDVGLQHSQGEA 120
Qy 142 CWTWLPASKORSSEGEKRVGGDDLILSVATERYLHTTKENEVSIVNASPHVTHWSQPY 201
Db 121 CWTWLPASKORSSEGEKRVGGDDLILSVATERYLHTTKENEQSIIVNASPHVTHWSQPY 180
Qy 202 GTGISRMKYGVGVGGDLRFPHGGDECLTIPSTWTXGQGNIVVYEGGSVMSQARSILWR 261
Db 181 GTGISRMKYGVGVGGDLRFPHGGDECLTIPSTWGREAGQNIIVYEGGVMAQARSILWR 240
Qy 262 LELARTKWAGGFINWHPMRIRHTTGRYLGVNDQNELYLVSREATTATSCAFCLRQEKD 321
Db 241 LELARTKWAGGFINWHPMRIRHTTGRYLGVNDSNELLYVKEEASATTTFCRLQEKD 300
Qy 322 DOKQVLEKDLLEVIGAPIIKYIGDSTVIVQHSETGLWSYKSYETKKYKGVKVEKQAILH 381
Db 301 DEKKVLEKDLLEVIGSPIIKYIGDSTVIVQHSETSLWSYKSYETKKYKGVKVEKQAILH 360
Qy 382 BEGKMDCLDFRSQEEESRTARVIRKCSLFTFKINGLETQENRRHSMFFASVNLGEM 441
Db 361 BEGKMDCLDFRSQEEESRTARVIRKCSLFTFI TALETQSNRRHSIFPKVNLNEM 420
Qy 442 VMCLEDLNYFQAQDEDMHEEKQNFALRNRODLFOEGILNLLLEAIDKINIVTSQ 501
Db 421 VMCLEDLNYFSQPEDDMHEEKQNFALRNRODLFOEGVNLNLLLEAIDKINIISQ 480
Qy 502 FLAGLAGDESQGWEMISGYLQLLAAI IKGNTNCAQFANSRLNWLFSRLSQASGE 561
Db 481 FLAGLAGDETQSWDLISTLYLQLLAAI IKGNTNCAQFANSRLNWLFSRLSQASSE 540
Qy 562 GTGMLDVHLICVLDSPALNNMRDEHIKVIISLLEKGRDPKVLVDVLCSCVGNQAVRS 621
Db 541 GSGMLDVHLICVLDSPALNNMRDEHIKVIISLLEKGRDPKVLVDVLCSCVGNQAVRS 600
Qy 622 SONNICDYLLPGKNLLQTLADVHSSVRPNI FVGRVEGSVAVRYKWFPEVTMDHIEKTH 681
Db 601 SONNICDPLLPKKNLLQTLADVHASIRPNI FVGRVDGSSMYQKWFPEVTMDHIEQTH 660
Qy 682 MPMHLRGWANTGVVYPGGGEKXGNGVGGDLYSYGFDGAYLWSGGRKTPVNRTHAE 741
Db 661 MPMHLRGWANTGVVYPGGGKXGNGVGGDLYSYGFDGAFWLTGGRKTLVVDALPEE 720
Qy 742 PYIRKGDVIGCALDITVPIINPMFNGVRVTSFTNENLEGMFPFVIVSCSSKLSCRELLGG 801
Db 721 PFIRKGDVIGVAIDLVSPIITFTNGVKVRSFDFNLDGMFFPVMSCSSKLSCRFLGG 780
Qy 802 EHGRLRVAAPGEGYPLVBSLLPQOITLSLEPCFYFGNLSKRALAGPPLVQDDTAFVPTPVD 861
Db 781 DHGRLKFAFPPMGFSALVQCLMPQOILSDPCFYFGNLAKKNVLAGPWLIEDDTAFVXPVD 840
Qy 862 TLQITLPPYVQIRDKLAENTHEMAMNKIEAGWMYGDQREDLHKIHPCLVPFRLPPAE 921
Db 841 TTGVTLPSSVDQIKELAEINHEMWNALNKIEAGWSGGEHRDDYHRIHPCLTHPEKLPAAE 900
Qy 922 KRYDIQAVQTLKTYLALGYVISLDPKPARIRNVRLPNEPMSQNGYKPAFLDLSAVTLT 981
Db 901 KRYDQAVQTLKTYLALGYVISLDPKPARIRNVRLPNEPMSQNGYKPAFLDLSAVTLT 960
Qy 982 PKWDELVDQLAENTHNLWABERIQQGWTYGLNEDSDMHRSPHLVPYKVDDAIKKANRDT 1041
Db 961 PKLEELVDQLAENTHNLWABERIQQGWTYGLNEDSENHRSPHLVPYAKVDPAIKKANRDT 1020
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Qy 1102 LTAGPMRVGWAHADMAPGMMLGQDENSFAFDGNEEKVYSGNTESFGQKQAVGDVGVFL 1161
Db 1081 LTSGPMRVGWARADCYPGAMLGSEDITSWAFDGHNVTKWAGSIHFVGVYAEAGDVGCFI 1140
Qy 1162 DLIDKTIISFSLNGELLMALGGETTADY--QGDNFVPACTGLGVQKARLYTYGQDVNTLK 1219
Db 1141 DVKEQTIISFSLNGELLMALGGETTADYTAEGVFPACTGLGVQKARLYTYGQDVNSLK 1200
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Db 1201 FFTTCGLQEGYEPFCVNMRRPVTHWTKOPIFENTEEMPDCRIDVTRIIPGADTPPHLK 1260
Qy 1280 ISHNTFETMEKANWELRLSLPVI CHNEFIDEAEKARRWVEIKDRQOILMKEA-VEAQM- 1337
Db 1261 ISHNTFETMEKANWELRLSLPVTCHGEFISEQEKARRWDEIKNOQVRLMREABIAAQM 1320
Qy 1338 ----PAHIDIMRSGFTMNDIKGLHYE-DNQEELPSSMKRLPSRPPRKGSMTRGVTIQ 1392
Db 1321 VQTAAAHMDHMLKGGFNMDIKGLTRNFDEHADAEDAHMMRGNPVRPPKGSLSRNIIT- 1377
Qy 1393 YNNLQGVNGMHRSTSEAEWAKYDGLAQCGLTPDDKDKRGRSPFKFRKRGSSSRAK 1452
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Qy 1453 SRKSKTPDPSPDTEVSPERGARRPNQIKVSOANQRNGNMARPSRTNLVYGSQVGLNMT 1512
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Qy 1513 PTQDRQMTTSTAQASATETVNGEIPDAECLKLINEFYGVRIYPGDPTHVIGWTTQ 1572
Db 1477 -PQGPQLSGSLNGQOPVETSGDEMDABCLKLINEFYGVRIYPPGDPTHVYVWTTQ 1535
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Db 1536 YHLHSEFNKNKVRGVSIVIEDDYEMAIERIDRQSCVYMRADLYNEVMAEATKAGASQ 1595
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Qy 1873 SLRSLQTESVRQKQMTDI-----AESITEISNLSPYFPPELVEAFVMOA 1918
Db 1836 SLRSLVTSVRQKQMTDI-----AESITEISNLSPYFPPELVEAFVMOA 1895
Qy 1919 LAEAVETNOVHNRDPVCGSNENFLPLIKLVLDRLLVGMWRDEVEKLLIWTNTPEDDPS 1978
Db 1896 LKDAVEINQVHNRDPVCGSNENFLPLIKLVLDRLLVGMWRDEVEKLLIWTNTPEDDPS 1955
Qy 1979 FDKEGKDEHRKGLLHMKNMAEAKLQMCYLLQHLNDIQLRHVEAIIAFAHDFVGLDQTDQ 2038
Db 1956 FEREGKDEHRKGLLTMKMAEAKLQMCYLLHLLYDTQLRHRVESIIAFSHDFVGLDQTDQ 2015
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QY 2039 LRRYIEIKOSDLPAAAKKTRPCRPPEQWNAIISFKHLEEDKENCPCGEELIARN 2098  
DB 2016 LRRYIEIKOSDLPAAAKKTRPCRPPEQWNAIISFKHLEEDKENCPCGEELIARN 2075  
QY 2099 EFHDTLMAHVSILHALQEPDAAENQF - PEAKPAGFKLYNIIINTVKLEEEAKAIBEPKK 2157  
DB 2076 DFHDSLMQKVSINALQEPDVEGTAEI BEVKGTPTKIYFNINTVKLEBEGPEVEPEKK 2135  
QY 2158 TPEEKFRKVLQTIWNWAEBSQIETPKLVREMFSLIVROYDAVGELIPALBKTYYINAKT 2217  
DB 2136 TPEEVFRKVLKTIWNAEBSQIENPKLVREMFSLILROYDVGELVRALEKTYVINTRA 2195  
QY 2218 KLDVAEMVGLSQRALLPVQMSQEBELMRKRLWKLNNHTFFQHPDLIRVLRVHENVM 2277  
DB 2196 RDDVAEMVGLSQRALLPVQMSQEBELMRKRLWKLNNATFFQHPDLIRVLRVHENVM 2255  
QY 2278 AVMMNTLGRRAQAQSDAQPSSQPVABE - DSKEKDTSHEMVAVACCRFLCYFCRTGRQNOKA 2335  
DB 2256 AVMMNTLGRRAQAQSDA - PTQSEVAEGAPSKEDTSHEMVAVACCRFLCYFCRTGRQNOKA 2314  
QY 2336 MFDHDFLLENSNIIISRLSGSTPLDVAYSSLMENTELALALBEHYLEKIAVYLSRCG 2395  
DB 2315 MFDHDFLLENSNIIISRLSGSTPLDVAYSSLMENTELALALBEHYLEKIAVYLSRCG 2374  
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QY 2456 ALRGEGEGILLKAIVDANKMSERIAADRLKREMEQEGDV - --NFSHPLPESDEDEDYIDTG 2512  
DB 2435 ALRGEGEGILFRAIVEANRMSERISDRCKWQD - EAGSTIAGLNFTHPLPEGEDEDEDYIDTG 2493  
QY 2513 AAILNFYCTLDLGRCPADAGVIALGXNESLRARAILRSLVPLBEDLQGVLSLRTFLNPP 2572  
DB 2494 AAILNFYCTLDLGRCPADASIVIRBQGXNESLRARAILRSLVPLBEDLQGVLSLRTFLNPP 2553  
QY 2573 AAGEERPKSDMPGSLIPGHQKQSVGLFLERVYGIETQELFYKLEBAFLPDRLRAAATMLDRN 2632  
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DB 2614 DGSESDMALSMNRYTGNISILPILIKHAYFYNEAENYASILLDATLHTVYRLSKNRMMLTKGQ 2673  
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DB 2793 NTDEBYGRQWAP - DQOYQWPNPDITNVHLDNLSLVOKFSEHYHDWASRRLEGG 2850  
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QY 2933 RSMRQSGSGRPPETI - VTDSATPPDYNPHVDWMTNLTLTREMNAERLADNAHDIIW 2990  
DB 2911 RGSTRQSK - ----FQINEFQEGSPFNYPNPHVDWMTNLTLTREMNAERLADNAHDIIW 2965  
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DB 2966 AKKKEELVTNGGHHQPLVPPYDLDLTDKCKDRERSQBFKLYQYQGYKLRHPKAPOS 3025  
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DB 3026 E-EGGATQAAVELRFSYSLEKLIQYIDRATINMMLKLPSTTFSRRSSFKTSTRDIKFFS 3084

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DB 3145 VRITVRCLQVLKIDAKSLVKNCPEFIRTSMLTFFNNVADDVGHITMNLQDGYAHLRG 3204  
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DB 3565 RR - SAISEGAPAVGKVKKKKKRDKKDKDKEVQASLWACLKLLPVGLNLPAGRQE 3623  
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DB 3624 LVQKCKRFLKMGSEODVAEFAKTQLTLPDKIDIPADEMSWQHYYYSKLGSKSKSNITVET - 3681  
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DB 3682 ALEKANVSNSEKDKTKQETVDRIVAMAKVIFGLHMDHPQMSKNVYRSVSIORKAV 3741  
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DB 3742 IACFRQTSLSHLPBHRACNIFARTYELWLEENIGQEWMTEDLTQSPEDAELEKSDVVE 3801  
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DB 3802 TDSKPDPLTQVTTCRGAMTERSGALQEDPLYSYAHIIAKSCGEEBEEGEGEGEG - --GG 3858  
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DB 3859 EGEBEGEG - TSIEHEQEMEKQKLLPHQARLADRGVAEMVLLHISASKGLPSEWMTQLQIG 3917  
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DB 3918 IAILRGGNIDITOMGMLNHLKDKDVGFFTSIAGLMNSCSVLDDAFERNTKAEGLVGLE 3977  
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DB 4038 ESIMDFWYHYSKELIDPAGKANFPKALGVASQVNTLTVIQQEPTONQALAHSLWD 4097  
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Db 4158 LVESASVVELLKVFDFMFLKLADLIESPSFHEVDMKNEGWTPKDFREKNEQSNYTFEE 4217  
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Qy 4360 KEKLEAFVNFCEDAIFEMTHASGLMAASEESVGGTKNREASY-NYMGDDDDDERAGDKPFR 4418  
Db 4338 KEKLEAFVNFCEDAIFEMTHASGLMATDGG--GNVNRDTRAYSINSEEEERARPIR 4395  
Qy 4419 RGLQSVKDGVATAFSSLSPSNIKAKIADMOMQMPAELAVGFFKMFYLYFYLVGVLVVV 4478  
Db 4396 RTITAVKEGLKFGVHMLSPANIKHQIGVMQTKSIPELIVGFFKIIFYFYVGVVAFCVV 4455  
Qy 4479 RYIFGVLLGMRGPOTDPPPEPTEEEKIGQLRHRLLATQSSRHLPALPPADDTGOMQVS 4538  
Db 4456 RYIFGILLNMRGPAQEPEEPVVEETFG-----RALPPLPUEEPPTVQ-- 4501  
Qy 4539 AFGDLITKEDNGOIQVKPHEPSTSTPSGEEAEVSPDESADHTEE-----QRPPSLI 4591  
Db 4502 AFGDLINKENGMKYVVVHESPANSSMBEGES--SPEDGAAAGELVEGPHPEPISIV 4559  
Qy 4592 DLLGGEQAKQAQERMEAAQAQAAMSIAEAKKAVQGPAPS-ALSOVDLSQYTRRAVS 4650  
Db 4560 DLLGGEAKKAQERQEAQKAQAAMASIEAEAKSSAPQETPAVHQIDFSQYTHRAVS 4619  
Qy 4651 FLARNFYNLKVALVLAFCINFLVLLFYKVTILDGEGGSGGLGIIAGGGSGSA---GS 4707  
Db 4620 FLARNFYNLKVALVLAFCINFLVLLFYKVTISFT-HEADSSAEELILGSGGGGADITGS 4678  
Qy 4708 ---GSGDGSGESGE-DDDALEVWHIDEDFFYMEHVIKMAAVLHGISVLSAILIGYVHLKVP 4763  
Db 4679 GFGSGDGGSGGDEMEDEIPBLVHVEDDFYMEHVLRINACLHLSVLSLAMIAYHLKVP 4738  
Qy 4764 LAIFKREKEIARLEFEGFLIAEQPEDDDFKSHWDKLVISAKSPFVNYWDFKVKKVRQK 4823  
Db 4739 LAIFKREKEIARLEFEGFLIAEQPEDDDFKSHWDKLVISAKSPFVNYWDFKVKKVRQK 4798  
Qy 4824 YSETYDPSISNMLGMEKTSFAQEEBSKGLIHIYINIDRWYQWKAGVTITONSFYS 4883  
Db 4799 YSETYDPSISNMLGMEKTSFAAQEESE-ETGIFKYIMNIDRWYQWKAGVTITDNFLYS 4857  
Qy 4884 LWYFSFVMGNFNNFFFAAHLDDVAGPKTLRTILOSVTHNGKQLVLTVMLLTIIVTYT 4943  
Db 4858 LWYFSFVMGNFNNFFFAAHLDDVAGPKTLRTILOSVTHNGKQLVLTVMLLTIIVTYT 4917  
Qy 4944 VIAFNFRKRYQBEDDEVRNCHMDLTCFVFNLYKVRAGGGIGDELEPPDGDSEYR 5003  
Db 4918 VIAFNFRKRYQBEDDEVRNCHMDLTCFVFNLYKVRAGGGIGDEIGDPGDDYEYR 4977  
Qy 5004 IIFDISPFFFIIVILLAIQGLIIDAFCGLRDQLESVKVEDMESNCFICGINKDFDKVPH 5063  
Db 4978 IIFDITFFFFFIIVILLAIQGLIIDAFCGLRDQLESVKVEDMESNCFICGINKDFDKVPH 5037  
Qy 5064 GPDTHVQREHNLANYMFLMLINKPDPTEYTGQETVYVNMWYTORCWDFFPVGDCFRKQYE 5123  
Db 5038 GPDTHVQREHNLANYMFLMLINKPDPTEYTGQETVYVNMWYTORCWDFFPVGDCFRKQYE 5097  
Qy 5124 D 5124  
Db 5098 D 5098

RESULT 12  
US-10-668-767-125  
; Sequence 125, Application US/10668767  
; Publication No. US2004017114A1  
; GENERAL INFORMATION:

; APPLICANT: Caspar, Timothy  
; APPLICANT: Cordova, Daniel  
; APPLICANT: Gutteridge, Steven  
; APPLICANT: Rauh, James  
; APPLICANT: Smith, Rejane  
; APPLICANT: Tao, Yong  
; APPLICANT: Wu, Lihong  
; TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors  
; FILE REFERENCE: BB1533 US NA  
; CURRENT APPLICATION NUMBER: US/10/668,767  
; CURRENT FILING DATE: 2003-09-23  
; PRIOR APPLICATION NUMBER: 60/412,795  
; PRIOR FILING DATE: 2002-09-23  
; PRIOR APPLICATION NUMBER: 60/427,324  
; PRIOR FILING DATE: 2002-11-18  
; NUMBER OF SEQ ID NOS: 149  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 125  
; LENGTH: 5112  
; TYPE: PRT  
; ORGANISM: Drosophila melanogaster  
; FEATURE:  
; OTHER INFORMATION: gi 2160477  
US-10-668-767-125  
  
Query Match 79.2%; Score 21234.5; DB 4; Length 5112;  
Best Local Similarity 78.8%; Pred. No. 0;  
Matches 4072; Conservative 441; Mismatches 546; Indels 109; Gaps 41;  
  
Qy 1 MAEAGGASQDDVSFLRTEDMVCLSCTATGERVCLAAEGFGRHCFLENIADKNIPDDL 60  
Db 1 MAEAGG-SQDDVSFLRTEDMVCLSCTATGERVCLAAEGFGRHCFLENIADKNIPDDL 59  
Qy 61 SQCVFIEQALSVRALQELVTAAGSETGKGTSGHRTLLYGNAILLRHNSDMYLACLS 120  
Db 60 SQCVFIEQALSVRALQELVTAAGSETGKGTSGHRTLLYGNAILLRHNSDMYLACLS 119  
Qy 121 SSSODKLAPDVGLOQHSQGEACWMTLHPASKQSEGEKVRGDDLIILSVVATERYLHTTK 180  
Db 120 SSSNDKLSPDVGLOQHSQGEACWMTLHPASKQSEGEKVRGDDLIILSVVATERYLHTTK 179  
Qy 181 ENEVSIVNASFHVTHMSVQPYGTGISMVYGVGVFGDVLRFPHGGDECLTIPSTWTKDG 240  
Db 180 ENEQSIVNASFHVTHMSVQPYGTGISMVYGVGVFGDVLRFPHGGDECLTIPSTWTKREA 239  
Qy 241 GQNVIVTEGGSVMSQARSLSRLELARTKWAGGFNNWTHPMRIRHITTTGRVLYGVNDQNELY 300  
Db 240 GQNVIVTEGGSVMSQARSLSRLELARTKWAGGFNNWTHPMRIRHITTTGRVLYGVNDQNELY 299  
Qy 301 LVSRREATTASCAFLRQEKDDOKVLEDKDLEIGAPIIKYGDSTVIVQHSSETGLWLSY 360  
Db 300 LVKKEEASIAITTTFSW-QEKDDEKKVLEDKDLEIGAPIIKYGDSTVIVQHSSETGLWLSY 358  
Qy 361 KSYETKKKGKVEEKQAILHEEGKMDGDLDFSRQSEESRTARVIRKCSLSFTKFNGL 420  
Db 359 KSYETKKKGKVEEKQAILHEEGKMDGDLDFSRQSEESRTARVIRKCSLSFTKFNGL 418  
Qy 421 ETLOENRRHNPASVNLGEMVNCLEDLINFAOPDEDMHEEKONKFRALNRQDLPOE 480  
Db 419 ETLOENRRHNPASVNLGEMVNCLEDLINFAOPDEDMHEEKONKFRALNRQDLPOE 478  
Qy 481 EGTILNLILEADKINVTISOGFLAGFLAGSGGSQSWEMISGYYQLLAAIIGKHNHTCAQ 540  
Db 479 EGTILNLILEADKINVTISOGFLAGFLAGSGGSQSWEMISGYYQLLAAIIGKHNHTCAQ 538  
Qy 541 FANSNRLNWLFSRLGSGQASGEGTGMLDVLHCVLIDSPALNMMRDEHIKVIISLLEKHGR 600  
Db 539 FANSNRLNWLFSRLGSGQASGEGTGMLDVLHCVLIDSPALNMMRDEHIKVIISLLEKHGR 598  
Qy 601 DPKVLDVCLSCVNGVAVRSSQNNICDYLPGKNLLQTLALVDHVSVRNIFVGRVVG 660  
Db 599 DPKVLDVCLSCVNGVAVRSSQNNICDYLPGKNLLQTLALVDHVSVRNIFVGRVVG 658



Db	2791	PDYSLSKMTDEDDYGRQMGAP--DQPYMPNPIDTNNVHLNDLNSLVQKFESEHYHDWA	2848
Qy	2866	SRKIENGWVYEGGWSDSQKTHPRILKPYNMLNDYKERYKEPVRESLKALLAIGHSVSEHSE	2925
Db	2849	SRLEGGWTYGDIRSDNDKHPRLKPYNMLSEYERERYRDPVRECLGALLAIGTWVSEHSE	2908
Qy	2926	VDIFSNRRSWMRRQSKSGRRPEI--VTDSATPDYDYNHPVDMTNLTLSREMOMNAERLA	2983
Db	2909	VEVPLNHRGSTRQSK-----POINEFQNGESPFPNYPNHPVDMGNTLTLSREMOMNAERLA	2963
Qy	2984	DNAHDIWAKKKEELVTNGGGIHPQLVPYDLDTKEKKKDRSQEFLKYLOYGYKLRH	3043
Db	2964	ENSHDIWAKKKEELNGCGVHIHPQLVPYDLDTKEKKKDRSQEFLKYWQYGYKLRH	3023
Qy	3044	PSKAPQSDTEQTGTGVAIELRFAYSLLLEKLIQYIDRATINMKLKPSTTFSRRSSFKTST	3103
Db	3024	PSKGAVE-EGGATQAAVELAFSLSLEKLIQYIDRATINMKLKPSTTFSRRSSFKTAT	3082
Qy	3104	RDIKFFSKAVILPLMEKYFSTHRNYFIAVATATNNVGAASLKEKEMVAALFCKLASILRSR	3163
Db	3083	RDIKFFSKVILPLMEKYFSTHRNYFIAIATATNIGAASLKEKEMVASIFCKLAALLRNR	3142
Qy	3164	LAAFGPDVRIITVRCLQVLVKGIDAKSLVKNCPFIRTSMLTFFNNVADDVGHITIMNLQDG	3223
Db	3143	LSAFGPDVRIITVRCLQVLVKGIDARTLTKNCPFIRTSMLTFFNQTSDDLTGNTILNQDG	3202
Qy	3224	KYAHLRGHLTKTSTSLGYINGVLLPILTAKEPDHLANCEYAGDALLDEIQVASYKMLGSLY	3283
Db	3203	KYSHLRGHLTKTSTSLGYVQVQVLPVLTAMPDHLAACDYGSDLLLDLDEIQVASYKILAALY	3262
Qy	3284	ALGTDAALTHDRKYLKTEIERHKPALGCLGAPSTFPVPAPLEPHLKNHQFSLNLRAD	3343
Db	3263	HLGTDGTLTHDRKYLKTEIERHRRPALGCLGAYSSCFVPAPLEPHLKNHQFSLNLRAD	3322
Qy	3344	HSLEAQDLMQKQECMPTLETILGEVDQFVESDKTYNEAPHIIDVLPPLCSLYLPFWMAQ	3403
Db	3323	HSLEAQDLMVKQESCMPTLETILGEVDQFVESDKTYNDAPHIIDVLPPLCAYLPFWWSQ	3382
Qy	3404	GPDNVTPGTGNHVTMTAEHNNQLLNKVLKLIKKNIGNENAPMWTIATYTTQOIIINSSE	3463
Db	3383	GPDNVSPTSNGHVTMTADHNPVLLRNVLKVIKKNIGNDNAPMWTIAAYTTQOIIINTSE	3442
Qy	3464	ELLRDSFLPLAERYKRTDNMFHKBESLRGFIKSTDDTSQVESQIQEDWQLLVRDIYSF	3523
Db	3443	ELLKDPFLPLAERYKVRTENMLHKEDSNRGRFIKSTDDTSQVETQLQEDWMLLVRDIYSF	3502
Qy	3524	YPLLIKYVDLQRNHLRNVPABEELYNHVAEIFNIWSKSYFLKEQNFISANEIDNMV	3583
Db	3503	YPLLIKYVDLQRNHLKDNIPABEELYNHVAEIFNIWSKSYFLKEQNFISANEIDNMA	3562
Qy	3584	LIMPTATRRVTAVDGTPOGGG--KKKKKHRDKRDKDKEYQASLMWACLKRLLPVGLNL	3641
Db	3563	LIMPTATR-SAISGAPAVGKVKKKKKRDKRDKDKEYQASLMWACLKRLLPVGLNL	3621
Qy	3642	PAGREQLVQCKDRFLKQMSQDVABPAKTQLTLPDKIDPADEMSQWHLYSKLGSKSK	3701
Db	3622	PAGREQLVQCKDRYKLMPEYDIEFARNQLTLPDKLDPSEMSQWHLYSKLG-KTE	3680
Qy	3702	SNITVETAENKAKI-----IDDTVERIVAMSKVLFGHLMDHDPQMSKNYRSVVS	3752
Db	3681	EPVD-EQALEKANVNSNEKGDKTQETVDRIVAMAKVLFGLHMDHDPQMSKNYRSVVS	3739
Qy	3753	IQRKRAVIACFRQTSLSHLPRHRACNIPARTYYELWLWEEENIGQVMIEDITQSFDAEL	3812
Db	3740	IQRKRAVIACFRQTSLSHLPRHRACNIPARSYYEQWLQEEVNVQGVVEDLTQTFEDSEK	3799
Qy	3813	KKSDVVEGEKPDPLTQLVTTFCRGAMTERSGALQEDPLMNSYAHIAKSCGEBEEBEGG	3872
Db	3800	SKKEGEETSDSPDLTQLVTTFCRGAMTERSGALQEDLLMNSYAOIAAKSTGKEEBEGGD	3859
Qy	3873	EEEGGGABAEDEGRASIHQEMEKOKLLPHQARLADRGAEMVLLHLHISAKGLPSEM	3932
Db	3860	BE---GGEGBEGEG-TSIIHQEMEKQKLLPHQARLSNRGAEMVLLHLHISAKGI PSEM	3915
Qy	3933	MKTLOIGISILRGNDIQMGMLNHLKDKXDVGFFTSIAGLMNSCSVLDDAFERNTKAE	3992
Db	3916	MTTNLNLGIALRGNDIQMGMLNHLKDKXDVGFFTSIAGLMNSCSVLDDAFERNTKAE	3975
Qy	3993	GLGVLEGGAAGEKNMHDABFTCALFRFIQULTCEGHNLDMQNYLRTQAGNTTTNNVVLCTV	4052
Db	3976	GLGVLEGGAAGEKNMHDABFTCALFRFIQULTCEGHNLDMQNYLRTQAGNTTTNNVVLCTV	4035
Qy	4053	DYLLRLQESIMDFYMHYSKELIDPAGKANFFKAIGVASQVFNLTLEVIQGPCTQNOOAL	4112
Db	4036	DYLLRLQESIMDFYMHYSKELIDPAGKANFFKAIEVASQVFNLTLEVIQGPCTLNOOAL	4095
Qy	4113	AHRLWDVAVGGFTPLFSHMQDKLSKUSSQVDLLKELLNLQKDMI PMWLSMLEGNVNGTI	4172
Db	4096	AHRLWDVAVGGFTPLFSHMQDKLSKUSSQVDLLKELLNLQKDMI TWMLSMLEGNVNGTI	4155
Qy	4173	GKQWDTLVESASNVLEILKYFDMFLKDLTSSASQFQIEDANNQDGVLPKDKKMEQQ	4232
Db	4156	GKQWDTLVESASNVLEILKYFDMFLKDLTSSASQFQFHEVDMKNEGVTTPKDFREKMEQS	4215
Qy	4233	KSYTPEIEIFLLACCTNHDKLDYIGFCDRPHPEAKBIGFNLAVALLTNLSEHMPNPRL	4292
Db	4216	KNYTPEEMDFLLACCBERNHEGKIDYRAFVBPHEPSKEIGFNLAVALLTNLSEHMPNPRL	4275
Qy	4293	ARFLETAGSVLNYFPFPLGRIEITMGSKRIERYFBIKESNIEQWEKPOIKESKRAFFYS	4352
Db	4276	ARFLETAGSVLNYFPFPLGRIEITLGSKRIERYFBIKDSNIEQWEKPOIRESKRAFFYS	4335
Qy	4353	IVTEGGDKKLEAFVNFCEDAIFEMTHASGLMAASESVGCTKNREASY-MYMGDDDDER	4411
Db	4336	IVTEGGDKKLEAFVNFCEDAIFEMTHASGLMATDDG--GCVNKRDTAYSSYMSSEEBER	4393
Qy	4412	AGKDPFRRLGQSKGVGATVAFSSLSPSNIKAKIADMQQMPAPAEAVGFQKFFFLFYFLG	4471
Db	4394	AARDPIRRTITAVKEGLKFGVHMLS PANIKHQIGVMQTKSIPELIVGFKKIIFYFYVTG	4453
Qy	4472	YGVLVVRYIFGVLLGLMQPQTDDEPPPEETEEKIQLRHRLLATOSSRHLPALPADD	4531
Db	4454	YAHFCVVRYIFGILLNMRGPAPEQBEEPVVEETFG-----RALPPLPLEEP	4501
Qy	4532	TGQMOVSACFLDITKEDNGOIQVKPHESPSTSPSSGEEAEVSPDESADTHER-----	4594
Db	4502	PGTVQ--AFGLDINKENGMYKVHVHESPANSSMEEGES--SPEDGAAASGELVEGEPH	4557
Qy	4585	QRPPSLIDLGGBOAKQAOERMEAAQAQAASAIIEAESKXAVQGPAPS-ALSQVDLSQ	4643
Db	4558	QEPISIVDLLGGEAAKKAQOERQEAQOEAAMASIEAEAKKSSAPQETPAVHQIDFSQ	4617
Qy	4644	YTRAVSFLARNFYNLKYVALVLAFCINFVLLEYKYSTLDGEGEGSLGDIITAGGSGS	4703
Db	4618	YTHRAVSFLARNFYNLKYVALVLAFCINFVLMFLFYKYVTSFT-HEADSSAEBELIUGSGG	4676
Qy	4704	GA---GS---GSGDGGESGE-DDDALVVHIDDFYMEHVIKMAAVALHSIVSLAILIG	4756
Db	4677	GADITSGFGCGSGDGGCGDGEDEPELVHVHEDDFYMEHVLRIACLSLVSMLAMLIA	4736
Qy	4757	YHHLKVPALAIKREKEIARKLEFDGLYIAEQPEDDDLLKSHWDKLVISAKSPVNVWDKPV	4816
Db	4737	YHHLKVPALAIKREKEIARLEFEGLFIAEQPEDDDPKSHWDKLVISAKSPVNVWDKPV	4796
Qy	4817	KKKVRAKYSTYDPSISNMLGMEKTSFSAQEEBEGSKGLIHYIINIDWRVQVWKAGVTIT	4876
Db	4797	KKKVRQKYSTYDPSISNLLGMEKSTFAAQESE-ETGIFKYIWNIDWRVQVWKAGVTFT	4855
Qy	4877	DNSFLSLWYFSFVSGNFNNFFFAAHLDDVAVGFKTLRTILOSVTHNGKQLVLTVMLLT	4936
Db	4856	DNAFLSLWTFVSFVSGNFNNFFFAAHLDDVAVGFKTLRTILOSVTHNGKQLVLTVMLLT	4915
Qy	4937	IIVYIVTVIAFPNFRKPYVQEEDEEVNRNCHDMLTCFVFNLYKGVRAAGGIGDELEPPDG	4996
Db	4916	IIVYIVTVIAFPNFRKPYIQEEDEEVDKCHDMLTCFVFNLYKGVRAAGGIGDIBGPDG	4975

QY 4997 DSEVYRIIFDISRFFFIIVILLAILOGLIIDAFAELRDQLESVKEDMESNCFICGINKD 5056  
DB 4976 DDEYVYRIIFDITFFFFVFIILLAIQGLIIDAFAELRDQLESVKDNMESNCFICGMGKD 5035  
QY 5057 YFDKVPHGFDTHVQREHNLANYMFLMLINKPDPTEYTGQTYVWNYTQRCWDFPFGVD 5116  
DB 5036 FFDIVPHGFDTHVQREHNLANYMFLMLINKPDPTEYTGQTYVWNYTQRCWDFPFGVD 5095  
QY 5117 CFRKQYED 5124  
DB 5096 CFRKQYED 5103  
RESULT 13  
US-10-668-767-56  
; Sequence 56, Application US/10668767  
; Publication No. US20040171114A1  
; GENERAL INFORMATION:  
; APPLICANT: Caspar, Timothy  
; APPLICANT: Cordova, Daniel  
; APPLICANT: Gutteridge, Steven  
; APPLICANT: Raub, James  
; APPLICANT: Smith, Rejane  
; APPLICANT: Tao, Yong  
; APPLICANT: Wu, Libong  
; TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors  
; FILE REFERENCE: BB1533 US NA  
; CURRENT APPLICATION NUMBER: US/10/668,767  
; CURRENT FILING DATE: 2003-09-23  
; PRIOR APPLICATION NUMBER: 60/412,795  
; PRIOR FILING DATE: 2002-09-23  
; PRIOR APPLICATION NUMBER: 60/427,324  
; PRIOR FILING DATE: 2002-11-18  
; NUMBER OF SEQ ID NOS: 149  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 56  
; LENGTH: 5126  
; TYPE: PPT  
; ORGANISM: Drosophila melanogaster  
US-10-668-767-56

Query Match 79.2%; Score 21218.5; DB 4; Length 5126;  
Best Local Similarity 78.6%; Pred. No. 0;  
Matches 4072; Conservative 442; Mismatches 545; Indels 123; Gaps 42;  
QY 1 MAEAEQASQDDVSFLRTEDMVCLSTATGERVCLAAEGFGRHCFLENIADKNIPDL 60  
DB 1 MAEAEQASQDDVSFLRTEDMVCLSTATGERVCLAAEGFGRHCFLENIADKNIPDL 59  
QY 61 SOCVFIEQALSVRALQELVTAAGSETGKGTSGHRTLLYGNAILLRHNSDMYLACLS 120  
DB 60 SOCVFIEQALSVRALQELVTAAGSETGKGTSGHRTLLYGNAILLRHNSDMYLACLS 119  
QY 121 SSSDKLAFDVLQHQSEACWTLHPASKORSEGEKVRVGGDDLIVSVATERYLHTTK 180  
DB 120 SSSDKLSFDVLQHQSEACWTLHPASKORSEGEKVRVGGDDLIVSVATERYLHTTK 179  
QY 181 ENEVSIVNASFHVTHWSVQPGTGISRMKYGVYFGGVDLRFPHGGDECLTIPSTWKD 240  
DB 180 ENEQSIVNASFHVTHWSVQPGTGISRMKYGVYFGGVDLRFPHGGDECLTIPSTWGRE 239  
QY 241 GQNVVYEGGSVNSQARSRLRLARTKWAGGFINWHPMRIRHITTCRYLGVNDONELY 300  
DB 240 GQNVVYEGGSVNSQARSRLRLARTKWAGGFINWHPMRIRHITTCRYLGVNDONELY 299  
QY 301 LVSRREATTASCAFCLRQEKDDQKQVLEDKLEVIAGPIIKYGDSTVIVQHSSETGLWSY 360  
DB 300 LVYKBEASATTTFSW-QEKDDKQVLEDKLEVIAGPIIKYGDSTVIVQHSSETGLWSY 358  
QY 361 KSYETKKGVGVKEEKQAILHEEGKMDGLDFSRQSEESRTARVIRKCSLFTKPIINGL 420  
DB 359 KSYETKKGVGVKEEKQAILHEEGKMDGLDFSRQSEESRTARVIRKCSLFTKPIINGL 418

QY 421 ETLOENRRHNPFPASVNLGEMVWVCLDLINYPAQPEDMEHEHEKONKFRALNRQDLFOE 480  
DB 419 ETLOENRRHNPFPASVNLGEMVWVCLDLINYPAQPEDMEHEHEKONKFRALNRQDLFOE 478  
QY 481 EGIINLILEAIDKINVTISQGFAGFLAGDESGQSWEMISGYLYQLLAAIIGKHNINCAQ 540  
DB 479 EGIINLILEAIDKINVTISQGFAGFLAGDESGQSWEMISGYLYQLLAAIIGKHNINCAQ 538  
QY 541 FANSNRLNWLFSRLGSQASGEGTGMLDVLHLCVLDLSPALNMMRDEHIKVIISLLEKHGR 600  
DB 539 FANSNRLNWLFSRLGSQASGEGTGMLDVLHLCVLDLSPALNMMRDEHIKVIISLLEKHGR 598  
QY 601 DPKVLDVLCISLVGNGVAVRSSQNNICDYLLPGKNLLQTLALVDHVSVRPNIIVGVRVG 660  
DB 599 DPKVLDVLCISLVGNGVAVRSSQNNICDYLLPGKNLLQTLALVDHVSVRPNIIVGVRVG 658  
QY 661 SAVYRWYFEVTDHIEKTTTHMPHLRIGWANTGYVPYGGGKGWGGVGDLLSYXGF 720  
DB 659 SSMYQKWYFEVTDHIEKTTTHMPHLRIGWANTGYVPYGGGKGWGGVGDLLSYXGF 718  
QY 721 DGAYLWSGGRKTPVNRTHABEPIYIRKGDVIGCALDLTPVIINFMFNGVVRVTGSFTNMLE 780  
DB 719 DGAYLWSGGRKTPVNRTHABEPIYIRKGDVIGCALDLTPVIINFMFNGVVRVTGSFTNMLE 778  
QY 781 GMFFPVISSCKSLSCRFLLGEGHGRLYAAPGEGSVPLVESLLPQOILSLBPCFYFGLNLSK 840  
DB 779 GMFFPVISSCKSLSCRFLLGEGHGRLYAAPGEGSVPLVESLLPQOILSLBPCFYFGLNLSK 838  
QY 841 RALAGPVLQDDTAFVTPVDTLOITLPTVYVQIRDKLAENIHMMWANNKIEAGWMYGDQ 900  
DB 839 NVLAGPWLIEDDTAFVTPVDTLOITLPTVYVQIRDKLAENIHMMWANNKIEAGWMYGDQ 898  
QY 901 REDLKHHPCLVPPERLPPAEKRYDIOQAVOTLXILALGYIISLDKPPAIRNRVLPNE 960  
DB 899 RDDYHRHPCLVPPERLPPAEKRYDIOQAVOTLXILALGYIISLDKPPAIRNRVLPNE 958  
QY 961 PFMQNGYKPAPLDLSAVTLTPKMDLVQLAENHNLWABERIQQGWYTYGLNEDSDMHR 1020  
DB 959 IFMQNGYKPAPLDLSAVTLTPKMDLVQLAENHNLWABERIQQGWYTYGLNEDSDMHR 1018  
QY 1021 SPHLVPPKVDADIKKANRDTASETVRTLLVYGYMLDPPPTGEQHEALLLEASKQKQADFR 1080  
DB 1019 SPHLVPPKVDADIKKANRDTASETVRTLLVYGYMLDPPPTGEQHEALLLEASKQKQADFR 1078  
QY 1081 TYRAEKNAVSSGKMYFEFEITLTPGMRVGHADMAPGMLQGDENSWAFDGYNEEKVY 1140  
DB 1079 TYRVERNAVSSGKMYFEFEITLTPGMRVGHADMAPGMLQGDENSWAFDGYNEEKVY 1138  
QY 1141 SGNTESEFGKQWAVGVGVFLDLIDKITSFSLNGELLMALDGGTTFADV--QGDNFVPA 1198  
DB 1139 SGNTESEFGKQWAVGVGVFLDLIDKITSFSLNGELLMALDGGTTFADV--QGDNFVPA 1198  
QY 1199 CTLVGQKARLYTQGVVNTLKYFTTCGLOEYBFCVNMKDDVTHWTKDQPIFENTDEM 1258  
DB 1199 CTLVGQKARLYTQGVVNTLKYFTTCGLOEYBFCVNMKDDVTHWTKDQPIFENTDEM 1258  
QY 1259 IDTRIDVTRIPAGSDTPCLKISHNTPETMEKANWELRLSLPVICHNEFTIDEAEKARW 1318  
DB 1259 IDTRIDVTRIPAGSDTPCLKISHNTPETMEKANWELRLSLPVICHNEFTIDEAEKARW 1318  
QY 1319 VEIKDQOILMKEA-VQAQM-----PAHIDQIMRSGFTMNDIKGLHYE-DNQEELPSSKM 1371  
DB 1319 VEIKDQOILMKEA-VQAQM-----PAHIDQIMRSGFTMNDIKGLHYE-DNQEELPSSKM 1378  
QY 1372 KRLPSRPKRGSMTRGVTIQNNYNNLQPGVNGMRSTSEAEWAKYDLGAQGLTPDQKDK 1431  
DB 1379 MRGNRPKRGSMTRGVTIQNNYNNLQPGVNGMRSTSEAEWAKYDLGAQGLTPDQKDK 1429  
QY 1432 RGRSPFKRSGESSDRKSRKTPDPEDSTEVSPEGRARRNPQIKVSOANQYNG 1491  
DB 1430 RGRSPFKRSGESSDRKSRKTPDPEDSTEVSPEGRARRNPQIKVSOANQYNG 1487  
QY 1492 MNARPSRTNLVGSQVGLNMAPTQDRKQMTTSTLAQSATETVGNBIFDAECLKLINEFY 1551

Db 1488 AEIPSPV-----PGPKQLSSNLGQOPVETSGDEMDFAECLKLINEFYF 1533  
Qy 1552 GVRYPGQDPHYVIGWVTTQYHLHSKDFNQSKVTKSSVIITDDYDRVENVNRQSCYV 1611  
Db 1534 GVRIFPGQDPHYVIGWVTTQYHLHSREFNKNKVRGSVIIEDDYEMAIERIDRQSCYV 1593  
Qy 1612 RADLYNEVWABATAKASQGMFTGCSVDITSGSVSTCGKDTSPFKMEPETKLPAPAI 1671  
Db 1594 RADELNEVTDASGKASQGMFVGCFCVDATGATGIIRFTECGKDTSHRMMEPDTKLPAPAI 1653  
Qy 1672 FVEATSEKIIQIEIGRATSPLPSAAVLPTSDKHVIPQFPRLKVQCLKPHQWARVNOQ 1731  
Db 1654 FVEATSEKIIQIEIGRTPPTLPLPSAAVLPTSDKHINQSPRLKVQCLRPHQWARVENTA 1713  
Qy 1732 LQVHALKSIDIRGWSMLCEDAVSMALHIPEEDRCIDILEPIEMDKLLSFHSHTLTYAA 1791  
Db 1714 LQVHALKSIDVRGWSMLCEDPVSMALHIPEEDRCIDILELIEWKLLSFHAHSLTYAA 1773  
Qy 1792 LCYQSNVRAAHALCTHVDQKOLLYAIOQYWSGRLRGQFYDILLJIALHLESHATTMEACKN 1851  
Db 1774 LCYQSNVRAAHALCQHVQKOLLYAIRSEYMSGRLRGQFYDILLJIALHLESHATTMEYCKN 1833  
Qy 1852 EFVILPGLKALVEEPMGHSLSLOTESVRPQMKWTDI-----AESITE 1897  
Db 1834 EYITPLGAELKELYSDEMQHSLSLVTESVRPQLRMTETITPPVIATSSMPSVSSEIIPD 1893  
Qy 1898 ISNLYSYFPFLEVAREFVMOALABAVENTQVHNRDPVGGSNENILFPLIKLVRLLLVGM 1957  
Db 1894 IDQLYSPKPLEVVQRQFVMEALKDAVEINQVHNRDPIGWTNENILFPLIKLDRLLLVGV 1953  
Qy 1958 MRDSEVKLLIMTNPETWDPSPFVKEGKDEHRKGLLHMKWAGAKLQWCYLLLOHLNDQLR 2017  
Db 1954 LTDEVDORLLVMIIDPETWQAFEREGKDEHRKGLLTKWMAEGAKLQWCYLLHLHYDTQLR 2013  
Qy 2018 HRVEAITAFADHFDGDLQDOLRYETELKQSDLPSAAVAKTREFRCPPEQWNAIISPK 2077  
Db 2014 HRVESIITAFSHDFDGLDQDOLRYEITKQSDLPSAAVAKTREFRCPPEQWNAIISCFK 2073  
Qy 2078 HLEEDKENCPCGBELIARMNEFHDITMAHVSLLALQEPDAAENQOE-PEAKPGAFGKLYN 2136  
Db 2074 NLEPDDQDNCTCGLELGRGDFHDSLMQKVSINALQEPDGVGEATAIEEVKTPITKIYN 2133  
Qy 2137 IINTVKELEBEAKAIEBPPKKTPEKFRKVLIOITIVNABESQIETPKLVREMPSSLVRQ 2196  
Db 2134 FINTVKELEEGKEVEBPKTPEBFRKVLIKTIVSWABESQIENPKLVREMPSSLVRQ 2193  
Qy 2197 YDAGELIRALEKTYVINAKTKLDAEMWVGLSQRALLPVQMSQEBEELMRKELKLVN 2256  
Db 2194 YDTVGEVLRALKETVYINTRARDDAEMWVGLSQRALLPVQMSQEBEELMRKELKLVN 2253  
Qy 2257 NHTFQHPDLIRVLVRHENVNAMVMTLIGRAQAQSDAQSPSSQPAVE--DSKEKDTSHEM 2314  
Db 2254 NATFQHPDLIRVLVRHENVNAMVMTLIGRAQAQSDA-PTQSEVAEGAPSKKEDTSHEM 2312  
Qy 2315 WVACCRFLCYCRTGRQNKAMFDPHFPFLLENSNILLSRPSLRGSTPLDVAYSLSMENTE 2374  
Db 2313 WVACCRFLCYCRTGRQNKAMFDPHFPFLDNANILLARPSLRGSTPLDVAYSLSMENTE 2372  
Qy 2375 LALALRHYLEKIAVYLSRCLQNSSELVEKGYDPLGWDPVGEGRYLDFLFCVWVNGES 2434  
Db 2373 LALALRHYLEKIAVYLSRCLQNSSELVEKGYDPLGWDPVGEGRYLDFLRYCVWVNGES 2432  
Qy 2435 VEENANVIRLLIRRPECLGPALGEGEGLKATVDANKSERIADRRLKREMQEGDV- 2493  
Db 2433 VEENANVIRLLIRRPECLGPALGEGEGLFRAIVEANRMSERISDRCKQD-BAEGTIA 2491  
Qy 2494 --NFSHPLPEDEDEDYDTGAAILNFYCTILVLDLGRCAPDAGVIALGKNESLARAILR 2551  
Db 2492 GLNFTPLPEGEDEDYDTGAAILNFYCTILVLDLGRCAPDASVIEQGNESLARASLR 2551  
Qy 2552 SLVPLEDLOGVLSLRFITLNNPAAGEERPCKSDMPGSLTIGHKQSVGLFRLVYGLTOLFL 2611

Db 2552 SLVPLEDLOGVLSLKTLSQTAPGEEKPKSDMPGSLLPNNKQISVLFLERVYGIEAQDLF 2611  
Qy 2612 YKLLIEAFIPDLBAATMLDRNDCESDMALSNRYIGNSITLPLLIKHAYVYNAENYASL 2671  
Db 2612 YRLLEDAFLPDLRTATYILDKSGSESDMALAMNRYIGNSITLPLLIKHKSKEYNENYASL 2671  
Qy 2672 LDATLHTVYRLSKVRMLTKQREAVSDFLVALTSAMQPSMLLKLLRKLTVDVSKLSSEYTT 2731  
Db 2672 LDATLHTVYRLSKVRMLTKQREAVSDFLVALTSQOPAMLLKLLRKLTVDVSKLSSEYTT 2731  
Qy 2732 VALRLTLTHYERCAKYVGTGAGQAGASSDEKRLTMMLFNSIFDSLKMDIYEPBLFG 2791  
Db 2732 VALRLTLTHFDRCAKYVGT--QOGSGYASSDEKRLTLLLFNSIFDSLNMMDYDPELFG 2790  
Qy 2792 KALPCLIAIGCALPPDYSISKNYDDDEFYKGEQAAGDLNPOYDPOPIPTINTSSVALNNDLNT 2851  
Db 2791 KALPCLIAIGCALPPDYSISKNTDEDYGRQMGAP--DQOYMPNPITDNNVHLNDLNS 2848  
Qy 2852 IVOKFSEHYHDAWASRKIENGWVYGEWSDSQKTHPRLKPYNNMLNDYEKERYKEPVRESL 2911  
Db 2849 LVOKFSEHYHDAWASRRLEGGWTYGDIRSNDNRKPRLKPYNNMLSEYERERYRDPVRECL 2908  
Qy 2912 KALLAIGWSVEHSEVDIPSNRSMRROSKSGGRPPEI--VTDSATPFDYNNHPVDMTNL 2969  
Db 2909 KGLAIGWTVVEHSEVEVPLNHRGSTRROSK----PQINEFQNEGSPFNYPHPVDMNSL 2963  
Qy 2970 TLSREMNWAERLADNAHDIWAKKKEBELVTNGGGIHPQLVPYDILLTDKCKKDRERSOE 3029  
Db 2964 TLSREMNWAERLAENSHDIWAKKKBELNGCGVIHPQLVPYDILLTDKCKKDRERSOE 3023  
Qy 3030 FLKYLQVQGYKLRHPSKAPQSDTEQTTGVVAIELRFAYSLLLEKLIQVIDRATINMKLLKP 3089  
Db 3024 FLKTMQIQGYKLRHPSKGAVE--EGGATQANAVELRFYSLLLEKLIQYLD RATINMKLLKP 3082  
Qy 3090 STTFRRSRSPKTRDIPKFSKAVLPLMEKYFSTRNYFIAVATATNNVGAASLKEKEMV 3149  
Db 3083 STTFRRSRSPKTRDIPKFSKVVLPLMEKYFSTRNYFIAIATATNNI GAASLKEKEMV 3142  
Qy 3150 AALFCKLASLRLRSLAAGFDPVIRVRCLOVLVKGIDAKSLVKNCEPFIKTSMLTFPNNV 3209  
Db 3143 ASIFCKLAALLRNLRSFAFGPDVIRVRCLOVLVKGIDARTLTKNCEPFIKTSMLTFPNNV 3202  
Qy 3210 ADDVGHITMNLQDKYAHLRGTHLKTSTSLGYINGVLLPILTAKFDFHLANCEYGAULLD 3269  
Db 3203 SDDLGNITLQQDQGYSHLRGTHLKTSTSLGYVQVQVLPVLTAMFADHLACDYGSDULLD 3262  
Qy 3270 EIQVASYKMLGSLYALGTDASTHDKYKLTETIERHKPALGCLGAFSSTFPVAFLEPHL 3329  
Db 3263 EIQVASYKILALYHLGTDLTHTDRKYLKTEIERHRPALGSLGAYSSCFPVAFLEPHL 3322  
Qy 3330 NKNQPSLLNRIADHSLAQDINQKMEQCHPTLETILGEVDQFVESDKTYNEAPHIITDV 3389  
Db 3323 NKNQYSLNRIADHSLAQDINVKMESCMPLNETILGEVDQFVESDKTYNDAPHIITDVI 3382  
Qy 3390 LPLLCVLPFWMAQGPNDVTPCTGNHVTWYTAESHMOLLKNLKLIIKNTGNENAPWMT 3449  
Db 3383 LPLLCVLPFWMAQGPNDVTPCTGNHVTWYTAESHMOLLKNLKLIIKNTGNENAPWMT 3442  
Qy 3450 IATYTOQIIINSFELLIRDSFLPLAERVRKRTDNMPHKEESLRGFIKSSDDTTSQVBSQI 3509  
Db 3443 IATYTOQIIINTSEELLKOPFLAERVKRTENMLHKEDEMRGFIKSSDDTTSQVBSQI 3502  
Qy 3510 QEDWQLLRDIYSFYPLLIIKYVDLQRNHWLRNVPENAEELYNHVAEIPN1WSKSOYFLKE 3569  
Db 3503 QEDWQLLRDIYSFYPLLIIKYVDLQRNHWLRNVPENAEELYNHVAEIPN1WSKSOYFLKE 3562  
Qy 3570 EQNFISANEIDNNVLTMPATRTVTTATDCTPGGG--KKKKHGRDKRDKKXEQVASLM 3627  
Db 3563 EQNFISANEIDNNVLTMPATRT--SAISEGAPVGGVKKKKKRRDKRDKKXEQVASLM 3621  
Qy 3628 VACLKRLLPVGLNLFAGREQELVQHCKDRFLKKMSQEDVAEFAKTQTLTLPDKIDPADEMS 3687  
Db 3622 VACLKRLLPVGLNLFAGREQELVQHCKDRFLKKMSQEDVIEFARNQTLTLPDKIDPADEMS 3681





Db 120 SSSNDKLSFDVGLQHSQGEACHWTVHPASQORSEGEKVRVGDDDLILVSVATERYLHTX 179  
Qy 181 ENEVSIVNASPHVTHWSVQPYGTGISRMKYVGYVFGDVLRFPHFGGDECLTIPSTWTKG 240  
Db 180 ENEQSIVNASPHVTHWSVQPYGTGISRMKYVGYVFGDVLRFPHFGGDECLTIPSTWGRE 239  
Qy 241 QONIVVYEGGSVMQARSLELARTKWAAGFFINWHPMRIRHTTGRVLYGVNDQNELY 300  
Db 240 QONIVVYEGGSVMQARSLELARTKWTGCFINWHPMRIRHTTGRVLYGVNDSNELI 299  
Qy 301 LVSRREATTASCFCLROEKDOKVLEDXLEVIGAPIIKYGDSTVIVORSETGLWLSY 360  
Db 300 LVKKEBASIAATTFSW-OEKDDEKKVLEDKVLEVIGSPIIKYGDSTVIVOCETSLWLSY 358  
Qy 361 KSYETKKGVGVKBEKQAILHEEGKMDGLDFSRSQBEESRTARVIRKCSLSFTKFINGL 420  
Db 359 KSYETKKGVGVKBEKQAILHEEGKMDGLDFSRSQBEESRTARVIRKCSLSFTQFITAL 418  
Qy 421 ETLOENRRHSFPFASVNLGEMWNCLEDLINYPAQDEDEMEHEEKONFRALNRQDLFOE 480  
Db 419 ETLOSNNRRHSIFFQKVNLENVMCLEDLINYFSQPEDDMEHEEKONFRALNRQDLFOE 478  
Qy 481 EGIILNLLIEADKKNVITSQCFLAGFLAGDESQOSWEMISGYLQOLLAIIKGNHTNCAQ 540  
Db 479 EGVNLLIEADKKNVITSQCFLAGFLAGDETGQSWDLISYLLQOLLAIIKGNHTNCAQ 538  
Qy 541 FANSNRLNWLFSRLGSQASGEGTGMDVLHCVLIDSPEALNMNRDEHIKVIISLLEKXGR 600  
Db 539 FANSNRLNWLFSRLGSQASGSGMDVLHCVLIDSPEALNMNRDEHIKVIISLLEKXGR 598  
Qy 601 DPKVLDVLCISCVNGVAVRSQNNICDYLLPGKNLLLOALVDHVSRRPNIIVGREG 660  
Db 599 DPKVLDVLCISCVNGVAVRSQNNICDFLLPGKNLLLOALVDHVASIRNIEIVGREGVDG 658  
Qy 661 SAVRKVYFVYTHMHEIKTHMPLHRIGWANTGYVYPYCGGKKGWGVGDLLYSVGF 720  
Db 659 SSMYQKVTFTVMOHIEGTTHMPLHRIGWANTGYVYPYCGGKKGWGVGDLLYSVGF 718  
Qy 721 DGAYLWSGGRTPVNRTHABEPYIRKGDVIGCALDLTVPIINFMFNGVRYTGSFTNFLE 780  
Db 719 DGAFLWTGGRKTLVVDALPEEPFIRKGDVIGVAIDLSPITFTFNGVKVGRGSPRDNLD 778  
Qy 781 GMFPFVIVSCSKLSRFLGGEHGRLYAABEGYSPLVESLLPOOILSLEPCFPFGMLSK 840  
Db 779 GMFPFVIVSCSKLSRFLGGEHGRKLPAPMGFSALVQCLMPQOILSLDPCFPFGMLAK 838  
Qy 841 RALAGPPLVQDDTAFVPTPVDTLQITLPTYVEQIRDKLAENIHEMWANKEAAGWYGDQ 900  
Db 839 NVLAGPMLIEDDTAFVPKPVDTTGVTLPSSVDQIKELAENIHEMWANKEAAGWYGEH 898  
Qy 901 REDLHKIHPCLVPPERLPAPAEKRYDIQAVQTLKTLIALGYIISLDKPPAIRNVRLPNE 960  
Db 899 RDDYHRHPCLTHEKLPAAEKRYDNQALAVQTLKTLIISLGYIITMDKPPAIRPVRLPNE 958  
Qy 961 PFMQSGYKPAPLDLSAVTLTPKMDLVDQLAENTHNLWABERIQOQWYGLNEDSDMHR 1020  
Db 959 IFMQNGYKPAPLDLSAVTLTPKLEELVDQLAENTHNLWABERIQOQWYGLNEDSDENHR 1018  
Qy 1021 SPHLVPYKVDADAIKKNRDTASETRVTLVYGYMDPPTGEOHEALLLEASKOKQADFR 1080  
Db 1019 SPHLVPYKVDADAIKKNRDTASETSANAPGLRITCLSSDGRNGTSGRGTTFQVVRIP 1078  
Qy 1081 TYRAEKYAVSSGKWYFEFEITAGPMRVGWAHADMAGMMLGODENSWAFDGYNEEKVY 1140  
Db 1079 TYRVERNYAVTSGKWYFEFEVITSGPMRVGARADCYPGMLGSEDTSWAFDGHNEEKVY 1138  
Qy 1141 SGNTESEFGKQWAGDVGVFIDLDTKITSFSLNGELLMALGGETTADV--QGDNFVPA 1198  
Db 1139 GGVSESEFGKQCGPDGVGVFIDLADHTITSFSLNGELLMALGGETTADVTAEGVGFVPA 1198  
Qy 1199 CTLGVGQKARLYTGDVNTLKYFTTCGLQEGYEPFCVNMKRDVTHWYTKQOPIFENTDEM 1258  
Db 1199 CTLGVGQKARLYTGDVNTLKYFTTCGLQEGYEPFCVNMRRPVTHWYTKQOPIFENTDEM 1258

Qy 1259 IDTRIDVTRIPAGSDTPPCLKISHNTFETMEKANWELRLSLPVICHNEFIDEAEKARRW 1318  
Db 1259 PDCRIDVTRIPGAGDTPPHLKISHNTFETMEKANWELRLSLPVTMGEFISBOEKARRW 1318  
Qy 1319 VEIKDROQIILMKEA-VEAQM-----PAHIDQIMRSGFTMNDIKGLHYE-DNQEBELPSSKM 1371  
Db 1319 DEIKNQYRLMRBAETAAMQOVQTAHMDHMLKGGFNMDIKGLTRNFDEHADAEADHM 1378  
Qy 1372 KRLFSRPPRKGSMTRGVTIQYNNLQPGVNGMHRSTSEAMAKYDLAGAQLTPDDKKOK 1431  
Db 1379 MRGNRPPRKGSLTRNIT---FETDMSAALDEMQRSTS-----VLDMNGLGEEMDDKK-K 1429  
Qy 1432 RGRSPKPFKRSKRGSSDRASKRSKTPDPFSTEVSPERGARRPNQIKVSOANQRYNG 1491  
Db 1430 RGRSPKPFK-FSKSRDQSRK-NGARTLDTLSLERRNTVAHGRNVVNOQMTTRAPTLLNN 1487  
Qy 1492 MNARPSRTNLYGSQVGLNMATPTQDRKQMTTSTLAQSATETVGNEIFDAECLKLINEFY 1551  
Db 1488 AEI PPPGV-----PQGPQLSGSNLGOQPVETSGDEMDEDAECLKLINEFY 1533  
Qy 1552 GVIYIPGQDPHTHYVIGWVTTQYHLHSHKDFNQSKVTKSSVITDDYDRVENVNRQSCYMV 1611  
Db 1534 GVIIPGQDPHTHYVVGWVTTQYHLHSREFNKNKVRGSVIEDDYEMAIERIDRQSCYV 1593  
Qy 1612 RADELNENWABATAKASQCMFICGSVDSTGTSVSFTCEGKOTSFKFKMEPETKLPFAI 1671  
Db 1594 RADELNENVTQDASGKASQCMFVGCVDATGATGIIRFTCEGKOTSHRMMMEPDTKLPFAI 1653  
Qy 1672 FVATSKEIILQIELGRSATSLSAAVLPTSDDKHVIPPQPPRLKVQCLKPHQWAVRNQS 1731  
Db 1654 FVATSKEIILQIELGRTPPTPLPSAAVLPTSDDKHINPQSPRLKVQCLRPHQWAVRNTA 1713  
Qy 1732 LQVHALKSLDIRGWSMLCEDAVSMLALHIPEEDRCDILEPIEMDKLLSPHSHTLYAA 1791  
Db 1714 LQVHALKSLDVRGWSMLCEDPVSMLALHIPEEDRCDILEPIEMDKLLSPHSHSLTYAA 1773  
Qy 1792 LCYQSNYRAAHALCTHVDQKOLLYATOSQVMSGRLQGFYDILLIALHLESHATTMEACKN 1851  
Db 1774 LCYQSNYRAAHALCQHVQKOLLYAIRSEYMSGRLQGFYDILLIALHLESHATTMEACKN 1833  
Qy 1852 EFVILGPPELKALYEBPDMGHLSRLSQTESVRPQMKMTDI-----AESITE 1897  
Db 1834 EYITPLGAELKELYSDEEMQHSRLSVTESVRQLRWTEITPPVIATSSMPSVSSEPIPD 1893  
Qy 1898 ISNLYSPYFPLEVAREFVMOALAEAVETNQVHNRDPVGGSNENLFLPLIKLDRLLLVGM 1957  
Db 1894 IDQLSPKPFLEVVRQFVMEALKDAVEINQVHNRDPIGWTNENLFLPLIKLDRLLLVGV 1953  
Qy 1958 MRDEDEKLLIMTNPETWDFSFKEGKDEHRKGLLHKMAEGAKLQMCYLLLOHLNDIQLR 2017  
Db 1954 LTDDEDVQRLVMDIPETWDOAFEREGKDEHRKGLLTKMAEGAKLQMCYLLLHLYDQLR 2013  
Qy 2018 HRVEALITAPAHDFVGLDQTLQRLRYTEIKOSDLPAAVAAKTRFCRCPPEQNNAILSFK 2077  
Db 2014 HRVESITAFSHDFVGLDQTLQRLRYTEIKOSDLPAAVAAKTRFCRCPPEQNNAILCFK 2073  
Qy 2078 HLBEEDEKENCPCGEBELIARNNEFHTLMAHVSJLHALQEPDAAENQBE-PEAKPGAFGLYN 2136  
Db 2074 NLEPDQDNCTCGLELRGLGRGLDFHDSLMQKVSJNALQEPDGVGVEGTAIEEVKTGPITKIYN 2133  
Qy 2137 IINTVKELEBEAKAIEBPPPKTPEEKPRKVLIOITIVNMAESQIETPKLVREMFSLVRQ 2196  
Db 2134 FINTVKELEBGPKEVEPEKTPPEEVRKVLITIVISWABESQIENPKLVREMFSLVRQ 2193  
Qy 2197 YDAVGEILIRALEKTYVINAKTKLDVAEMVGLSQIRALLPVQMSQEBEELMRKELWLVN 2256  
Db 2194 YDTVGEILVRALEKTYVINTEARDVAEMVGLSQIRALLPVQMSQEBEELMRKELWLVN 2253  
Qy 2257 NHTFFQHPDLIRVLRVHENYMAVMNTLGRRAQASDAQSSQPVAB--DSKEKDTSHEM 2314  
Db 2254 NATFFQHPDLIRILRVHENYMAVMNTIGRRAQASDA-PTQSEVAREGAPSKSKENDTSHEM 2312



QY 2315 VVACRFLCYFCRTGRQKAMFDFHDFELLENSTILLRSPSRGSGTPLDVAYSSLMENTE 2374  
Db 2313 VVACRFLCYFCRTGRQKAMFDFHDFLLDNANILLARSPSRGSGTPLDVAYSSLMENTE 2372  
QY 2375 LALALREHYLEKIAVYLSRCGLQNSSELVEKGYDPLGWDPEGEERYLDFLRCVWVNGES 2434  
Db 2373 LALALREHYLEKIAVYLSRCGLQNSSELVEKGYDPLGWDPEGEERYLDFLRCVWVNGES 2432  
QY 2435 VEENANLVRLIRPECLGPALRGEGLLKAIVDANKMSRRIADRRLKLRMEQEGDV- 2493  
Db 2433 VEENANLVRLIRPECLGPALRGEGLFRAIVEANRMSRISDRCKMQD-EAEGTIA 2491  
QY 2494 --NFSPHLPESDEDEDYIDTGAAILNFYCTLVLLGRCAPDAGVIALGKNESLRARAILR 2551  
Db 2492 GLNFTHLPPEGEDESDYIDTGAAILNFYCTLVLLGRCAPDASVIEQGNESLRARASILR 2551  
QY 2552 SLVPLEDLOGVLSLAPTLNPAAGEBERPKSDMPGSLIPGHKQSGVGLFERYVGIETQELF 2611  
Db 2552 SLVPLEDLOGVLSLFTLSQTAPGEEKPKSDMPGSLIPNNKQSIIVLFILERVYGIETQELF 2611  
QY 2612 YKLLREAFPLDRAATMLDRNDGCSDMALSMNRVYIGNSILPLLKHAFFYNEAENYASL 2671  
Db 2612 YELLEDAPFDDURTATILDKSDGSESDMALANRVIIGNSILPLLKHAFFYNEAENYASL 2671  
QY 2672 LDATLHTVYRLSKNRMLTGOREAVSDFLVALTSAMQPSMLLKLRKLTVDVSKLSEYTT 2731  
Db 2672 LDATLHTVYRLSKNRMLTGOREAVSDFLVALTSQMPAMLLKLRKLTVDVSKLSEYTT 2731  
QY 2732 VALRLTLHYERCAKYGTGAGQAGFAGASSDEEKRLTWMFLNSNIPDSLSKMDYPELFG 2791  
Db 2732 VALRLTLHFDRCAKYGTG-QGQSGYAGSSDEEKRLTWMFLNSNIPDSLSKMDYPELFG 2790  
QY 2792 KALPCLIAIGCALPPDYSKNYDDEFYCKEQAAGDLNPOVDPOPINTSSVALANDLNT 2851  
Db 2791 KALPCLIAIGCALPPDYSKNTDDEYYQRQMGAP--DQPQYMPNPIDTNNVHLLDNLNS 2848  
QY 2852 IVQKSEHYHDWASRKIEGWYVYEGWSDSOKTHPRLPKYNMLNDYKERYKEPVRESL 2911  
Db 2849 IVQKSEHYHDWASRLLEGWYTGDIRSDNRKHPRLKPYNMLSEYERERYDVPRECL 2908  
QY 2912 KALLAIGMSVHSEVDIPSNRSMRRQSKSGRRPEI--VTDSATPPDYPHPVDMNVL 2969  
Db 2909 KGLLAIGWTVHSEVEVPLNHRGSTRQSK----PQINEFQNEGSPFNYPHPVDMNVL 2963  
QY 2970 TLRSEMNMAERLADNAHDIWAKKKEELVTGGGHPQIPVYDILLTDKKEKDRERSOE 3029  
Db 2964 TLRSEMNMAERLAENSHDIWAKKKEELVTGGGHPQIPVYDILLTDKKEKDRERSOE 3023  
QY 3030 FLKYLOQYQYKLRHPSKAPQSDTEQTTGVAITELREFAYSILLEKLIQYIDRATINMKLLKP 3089  
Db 3024 FLKYMOYQYKLRHPSKAGAVE--EGGATQAVALREFYSYILLEKLIQYIDRATINMKLLKP 3082  
QY 3090 STTFSRRSFKTSTRIDIKFFPSKAVLPLMEKYFSTHRNYFIAVATATNNYGAASLKEKEMV 3149  
Db 3083 STTFSRRSFKTATRIDIKFFSKVVLPLMEKYFSTHRNYFIAVATATNNYGAASLKEKEMV 3142  
QY 3150 AALFCKLASLLRSLAAGPDVRAITVRCLOVLVKGIDAKSLVKNCEPFTRTSMLTFFNNV 3209  
Db 3143 ASIFCKLAALLRNLRSFAFPDRAITVRCLOVLVKGIDARTLTKNCEPFTRTSMLTFFNNV 3202  
QY 3210 ADDVGHITMNOGKYAHLRGTHLKTSTSLGYINGVLLPLTLAKPDHLANCEVGADLLD 3269  
Db 3203 SDDLGNITLNOQDGKYSHLRGTHLKTSTSLGYVNVQVLLPVTAMFDHLAACYDGSLLD 3262  
QY 3270 EIQVASYKMLGSLYALGTDASTHDKYLTETIERHKPALGSCLAGFSSTFFVAFLEPHL 3329  
Db 3263 EIQVASYKILAAALYHLGTGTTLTHDKYLTETIERHKPALGSCLAGFSSTFFVAFLEPHL 3322  
QY 3330 NKHNQFSLNRIADHSLAQDINQKMEQCMPTLETILGEVDQVQVESDKTYNRAPIIDV 3389  
Db 3323 NKHNQFSLNRIADHSLAQDINQKMEQCMPTLETILGEVDQVQVESDKTYNRAPIIDV 3382  
QY 3390 LPLLCSYLFPFWAQGPDNVTPTGGNHVTVTAHMMNQLKLVLLKLNIGNENAPWMTR 3449

Db 3383 LPLLCAYLFPFWSGPDNVSPTSNGHVTVMTADHNNPLLRNVLKMIKKNIGNENAPWMTR 3442  
QY 3450 IATVTOQIIINSSEBELLRDSFPLAERVRKTDNMHFKESLRGFIKSTDDTTSQVESQI 3509  
Db 3443 IAAVTOQIIINTSSELLKDPFLPLAERVKKXTENMLHKEDSMRGFIKATDDTTSQVETQL 3502  
QY 3510 QEDWOLLVRDIYSFYPPLIKYVDLQRNHLNRRNVPEABELYNHVAEIPNIWSKSYFLKE 3569  
Db 3503 QEDWOLLVRDIYSFYPPLIKYVDLQRNHLNRRNVPEABELYNHVAEIPNIWSKSYFLKE 3562  
QY 3570 EONFISANEIDNMVLIPTATERTVAVTDGTPQGG--KKKKXHRDKKDKKQVQASLM 3627  
Db 3563 EQNFISANEIDNMALIMPTATRR--SAISEGAPAVGGVKVKKKKKRRDKKDKKQVQASLM 3621  
QY 3628 VACLKRLLPVGLNLPAGREQELVQCHCKDRFLKMKSEQDVAEFKTLQTLPLDKIDPADBMS 3687  
Db 3622 VACLKRLLPVGLNLPAGREQELVQCHCKDRYLKKMPEYDVEFARNQLTLPDKLDPSDEMS 3681  
QY 3688 WOHYLYSKLGSKSNSNITVETAENKAKI-----IDDTVERIVAMSKVLFGHLMIDH 3738  
Db 3682 WOHYLYSKLG-KTEBEPVD-EQALEKANVNSNEKGDKTKQETVDRIVAMAKVLFGHLMIDH 3739  
QY 3739 PQQSKNYRVSWSIORKRAVIACFRQTSLSHSLPRHRACNIFARTYYELMLEENIGQEV 3798  
Db 3740 PQQSKNYRVSWSIORKRAVIACFRQTSLSHSLPRHRACNIFARSYYEQLQEEENVQEV 3799  
QY 3799 MIEDLTQSFDAELKKSVDVVEGEPDPLTQLTTCRCGAMTERSGALQEOPLVMSYAH 3858  
Db 3800 MVEDTQTFEUSEKSKKEGETDSKPDPLTQLTTCRCGAMTERSGALQEOPLVMSYAH 3859  
QY 3859 IAKSCGEEBEGGEEBEGGEEAEAEDEGRASIIHEQEMEKQKLLPHQARLADRGAEMVL 3918  
Db 3860 AAKSTGKEEBEGGDEE---GGEGGEGEG--TSIHEQEMEKQKLLPHQARLSNRGAEMVL 3915  
QY 3919 LHSASKGLPSEMVMKTLQGLISILRGNDIIOQMGLNHLKDKDVGFSTAGLWNSCS 3978  
Db 3916 LHSASKGIPSEMVMKTLNGLTALIRGNDIIOQMGLNHLKDKDVGFSTAGLWNSCS 3975  
QY 3979 VLDDAFERNTKAEGLVGLEGAAAGEKNMHDAEFTCALFRFQLTCEGHNDWQVLRTO 4038  
Db 3976 VLDDAFERNTKAEGLVGLEGAAAGEKNMHDAEFTCALFRFQLTCEGHNLWQVLRTO 4035  
QY 4039 AGNTTVNVMVICTVDYLLRQESIMDFYHYSSKELIDPAGKANFFKAIGVASQVFNLT 4098  
Db 4036 AGNTTVNVMVICTVDYLLRQESIMDFYHYSSKEIIDPAGKANFFKAIGVASQVFNLT 4095  
QY 4099 EYIQGPCTONQOALAHSLRDLWDAVGGLFLFSHMQDKLSKSSQVDDLKELLMLQKDMTPM 4158  
Db 4096 EYIQGPCTONQOALAHSLRDLWDAVGGLFLFSHMQDKLSKSSQVDDLKELLMLQKDMTPM 4155  
QY 4159 MSLMEGNVNGTICKQWVDTLVESASNVLELTKYFDMFLKLDLTSSASFOEIDANNNG 4218  
Db 4156 MSLMEGNVNGTICKQWVDTLVESASNVLELTKYFDMFLKLDLTSSASFOEIDANNNG 4215  
QY 4219 WVLPKDFEKKQKQSYTPEETIEFLACCTNHDGKLDYIGFCDRFHPEPAKEIGFNLAVL 4278  
Db 4216 WTPKDFEKKQKQSYTPEEMDFLLACCERNHEKIDYRAFVEHFHPEKIGFNLAVL 4275  
QY 4279 LTNLSEHNPENRPLARFLETAGSVLNYPEPFLGRITIEIMGGSQRIERVYFEIKESIEQWE 4338  
Db 4276 LTNLSEHNPENRPLARFLETAGSVLNYPEPFLGRITIEIMGGSQRIERVYFEIKESIEQWE 4335  
QY 4339 KPQIKESKRAFFYSIVTEGGDKLEAFVNFCEDAIFEMTHASGLMAAEESSVGGTHORE 4398  
Db 4336 KPQIKESKRAFFYSIVTEGGDKLEAFVNFCEDAIFEMTHASGLMATDDG--GGNVKRD 4393  
QY 4399 ASY-NYMGDDDDERAGKDPFRRLGLOSVDGVATAPSSLSPSNIAKAKIADMQMPAEALAV 4457  
Db 4394 TAYSYMSEEBEERARDPPIRITITAVKEGLKFGVHMLSPANIKHQIGVMQTKSPILLIV 4453  
QY 4458 GFFKQFFYLYGYGVLVVRYIFGVLLGLMRGPQTDPPPEETEEKIGQLRHLRLAT 4517

Db 4454 GFFXIIYFYITGYAHFCVVRVYIFGLIILNLMRGPAPEQBEEPPVVEBETFG----- 4504  
Qy 4518 QSSRHLPALPADDTGQMVSAGFALDITKEDNGOIQVKPHESPSTSTPSSGEEAEVSPDE 4577  
Db 4505 ---RALPPLPEEPGTVQ--AFGLDINKENGMYKVVVHESPANSSMEEGES--SPED 4557  
Qy 4578 SADHTE-----ORPPLDILGGEOAKQAOERMEAOQAQAASAEAKKAVOG 4630  
Db 4558 GAASSELVEGEHPQEPISIVDLGGEAAKAAQOEQAQAQAANASIEAEAKSSSA 4617  
Qy 4631 PAPS-ALSOVDLSQVTRAVSFARNFNLKYVALVLAFCINFVLLPVKYKYSTLDGEGEG 4689  
Db 4618 POETPAVHQIDFSQVTHRAVSFLARNFNLKYVALVLAFSINFMLLYKYKYSTFT- 4676  
Qy 4690 SGLDIIAGGSGSGA---GS---GSGDGSGESGE-DDDALEVVIHDEDFPFYMEHVIKMA 4742  
Db 4677 SABELILGSGSGGADITGSGFGSGDGGSGDGEDEIPELVHVDEDFPFYMEHVLRIA 4736  
Qy 4743 AVLHSIVSLAILIGYHYHLKVP LAIFKREKETARKLEFDGLYIARQPEDDDLKSHWDKVI 4802  
Db 4737 ACLHSLVSLAMLIAYHYHLKVP LAIFKREKETARKLEFEGLFIARQPEDDDFKSHWDKVI 4796  
Qy 4803 SAKSFPVNYWDKFKVKVRAKYSETYDFDSTSNMLGMEKTSFSAQEBEGSKGLIHYINI 4862  
Db 4797 SAKSFPVNYWDKFKVKVROKYSITYDFDSTSNLGMKSTFAAQESE-ETGIFKYIWN 4855  
Qy 4863 DWRQVQWKAGVTITDNGFLYSLWTSFVSVMGNFNFFFAHLLDVAVGFKTLRTILQSVT 4922  
Db 4856 DWRQVQWKAGVTITDNGFLYSLWTSFVSVMGNFNFFFAHLLDVAVGFKTLRTILQSVT 4915  
Qy 4923 HNGQLVLTVMLLTIIVYIVIAFNFRKPYQOEDEDEVNRNCHDMLTCEVENLYKGVR 4982  
Db 4916 HNGQLVLTVMLLTIIVYIVIAFNFRKPYIQEEDSEVNDKCHDMLTCEVFLYKGVR 4975  
Qy 4983 AGGIGBELEPPDGDSDSVRIIFDISPFPIIIVLAILQGLIIDAFGLRDQLESVKE 5042  
Db 4976 AGGIGBEIGDPDGDSDVEYRIIFDITFFPVIILAILQGLIIDAFGLRDQLESVKD 5035  
Qy 5043 DMESNCITGINKDYFKVPHGFTHVQREHNLANYMFFLMLINKPDTEYTGQETVWN 5102  
Db 5036 NMESNCITGKMGKDFDIPVHGFDTHVQKEHNLANYMFFLMLINKPDTEYTGQETVWN 5095  
Qy 5103 MYTORCWDFFPVGDCFRKQYED 5124  
Db 5096 MYQORSWDFFPVGDCEFRKQYED 5117

RESULT 15

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Query Match 79.1%; Score 21191.5; DB 4; Length 5112;  
Best Local Similarity 78.6%; Pred. No. 0;  
Matches 4061; Conservative 450; Mismatches 548; Indels 109; Gaps 41;

Qy 1 MAEAGGASEQDDVSFLRTEDMVCLSCTATGERVCLAAEGFGNRHCFLENIADKNIPDDL 60  
Db 1 MAEAGG-SEQDDVSFLRTEDMVTLSCTATGERVCLAAEGFGNRHCFLENIADKNVPPDL 59  
Qy 61 SQCVFVEQALSRAIQELVTAAGSETGKGTSGSHRTLTYGNAILLRLHNSDMVYLAQLST 120  
Db 60 SQCVFVEQALSRAIQELVTAAGSETGKGTSGSHRTLTYGNAILLRLHNSDMVYLAQLST 119  
Qy 121 SSSQDKLAFDVGIQHQSQGEACWMTLHPASKQRSEGEKVRVGDDLLVSVATERYLHTTK 180  
Db 120 SSSNDKLSFDVGLQEHQSQGEACWMTVHPASKQRSEGEKVRVGDDLLVSVATERYLHTTK 179  
Qy 181 ENEVSIVNASFHVTHWSVQPYGTGISRMKVGVVFGDVLRFPHGGDECLTIPSTWTKDG 240  
Db 180 ENEQSIVNASFHVTHWSVQPYGTGISRMKVGVVFGDVLRFPHGGDECLTIPSTWREA 239  
Qy 241 GQNIIVVEGGSVMSQARSRLWRLELARTKWAGGFINWHPMRIHITTTGRVLYGVNDONELY 300  
Db 240 GQNIIVVEGGSVMSQARSRLWRLELARTKWAGGFINWHPMRIHITTTGRVLYGVNDONELY 299  
Qy 301 LVREBATTASCAFLRQEKDQKQVLEDKDLEVIGAPIIKYGDSTVIVQHSETGLWSY 360  
Db 300 LVKKEEASIAITTFSW-QEKDDEKQVLEDKDLEVIGAPIIKYGDSTVIVQHSETGLWSY 358  
Qy 361 KSYETKKKGKGVKEEQAAILHEEGKMDGLDPSRSEESERTARVIRKCSLFTKFNGL 420  
Db 359 KSYETKKKGKGVKEEQAAILHEEGKMDGLDPSRSEESERTARVIRKCSLFTKFNGL 418  
Qy 421 ETIQENRRHSFFKQVNLNEMVNCLEDLINYPQOPEDMEHEKONFRALNRQDLFOE 480  
Db 419 ETIQENRRHSFFKQVNLNEMVNCLEDLINYPQOPEDMEHEKONFRALNRQDLFOE 478  
Qy 481 EGIINLILAEADKINIVITTSQGLAGFLAGDESQSWEMISGYLYQLLAAAIKGNHTNCAQ 540  
Db 479 EGVNLIILAEADKINIVITTSQGLAGFLAGDESQSWEMISGYLYQLLAAAIKGNHTNCAQ 538  
Qy 541 FANSNRLNMLFSRLGSAQSGEGTMDLVHLCVILDSPEALNMRDEHIKVIISLLEKXGR 600  
Db 539 FANSNRLNMLFSRLGSAQSGEGTMDLVHLCVILDSPEALNMRDEHIKVIISLLEKXGR 598  
Qy 601 DPKVLDVLCSCVGVAVRSSQNNICDYLPGKNLLQTLALVDHVSSVRPNFVGRVGE 660  
Db 599 DPKVLDVLCSCVGVAVRSSQNNICDYLPGKNLLQTLALVDHVSSVRPNFVGRVGE 658  
Qy 661 SAVYRWYFEVITMDHIEKTHMMPHLRIGWANTTGVYVYPGGGKMGNGVGGDLYSYGF 720  
Db 659 SSYQKRYFEVITMDHIEKTHMMPHLRIGWANTTGVYVYPGGGKMGNGVGGDLYSYGF 718  
Qy 721 DGAYLMSGGRKTPVNRTHAEEPIYRGDVTGCAOLDLTVPIINFMFNGVRVTGFTNFLE 780  
Db 719 DGAYLMSGGRKTPVNRTHAEEPIYRGDVTGCAOLDLTVPIINFMFNGVRVTGFTNFLE 778  
Qy 781 GMFPFVYSCSSKLSCLRGHGRRLRYAAPEGVSLVESLLPQOILSLSPCFYFGLSK 840  
Db 779 GMFPFVYSCSSKLSCLRGHGRRLRYAAPEGVSLVESLLPQOILSLSPCFYFGLSK 838  
Qy 841 RALAGPPLVQDDTAFPVTPVDVTLTIPTVVEQIRDKLAENIHEHWMANNKIEAGMYGDQ 900  
Db 839 NVLAGPWLIEDDTAFVPPKPVDTTGTPLPSSVDQIKELAEINHEHWMALNKEACWSGEH 898  
Qy 901 REDLKHITHPCLVPPERLPPAEKRYDIQLAVQTKLITLALGYISLDKPPAIRNVRPLNE 960  
Db 899 RDDVHRHPCLVTHFEKLPAAEKRYDNLAVQTKLITLALGYISLDKPPAIRNVRPLNE 958  
Qy 961 PFMQSNQYKPAPLDLSAVTLTPKMDDELVDQLAENTHNLWARERIQQGVTLGNLSDSMHR 1020

Db 959 IFMQNGYKPAPLDLSAVTLTKLEELVDQLAETHNLWABERIQOQWYTGLENSDENHR 1018  
 Qy 1021 SPHLVPYKVDADAKKANRDFTASEVTLLVYGYMLDPTTCEQHEALLLEASKQKQADFR 1080  
 Db 1019 SPHLVPYAKVDEAKKANRDFTASEVSANAPGLRICGSSDGRNGGTSGRRITPQVRRIP 1078  
 Qy 1081 TYRAEKYAVSGKWYFEFEILTAGPMRVGWAHADMAPGMLGDENSFAFDGYNEEKVY 1140  
 Db 1079 TYRVERNAVTSKWYFEFEVLTSKPMRVGWARADCYFGAMLGSEDTSWAFDGHNVTKQH 1138  
 Qy 1141 SGNTEFQKQWAGVGVGFDLDLIDKTSFSLNGELLMALGGETTPADV--QGDNFVPA 1198  
 Db 1139 AGSIEHFGVREAGDVIGCFIDVKEQITISFSLNGELLMALGGETTPADVTAEGVGFPA 1198  
 Qy 1199 CTLVGVQKARLYTGODVNTLKYFTTCGLQEGVEPCVNMKRDVTHWYTKDOPIFENTDEM 1258  
 Db 1199 CTLVGVQKARLYTGODVNSLKFFTTCGLQEGVEPCVNMRRPVTWYTKDOPIFENTDEM 1258  
 Qy 1259 IDTRIDVTIRIPAGSDTPCLKISHNTFETMEKANWELRLSLPVTICHNEFIDEAEKARRW 1318  
 Db 1259 PDCRIDVTIRIPAGGADTPHLKISHNTFETMEKANWELRLSLPVTICMGEFTISEQEKARRW 1318  
 Qy 1319 VEIKROQOILMKEA-VEAQM-----PAHIDQIMRSQFTMDIKLHYE-DNOEELPSSKM 1371  
 Db 1319 DEIKNQYRLMREAEIAAQMOVQTAHMDHMLKGFNNNDIKGLTRNFDHADAADHM 1378  
 Qy 1372 KRLPRPRKSGMTGVTIONYNNIOPQOVNGMHRSTSEAEWAKYDLGAQGLTDPDKKOK 1431  
 Db 1379 MRGNRPKRLSLTNIT---FETDMSAALDEMQRSTST-----VLDMNGLGEEMDDKK-K 1429  
 Qy 1432 RGRSPFKFRSGRESSDRAKRSKTPDPFSDTEVSPERGARRNPQIKVSAQNRVNG 1491  
 Db 1430 RGRSPFKFP-SKSRDQGREK-MGARTLDTSLERNTVAHGNVNVQWMTTRAPTFLRNN 1487  
 Qy 1492 MNARESRNLXGSOVGLNMAPTDQRKQMTTSLAQSATETVGNBIFDAECLKLNEYFY 1551  
 Db 1488 AEIPSPV-----POGPKQLSGSLGQOPVETSGDEMFAECLKLNEYFY 1533  
 Qy 1552 GVRIPGQDPTHVYIGWTTQYHLHSKOPNQSKVTKSSVIIITDDYDRVVENVNROSCYV 1611  
 Db 1534 GVRIPGQDPTHVYIGWTTQYHLHSREFNKNKVRGSIYIBDDYEMAIERIDROSCYV 1593  
 Qy 1612 RADELVNEVMAEATAGKASQGMFICGSVDVTSFGVSFTCEGKDTSFKPMETKLFPAI 1671  
 Db 1594 RADELNEVMTQASGKASQGMFVCGFVDATLGIIRFTCEGKDTSHRWMEPDKLFPAI 1653  
 Qy 1672 FVEATSKETLOELGRSATSLPSAAVLPTSDKHVIPQPPRLKQVCLKPHQWARPVNO 1731  
 Db 1654 FVEATSKETLOELGRTPPTLPSAAVLPTSDKHINPQSPRLKQVCLKPHQWARPNTA 1713  
 Qy 1732 LOVHALKUSDTRGWSMLCEDAVSMALHIPEDRCIDILEPIEMDKLLSFHSHTLTLYAA 1791  
 Db 1714 LOVHALKUSDVRGWSMLCEDPVSMLALHIPEDRCIDILEPIEMDKLLSFHAHSHTLYAA 1773  
 Qy 1792 LCYQSNYRAAHALCTHVDOKLLEYAIOQOYMSGPLRQGFYDLIALHLESHATTWEACN 1851  
 Db 1774 LCYQSNYRAAHALCORVDQKLLYAIRSEYMGGPLRQGFYDLIALHLESHATTWEVCN 1833  
 Qy 1852 EFVILPGLPELKYBEPDMGHLSRLSIQTESVRFPMQMTDIAESITEISNLSPFYFPLEVA 1911  
 Db 1834 EYITPLGAELEKELYDEENQHSRLSVTESVRPQLRMTETIETPIDQLYSPKPLEVV 1893  
 Qy 1912 REFVMOALABAVETQVNRDPVGGSENFLPLIKLVDRLLLVGMRRDEVEKLLIWTN 1971  
 Db 1894 RQFVMEALKDAVEINQVNRDPGTGWTNENLFLPIKLTDRLLVGLVTDDEVDQRLVMD 1953  
 Qy 1972 PETWDSFQEGKDEHRKGLLHMWMAEGAKLQWYLLQHLNDIOQLRHRVEAIIAFAHDFV 2031  
 Db 1954 PETWDAFEREGKDEHRKGLLHMWMAEGAKLQWYLLHLLHYDTQLRHRVESIIAASHDFV 2013  
 Qy 2032 GLOLTDOLRYTEIKQSDLPSSAAKKTREFCPPREQMNAILSFHGLEEDKENCPCGE 2091

Db 2014 GDLQTDOLRYTEIKQSDLPSSAAKKTREFCPPREQMNQILCFKNLEPDDQDNCTCGL 2073  
 Qy 2092 ELIARMNEFHTLMAHVSYSLHALQEPDAAENQEB-PEAKPGAFGKLYNIINTVKELEEEAKA 2150  
 Db 2074 ELRGLGDFHDSLMQKVSJNALQEPDGVGTAIEBVTGPTTKIYNFTINTVKELEEGPKE 2133  
 Qy 2151 IEPPPKTPEBKPKVLIQTIIVNWAESQIETPKLVREMFSLLVROYDANGELTRALEKT 2210  
 Db 2134 VEPEKKTPEBPKVLIKTIIVNWAESQIENPKLVREMFSLLRQYDVTGELVRALBKT 2193  
 Qy 2211 YVINAKTKLDAVEMWVGLSQRALLPVQMSQEEBELMRKRLKWLNNHTFQHPDLIRVL 2270  
 Db 2194 YVINTRADDVAEMWVGLSQRALLPVQMSQEEBELMRKRLKWLNNATFQHPDLIRIL 2253  
 Qy 2271 RVHENVMAVMNTLGRRAQASDAQSPSPVAE--DSKEDTSHEMVACCRFLCYFCRT 2328  
 Db 2254 RVHENVMAVMNTLGRRAQASDAQSPSPVAE--DSKEDTSHEMVACCRFLCYFCRT 2312  
 Qy 2329 GRQOKAMFDFHDFLENSNILLSPRLSGSTPLDVAISSLMMENTELALAREHYLEKIA 2388  
 Db 2313 GRQOKAMFDFHDFLENSNILLSPRLSGSTPLDVAISSLMMENTELALAREHYLEKIA 2372  
 Qy 2389 VYLSRCGLQSNSELVEKGYDGLGWDVPEGERYLDLFRFCVWNGESVEENANLVIRLLIR 2448  
 Db 2373 VYLSRCGLQSNSELVEKGYDGLGWDVPEGERYLDLFRFCVWNGESVEENANLVIRLLIR 2432  
 Qy 2449 RPECLGALRGEGEGLLAKAIVDANKMSERIADRRKLREMEQEGDV--NFSHPLPESDED 2505  
 Db 2433 RPECLGALRGEGEGLLAKAIVDANKMSERIADRRKLREMEQEGDV--NFSHPLPESDED 2491  
 Qy 2506 EDYIDTGAAILNFYCTLLVDLGRCAPDAGVATLAKNESLRARAILRSLVPLEDQGVLSL 2565  
 Db 2492 EDYIDTGAAILNFYCTLLVDLGRCAPDAGVATLAKNESLRARAILRSLVPLEDQGVLSL 2551  
 Qy 2566 RFTLNNPAGGERPKSDMPGSLIPGHKOSVGLFLERVYGIETQELFYKLLBEAFPLDRA 2625  
 Db 2552 KPTLSQTAGBEKPKSDMPGSLIPGHKOSVGLFLERVYGIETQELFYKLLBEAFPLDRA 2611  
 Qy 2626 ATMLDRDGCESDMALSMNRYIGNSILPLLIKHAYFYNEAENYASLLDATLHTVYVLSKN 2685  
 Db 2612 ATILDKSGESDMALSMNRYIGNSILPLLIKHAYFYNEAENYASLLDATLHTVYVLSKN 2671  
 Qy 2686 RMLTKGOREAVSDFLVALTSQMPAMLLKLRKLTVDVSKLSEYTTVALRLLTLHYERCA 2745  
 Db 2672 RMLTKGOREAVSDFLVALTSQMPAMLLKLRKLTVDVSKLSEYTTVALRLLTLHYERCA 2731  
 Qy 2746 KYGSGTAGOGAFGASSDEEKRLTMMFLSNIFDSLSKMDYBPFLFGKALPCLIAGCALP 2805  
 Db 2732 KYGST-QOGSGYASSDEEKRLTMMFLSNIFDSLSKMDYBPFLFGKALPCLIAGCALP 2790  
 Qy 2806 PDYLSKNYDDEFYKQQAAGDLNPOYDPOPIINTSSVALANDLNTIIVQKFESEHYHDWA 2865  
 Db 2791 PDYLSKNYDDEFYKQQAAGDLNPOYDPOPIINTSSVALANDLNTIIVQKFESEHYHDWA 2848  
 Qy 2866 SRKIENGWYGEHSDSOKTHPRKLPYNNLDYKERYKEBPVRESLKALLAIGWSEHSE 2925  
 Db 2849 SRLEGGWYGDIRSDNDRKHPRKLPYNNLDYKERYKEBPVRESLKALLAIGWSEHSE 2908  
 Qy 2926 VDIPSNRSSMRQSKSGRRPEI--VTDSATPDYNNPVDMTNLTLSREMNMAERLA 2983  
 Db 2909 VEVLNHRGSTRQSK-----PQINEFQNEGSPFNYPHPVDMSNLTLSREMNMAERLA 2963  
 Qy 2984 DNAHDIMAKKKEELVTNGGGIHPOLVPYDILLTDEKKKDRSROEFKLYQYQYKLRH 3043  
 Db 2964 ENSHDIMAKKKEELVTNGGGIHPOLVPYDILLTDEKKKDRSROEFKLYQYQYKLRH 3023  
 Qy 3044 PSKAPQSDTEQTTGVAIELRPAYSLEKLIQYIDRATINMKLLKPSTTFPSRRSFKST 3103  
 Db 3024 PSKGAVE-EGGATQAAVELRFSYLLKLIQYIDRATINMKLLKPSTTFPSRRSFKST 3082  
 Qy 3104 RDIKFFSKAVLPLMEKYFSTHRNYFIAVATATNNYGAASLKEKEMVAALFCKLASILRR 3163  
 Db 3083 RDIKFFSKAVLPLMEKYFSTHRNYFIAVATATNNYGAASLKEKEMVAALFCKLASILRR 3142





Qy 1857 LG-----PELKALYBEPOMGHLSRSIQTES-----VRPQWMTDIAESI 1895  
Db 117 YGNVIQLHLKSNKYLTVNKKLPALLEKNAMRVTLDEAGBGSWFYIQPFYKLSIGDSV 176  
Qy 1896 TEISNLSPYPPLEVARFVMOALAEAVETNQVHNRPVGGSENENLFLPLIKLVDRLLLV 1955  
Db 177 -----VIGDKVLPVNPVAGQPLHASSH-----QLVDN---P 204  
Qy 1956 GMMREDEVE-----KLLIMTNPETWDPSPFKBKGDEHRKG--LLHMKMAEGAKLQMCYLL 2008  
Db 205 GCNEVNSVNCNTSWKILVFMK---W-----SDNKDDILKGGDVVRLFAHEQKELTCD-- 254  
Qy 2009 QHNDIQLHRHVEAIIAFADHPFVGDLQDQLRRYTEIKQSDLPASAIAAKTTRCPCPRE 2068  
Db 255 -----EHRKK-----QHVFL-----RTTGRQS--ATSATSSKALWEVVEVQHD 290  
Qy 2069 -----QMNAILSFKHLEEDKENCPCGEBELIARMNEFHDTLMAHVSLSHALQPDAAEN 2121  
Db 291 PCRGAGYWNLSLFRFKHL-----ATGHVLAEEV-----DPD----- 321  
Qy 2122 QEPEAKPGAFGLKYNIIINTVKELBEEAKAIBEPKKTPEE-----KFRKVLIIQITVN 2173  
Db 322 -----FEEF-----CLEFQSPVDPDQDASRSRLRNAQEKWVYSLVS 357  
Qy 2174 WABESQIET-----PKLVREMFSLVROYDAVGELIRALEKTYVINAKTKLDVAE----- 2223  
Db 358 VPEGNDISSIFELDPFTTLRGGDSLVPR--NSYVRLHLCNTWVHSTNIPIDKEEEKPVM 415  
Qy 2224 MWVGLSOIR-----ALLPVQMSQEBE-----ELMRKRLWK 2253  
Db 416 LKIGTSPVKDEKAFAIVPSPAEVRDLDPANDASKVLGSIAGKLEKGTITONERSVTX 475  
Qy 2254 LVNNHTFF-----QHPLDIRV-----LRVHENVMVMMNTLGRRAQAQSDAQP 2296  
Db 476 LLEDLVFVTGNTSGQDVLVWFVSKPNRRQKLMREQNILKQIFKLLQALPFTDCGDG-- 533  
Qy 2297 SSQPVAEDSKEDTSHENVACCRFLCYFC-----RTGRONKAMFDFHDFLENSNILL 2351  
Db 534 ---PMLREELGQDQRAFFRHCIR--LCYVRLRHSQQDYRKNOEYIAKQFGFMQK----- 583  
Qy 2352 SRPSLRGSTPLDVAYSSIMMENTALALAREHYLEKIAVYLSRCGLQNSSELVEKGYPDLG 2411  
Db 584 -----QIGYDVLAETITAL-----LHNNRKLLEKHITAAE 614  
Qy 2412 WDPV-----EGERYLDPLR--FCVWNGESV-----EENANLVI---RLLR 2448  
Db 615 IDTFVSLVRKNREPRFLDYLDLCVSMN--KSIPVTQELICKAVLNPTNADILITKLVL 673  
Qy 2449 RPECLGPALRGEGLLKAIYDANKM-----SERIADRRKLREMEQEGDVNFSHPILPES 2502  
Db 674 RPEPEG--VSSTGENALEAGEDEEVWLFWRDSNKETRSKSVRELAQDAKEG-----Q 724  
Qy 2503 DEDEDYIDTGAAILNFYCTL-----VDLLGRCAPDAGVIALGKNESLR 2545  
Db 725 KEDRDVLSYRYQNLFPARMCLDROYLAINEISQGLVDLILRCMSDENL-----PYDLR 779  
Qy 2546 A---RAILRSVLPLEDQGLVLSLRTFLMNPAAAGERPKSDMPGSLIPHQKOSVGLFLERV 2602  
Db 780 ASFCRLMLHMHVDRDPQOVTPVKYA-----RLWSEIPSEIADDDYSSGASKD-- 828  
Qy 2603 YGITOELFYKLE--EAFPLDPLRAATMLDRNDGCESDMALSMRYTGNSTILPLIKHAY 2660  
Db 829 ---BIKERFACTMEFVEEYLRDV--VCORFPFSDKEKNKLTPEVVYNLARNLI-----YFG 878  
Qy 2661 FYNEAENYASLLDAT-----LHTVYRLSKNRMLTGQREAVSDFLVALTSAMQP 2709  
Db 879 FY-----NFSDDLRLTKILLAILDCHVTITIPISK---MAKGE----- 915  
Qy 2710 SMLLKLRLKLVDSKLSYTTVAL-----BLTLHYERCAYKYYGSTGAGOGAFG----A 2760  
Db 916 -----NKGNDVEKLSKNVMSRSHGVGELMTQVVLRGGLPMTPMMAAPEGNVQQA 968  
Qy 2761 SSDEEKRLTMMLFSNIFDLSL-----KMDYEPFLFGKALPCLIIAIGCALPDPYLSLKNYD 2815

Db 969 EPEKEDIMVMDTKLKIEIILQFILNVRLDYR-----ISCLLCI-----FK 1008  
Qy 2816 DEFYGKEQAAGDLNDNQYDQDPQINTSSVALNNDLNTIVQKFSBYHDAMASRKIENGWY 2875  
Db 1009 REF-----DESNQ-----TSETSSGNSQ----- 1028  
Qy 2876 GEGMSDSQKTHPLKPVNMLNDYEKERYKEPVRESLKALLAIGWSVEHSEVDIPSNRRSS 2935  
Db 1029 -EG-----PSNVPGALDFEHIEQA--EGIPGGRKVYFHEENTPLDLDH----- 1070  
Qy 2936 MRQSKSGGRPEIIVTDSATPFYNNPDPVDMTNLTLSREMNMAERLADNAHDIIWAKKK 2995  
Db 1071 -----GGRTFLRVLLHLTHDYPP-----LVSGALQLLFRHFSQREVLQAFQV 1115  
Qy 2996 EELVTNGGGIHPOLVPYDLTLTDEKKKDRORSQEFKLYQYQYKULHRPSK-----APQS 3050  
Db 1116 QLLVTS-----QVDVNYKQIKODLDQLRASIVEKSELWVYKGGQPDETMDGASGEN 1165  
Qy 3051 DTEQTTTGVAIELRPAYSLEKLIQYIDRATINNKLLKPSTTFSSRRSSFTKTRDIKFFS 3110  
Db 1166 EHKTEEG-----NNKPKHEST-----SSY----- 1186  
Qy 3111 KAVLPLMEKYFSTRNYFIAVATATNNGAASLKEKEMVAALFCKLASLRLSLAFAQPD 3170  
Db 1187 -----NVRVV-----KEIL----- 1195  
Qy 3171 VRITVRLQVLVIGIDAKSLVKNCPEPIRTSMLTFFNNVADDVGHITMNLQDGYAHLRG 3230  
Db 1196 IRLSKLCVQ-----ESASVRKS-----RKQORLLRNM-----G 1224  
Qy 3231 THLKTSTSLGYINGVLLPILITAKFDHLANCEYGADLLLDLDEIOVASYKMLGSLYALGTDS 3290  
Db 1225 AH-----AVVLELQIPI-----EKAEDTKQMEIMRLAHEFLQNF----- 1259  
Qy 3291 LTHDRKYLKTEIBERHKPALGSCGLGSAFSTPPVPAFLEPHLNKNQFSLNLNIAHSLBAQD 3350  
Db 1260 -----CAGNQNQ-----ALLHKHINLFLNPGILEAVTMQHI--- 1291  
Qy 3351 IMQMBQCMPTLETILGEVDQFVESDKTYNEAPHI IDVVLPLLCSYLPFWWAQPDNVTP 3410  
Db 1292 FMNFQLCSEINERV--VQHFV-----HCIE----- 1315  
Qy 3411 TCGNHYTMTVAEHNQLLKNVLKIKKNIGNENAPMWTIATVTTQIIINSSEBLL--- 3466  
Db 1316 THGRNQYI--KFLQITIVKAEGRFIKK-----CODMMAELVNSGEDVLVFN 1361  
Qy 3467 -RDSFPLAERVRKRTDNM-----PHKEESLRGFIKSDTDDTSQVESIQIEDWOLL 3516  
Db 1362 DRASFQTLIQMMSERDRMDENSPLMYHIHLVELL-----AVCTEGKNVYTEIKCNLLP 1416  
Qy 3517 VRDIYSPY-----PLLIKYVDLQRNHWLRNNVPEABELY--NHVAEIPNIMSKSQYFL 3567  
Db 1417 LDDIVRVVTHEDCITPEVKIAYINF-LNHCVYDTEVENKEIYTSNHHMKLF----- 1465  
Qy 3568 KEQNFISANEIDNMVLMPTATRTATRVATVDTGTPQGGGKKKKHKKRDKK--DKEVOASL 3626  
Db 1466 ---ENFL---VD-----ICRACNNTSD-----RKHADSIKEYTEIIVMSI 1500  
Qy 3627 MV-----ACLKRLLPVGLNLPAGREQELVQCHCKDRFLKKNSEQDV-----AE 3668  
Db 1501 VTTFFSSPDSQSTTLTQTRQPVFVQLLQGVFR--VYHC--NWLMPQSKASVESICIRVLSD 1556  
Qy 3669 FAKTQ-LTLPDKID-----PADEMSWQHLYSKLGSKSKSNIT----- 3705  
Db 1557 VAKSRATAIPVDLDSQVNNLFLKSHSIVQKTAMNR--LSARNAARDSDVLAASRDYRNI 1614  
Qy 3706 VETAENKAKIIDTVERIV-AMSKVLFGHLMIDHPQOMSKNVYRSVVSIOKRAVIACFR 3764  
Db 1615 IERLQDIVSALEDRLRPLVQAEISVL--VDVLRPELL-----PFENTDARK--CES 1663  
Qy 3765 QTSIHLSPRH-----RACNIFARTYELWLEENITGOEYMIEDLTQSFEDAEL-- 3812

Db 1664 GGFICKLIKHTKOLLENEEKLCKIKVQLTREMMTKDRGYGEKLSID---ELDNAELPP 1720  
Qy 3813 --KSDVVEEGKPDPLQLVTTFCRGAMTERSGALQSDPLYSVAHIIAKSCGEBE-- 3868  
Db 1721 APDSENATEELEPSPPLQLED-----HKGEALRQVLVNRYYGNV--RPSGRRESLT 1771  
Qy 3869 -----EGGGBEEGGGAEAEDEGRASIIHEQEMEKQKLLFQHQLARLADRGVAEMVL-LH 3920  
Db 1772 SFGNGPLSAGGPKPGGG--GGGSGSSMSRSGEMSLAEV--QCHDKEGASNLVIDLI 1825  
Qy 3921 ISASGKLSEVMWKTLQIGISILRCGNIDIQMGMLNHL-KDKKGVFF----- 3967  
Db 1826 MNASS---DRVFHESILLAIALEGNTTIOHSFPCRLTEDKSKSEKFKFVDRMKVAQQ 1882  
Qy 3968 ---TSIAGLMNSCVLDLDAFERNTKAEGL----- 3994  
Db 1893 EIKATVNTSDLGNNKKDDVDROPSPRKAKKEPTTOITEVRDQLLEASAAATRKATTT 1942  
Qy 3995 -----GVGLEGAAGEKNMHAETCA-----LFRFTQLTCEGHNDWQNYL 4035  
Db 1943 FRREADPDHYQPGSGTQ-ATADKAKDDELSAVITIMQPIILRFQLLCEHNHRDLQNFL 2001  
Qy 4036 RTQAGNTTNNVICTVYLRLQBS-----IMDFYWHYSKELIDPAGKANFPKAGV 4089  
Db 2002 RCQ-NNKTNYNLVCTLOFLDCICGSGTTGGLGLGLYINE-----KNVAL 2045  
Qy 4090 ASOVENTLITEVLOQCTOQALAHSLWDVGGFLFLFSHMDKLSKHSQVDLLKELL 4149  
Db 2046 INQTLSETEYCGPGCHENQNCIA-----THESNGIDIITAI- 2082  
Qy 4150 NIQKDMIPMLSMLEGNVNGTIGQVMDTILVE-SASNVELILKYDFMFLKLKOLITSSAS 4208  
Db 2083 -ILNDINP-----LGKRWDLVLELAKNASKLL-----LAIMESHDSN 2122  
Qy 4209 FOEIDANNDGWLPKDFKEMEQKSYTPEETIEFLACETNHDGKLDYIGFCDFRHPA 4268  
Db 2123 ABIRILYN---MRPKELVEVI--KKAQMGEVEF-----EDGENGE-----DGAASP- 2163  
Qy 4269 KEIGENLAVLLTNLSEHPNEPRLARFLETAGSV-----LNYPEFLGRIETMGSKIE 4323  
Db 2164 RNVGHNIVILAHQLARH---NKELOSMLKPGQVDGEALFEYAKHTAQIETVRLDRME 2220  
Qy 4324 RYVFPIKESNIBQWEKPOI-----KESKRAFFSYIVTEGGDK-EKLEAFVNPCEDAIFEM 4377  
Db 2221 QIVFPV-----PSICEFLTRESKLRIYTT--TERDEGSKINDFFLRSEDLFNM 2268  
Qy 4378 THASGLMAASESVGGTKNREASYMGMDDDERAGKDPFRGLQSVKDGVATAFSSLS 4437  
Db 2269 NWOKKLA-----QPVLYWCARNMSFW-- 2290  
Qy 4438 SNIKAKIADMQMPAELAVGFFKMFYLYLGYGLVIVVRYIFGVLLGLMRGPOTDEP 4497  
Db 2291 SSIISFNLAIVMLNLLVA-----FFYPFKVGSGTL----- 2319  
Qy 4498 PPEPTEEEKIGQLRHLLATQSSRHLPALPPADDTGQMVSAGFLDITKEDNGQIQVKPH 4557  
Db 2320 -----EPH 2322  
Qy 4558 ESPSTSTPSGSEAEVSPDESADTHEQRPSPSLIDLLGGEQAKQAQERMEAAQAQAA 4617  
Db 2323 WS----- 2324  
Qy 4618 SAIEAESKAVOGPAPALSQVDLSQYTRAVSFARPNYKLYVALVLAFCINVFLLFY 4677  
Db 2325 -----GLLTWAMLISLAIVIAL--- 2341  
Qy 4678 KYSTLDGEGGSGLDIITAGGSGGAGSGSGSGESGSDDDDALEVHIDEDFYMEH 4737  
Db 2342 -----KPHGIRALIA----- 2352  
Qy 4738 VIKMAAVLHISVLSAI-----LIGYHYLKVPLAIFRKEKEIARKLEFDGLYIAEQPEDDD 4792  
Db 2353 ----STILRLIFSGLQPTFLFLGAFN-----VCNKLIIF----- 2382

Qy 4793 LKSHWDKLIVASISGFPVNYMDKFVKKVRAKRYSETYDFDSISNMLGMEKTSFSAQEEBGS 4852  
Db 2383 ----- 2382  
Qy 4853 KGLHYIINIDRWYQVWKAGVTITDNSFLYSLWYFSVMGNF--NNPFFAAHLLDVAVGF 4911  
Db 2383 --LMSFVNGCGTFFRGYRA--MWLDVBFLLHLLVLCAMGLFVHEFFYSLLLPDLVYRE 2438  
Qy 4912 KTLATILQSVTHNGKQLVLTVMLLTIIVYIVTIAFNFFKFFV----- 4955  
Db 2439 ETLNVIKSVTRNGRSIILTAVALIILVYLSIYGVYLFKDDFILEVDRLPNETAVPTG 2498  
Qy 4956 -----QEEDDEVNRNCHDMLTCTFVNLYKQVR 4982  
Db 2499 ESLASEFLFSDVCRVSEGENCSSPAPREELVPAEBEQDKEHTCETLLMCIVTVLSHGLR 2558  
Qy 4983 AGGIGIGELEPPDGDSDS-EVYRIIFDISFPFFIIVILLAILOGLIIDAFAELRDQLESVK 5041  
Db 2559 SGGGVGVDLRKPSKEEPLFAARVYDILLFFFWVIIIVLNLIFGVIIIDTFADLRSEKQKE 2618  
Qy 5042 EDMESNCFICGINKDYFDKVPHGPDTHVQREHNLANTYMFELMHLINKPDTVETGOETVW 5101  
Db 2619 EILKTTFCIGLERDKDFDKNTVTFEHKEHNNMHWYLCFIVLVKVKDSTETGYESYA 2678  
Qy 5102 NMVTCRCWDPPP 5113  
Db 2679 EMIKERNLDWPP 2690

RESULT 2

US-10-505-928-784  
; Sequence 784, Application US/10505928  
; Publication No. US20060089532A1  
; GENERAL INFORMATION:  
; APPLICANT: Ludwig Institute for Cancer Research et al.  
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES  
; FILE REFERENCE: 28967/39178  
; CURRENT APPLICATION NUMBER: US/10/505,928  
; CURRENT FILING DATE: 2004-08-27  
; PRIOR APPLICATION NUMBER: US 60/363,019  
; PRIOR FILING DATE: 2002-03-07  
; NUMBER OF SEQ ID NOS: 866  
; SOFTWARE: PatentIn 3.2  
; SEQ ID NO 784  
; LENGTH: 2671  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-505-928-784

Query Match 2.2%; Score 601.5; DB 6; Length 2671;  
Best Local Similarity 17.4%; Pred. No. 9.2e-28;  
Matches 625; Conservative 475; Mismatches 1060; Indels 1427; Gaps 149;

Qy 1932 DPVGGSENFLPLIKLVDRLLVGMWRDEVEKLLIMTNPETWDPSPDEKGDHHRKGL 1991  
Db 39 EPAAGDLDN---PPKKFRDCLFKVCPMRYSAQK-----QYWKAKQTKDKEKIADV 88  
Qy 1992 LHMKAAGAKIQMCLYQLHND-----IQURH-----RVEAII 2024  
Db 89 LLOKLQHAQAQME-----QKQNDTENKKVHGWDVKYGSVIQLLHMKSNKYLTWNKRLPAL 143  
Qy 2025 -----APAHDF-----VGD---LQTDLRRYTEIKOSDLP 2052  
Db 144 EKNAMRVTLDATNGESWLFQPPFWKLSRNGDNVVGDKVILNPNVACQPLHASNYEUSD 203  
Qy 2053 AVAAKKTREPPCPPEOMNAILSEK-HLEE-----EDKENCPCGEELIARN 2098  
Db 204 NAGKEVNSVNCNTSKINLFMQFRDLHEEVLKGDVVRLPHAEQEKELTC-DEYKGLQ 262  
Qy 2099 EFHDTLM-----AHVSLHALQEPDAAENQEPKPAFGKLYNIINTVKELEE-EAKAIE 2152  
Db 263 VFLRTLRLQSATSATSSNALWEVHVHDPCKRGAGHNGLYRF-----KHLATGNYLAAE 318







450	Db	-----QNTLAQVFGIL--KAPPEKAGSGMLRLEDLGDQR 483
2310	Qy	TS--HEMVACCRFLCYFCRTGRQNKQAMFDFDLLENSNILLSRPSLRGSTELDVAYS 2367
484	Db	YAPKYMLRLCYRVLRHSQDYQRNQ-----PYIAKNFCVMQSQ-----LCYD 526
2368	Qy	SLMENTELAL-----ALREHYLEK-IAYVLSRCSGLOSSELVBKGYPDLGWDPEVEGRY 2420
527	Db	ILAEEDTITALLHNRNKLLEKHITAKETIETFVSL-LARNRE-----PRF 568
2421	Qy	LDLRFVCVWNGESVEENANLIVIRLLRPPCICGPAIRGECEGLLKAIVDANKMSERIAD 2480
569	Db	LDYLSDLCVSNSTTAPVQTEUICKFM-----LSP--GNADILIQT-----606
2481	Qy	RRKREMEQEDVNFSPHLPDESDEDED---YIDT-----GAATLNFVCTLVLLGLRCAP 2531
607	Db	--KVVSQADNPM-E-SIILSDDIIDEEVWLYWIDSNEKPHGKAIRH-----649
2532	Qy	DAGVIALGKNBSLRARAILRSLVPLEDLQGVLSLURFTLNNPAAGEERPKSDMPGSLIPGH 2591
650	Db	---LAQEAKEGTXA-----DLEVLTYRYQLNLFAR-----677
2592	Qy	KQSVGLFLERY-----GIETO---ELFYKLLBEAFLP-DLRAATMLDRNDGCSDDMALSM 2643
678	Db	-----MCLDRQYLAINGISTQLSVDLILRCVSDSLSLFDLRASF-----CRILMLMHV 725
2644	Qy	NRVIGNSILPLLIKHAYFYN-----AENVASLLDATLHTVYRLSKNRMLTKG--QREA 2695
726	Db	DRDQESVVP--VYIARLWTEIPTKIITHEYDSITDS-----SRNDMKRKFALTMEF 775
2696	Qy	VSDLEVALTSAMQSPMLLKLRKLTVDV-----SKLSEYTTVALRLTL- 2739
776	Db	VEEYLKEVNPQPP-FGDKEKNKLTFEVHLARNLIYFGVFSFSELLRTRTLAILDIV 834
2740	Qy	-----HYERCACYGTGACQAGFAGSSDBEKKLTWMLFS--NIF-----2777
835	Db	QAPMSSYFERLSKF---QDGGNNVMRTIHGVGEMNTQVLSRGSIFPMSPVDPVPSIHPS 891
2778	Qy	-----DSLKMDYEPFLFGKALPCLIAIGCALPPDYSLSKNYDDEFYKGEQAAGDLD 2829
892	Db	KQGSPTHEDEVMTDKLII-ELQPLSLVRL---DYRIS---YMLSIYKE--FGE-D 941
2830	Qy	NPOYDPOPINTSSVALNNDLNTIVQKFSSEHYHDASWKIENGWVYGEWSDSOKTHPRL 2889
942	Db	NDNAETSASGSDPTLLPSAIVPDIDEIAAQAEFTWAGRKEKNPVQLDD---EGGRTEFLRV 998
2890	Qy	KPYNMLNDYKERYKEPVRESLKALLAIGWSVEHSEVDIPNNKSSWRRQSKSGRRPEI 2949
999	Db	LIHLIMHDY-----PPLLSGALOLLF-----KHFSQRAEVLQAFKQVL 1037
2950	Qy	VTDSATPDYNPHPVDMTNLTLTSEMOMAERLADNAHDIAWKKKEELVNTGGIHPQL 3009
1038	Db	LVSNQVDVNYQKIIKADLDQRLTVEKS-----ELWVEKSN--YENGE-----1078
3010	Qy	VPYDLLADKEKKDRERSQE--FLKYLYQGYKHLRPSKAPQSDTEQTTGTGVAIELRFAY 3067
1079	Db	-----IGESQVKGGEPIEESNILSPVQ-----DGTKKPQIDSNKSN-----Y 1117
3068	Qy	SLEBKLQYIDRATINMKLKPSTTFRRRSFKTSTRDIKFFSKAVLPLMEKYPFSTRHNY 3127
1118	Db	RIVKEILIRLSKLCVQNK-----DEKNNEVNL-----AH---TFLQNFCEGNPQNVLL 1194
3128	Qy	FIAVATATNVNGASLKEKENVAALFCKLASLLRSLAAFGPDVRIIVTRCLOVLVKGIDA 3187
1145	Db	L-----KNMGHS-----VVLDLQIPIYE-----1163
3188	Qy	KSLVKNCPEFIRTSMLTFFNNVADDVGHITMNLQDKYAHRLGTHLKTSTSLGIVINGVLL 3247
1164	Db	---KN-----DEKNNEVNL-----AH---TFLQNFCEGNPQNVLL 1194
3248	Qy	PILTAKEFHILANCEYGADLLDEIQVASYKMWLSGLYALGTDSLUTHDRKYLKTEIERHKKP 3307
1195	Db	-----HKLNLFLTPG-----LLEAETMRH-- 1214

Qy	3308	ALGSCLGAFSTFPFAFLPHLNKHNQFSLNRIADHSLSEADQIMQKMEQCMPT-	3361
Db	1215	-----IFM-----NNYHLCNEISER-----VQHFVHCIEITHGRHVE	1246
Qy	3362	-----LETILGEVQOFVESDKT-----YNEAPHIIDVVLPLLCSLYLPFW	3401
Db	1247	YLRFLQITIVKADGQYKVKCCQDMVTMELLINGGEDVLIFYNDRAS-FPILLHMMCSERDRGD	1305
Qy	3402	AQCPDNVPTGGNHVTMTVAEHNQLL-----KNVLKLIKIGNENAPWMTRIAFYQ	3455
Db	1306	ESGP-----LAYHTLV-----ELLAACTEGNVYTEIKCN-----	1336
Qy	3456	QIIINSSEELRDSFLPLAERVRKRTDNMHPKBEESLGRGFIKSSTDTSQVESQIQEDMWL	3515
Db	1337	-----SLLPLDDIVR-----VVTHDDCIPEVK-----	1358
Qy	3516	LVRDIYSFYPLLIIKYVDLQRNHWLRNNVPABEYL--NHVAEFLNIWSKSYFLKERQNF	3573
Db	1359	-----IAYNVFV--NHCYVDTEVEMKEIYTSNHIWKLF-----ENF	1392
Qy	3574	ISANEIDNMVLIPTATRRVTAVTDGTPQGGKKKKHRRDKDKDKEVQASLM-----	3627
Db	1393	LV-----DMARVCNVTITDR-----KHADIFLEKC--VTESIMNIVSGF	1428
Qy	3628	-----VACLKRLPLPVGLNLFAG-----REQELYQHCKDRFLKMKSEODVA	3667
Db	1429	FNSPFSDNSTSLQTHQPVFIQLQASAFRIYNCWTWPNPAQKASVESC-----INTLA	1479
Qy	3668	EFAKTO-LTLPDKIDPADEMSWOHYLYSKLGSKSKSNITVETAEKAKIIDDTVERIVAM	3726
Db	1480	EVAKNRGIAIPVLDLSQ-----VNTLFMKSHSNMVQRAAMG-----WRLSAR	1521
Qy	3727	S-----KVLFCGLHMDHPQMSKNVRSVSVSIQRKRAVIACFRQTSLSHL--PRHRA--	3776
Db	1522	SGRPFKEALGGPAWD-----YRNI--IEKLQDVVASLE-----HOFSPMQAEPSSL	1566
Qy	3777	-----CNIFAR--TYEELWLEENIIGOEVMIEDITQSFEDAELK	3813
Db	1567	VDVLYSPELLFPGSDARIRCGAFMSKLIINHKKLMEKE--EKLCIKILOTLREMLEK	1622
Qy	3814	KSDVVEGEKXPDPLTQLVTT-----FCRGAMTERGALQEDPLYSYAHIIAKSCGEE	3867
Db	1623	KDSFVBEQ---NTRLRKILLNRYFKGDYSIGVNGHLSGA-----YSKTAQV-----	1664
Qy	3868	EEGGEEEEGGEEAEDEGRASIIHQEMEKQLLPHQARLADRGVAEMVLLHISASKGL	3927
Db	1665	-----GGSFSGSDSKMGISMSDI-----QCULDEKGASELVIDIVNTKN--	1705
Qy	3928	PSEVMWKTLOLGISILRGHIDIQMGMLNHL-KDKKDVGFFTSIAGLMNSC-----	3977
Db	1706	-DRIFSEGIFLGIALLGEGNTQYQSYFQQLHEQKSEKFKVLYDRMKAQKEIRSTVT	1764
Qy	3978	-SVLDDDAFERNTKAE-----GLGVLEGAAGERNMHDAFTCA-----	4015
Db	1765	VNTIDLGNKKRDDDELMTSGPRMRYRDSLTHLKEGMKGOLTEASSATSKAYCYVREMD	1824
Qy	4016	-----LRFRIOLTCBGNLDMQNYLRTQAGN	4041
Db	1825	PEIDIMCTGPEAGNTEKSAEVTMGPAIIMOPILRFLQCCENHRELFQNFURNO--NN	1883
Qy	4042	TTTVNVVICVDYLLRLQES-----IMDPYHYSKSELIDPAGKANFFKAIQVSGVFN	4095
Db	1884	KTYNVLVCETLQFLDCICGTTGGLGLGLYINE-----KNVALVQNLE	1928
Qy	4096	TLTEVIQGPCTQNOQALAHSLRLWDVAGGFILFLFSHMQDKLSKISSQVDLLKELLNQOM	4155
Db	1929	SLTEYCGQPCHEHOTCIA-----THESSNGIDI--	1956
Qy	4156	IPMKLSMLEGNVNGTIGKQMVDTLVESASNVELILKYFDMFLKLKDLTSSASFOEIDAN	4215
Db	1957	IATIL-----NDIN--PLGKYRMDVLVQLKNNAKLL-----LAIMSRHDSENARILFN	2005

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QY 4216 NDGWLVPKDFKEMQKSYTTEIEFLAACCTNHGDKLDYIGFCDRFHEPAKIGFNL 4275
Db 2006 ----MRPRELVDM--KNAYNQ-----LECDHGDEGGDGV-----PKDVGHI 2046
QY 4276 AVLLTNLSHMEPEFLARLETAGS-----VLNYPEPFLGRIEMGSGKRIERVPE 4328
Db 2047 YILAHQARH-----NKLQOMLKPGSDPDDEGDEALKYANHTAQIEIVHRDRTMEQIVPP 2102
QY 4329 IKESNIEQWKEPKIKESKRAFFSVITEGGDKLEAFVNFCEDAIFEMTHASGLMAASE 4388
Db 2103 VP-----NICE-----YLTRSK 2115
QY 4389 ESVGTKNREASYMYMGDDDDDERAGKPPFRGLQSVKDGAVATAFSSLSFNKAKIADMQ 4448
Db 2116 CRVFNTER-----DEQGSK-----VND-----2133
QY 4449 QMPPELAVGFKMFYLYLYGYLVVVRVIFGVLLGLMRGPOTDEPPPTREEKIG 4508
Db 2134 -----FFQ-----QTEDLYNEMKWKI- 2151
QY 4509 QLRHRLATQSSRHLPALPPADDTGQMOVSAGFLDITKEDNGIQVVKPHESPSTPSSG 4568
Db 2152 --RNPALWFSRH-----ISLWG-----2168
QY 4569 EBAVSPDESADHTERQRPPLSLDLIGGEQAKQAEQERMEAOAQAQAAASAIEAESKAV 4628
Db 2169 -----2168
QY 4629 QGPAPALSQVLSQYTRRAVGFARNFYNLYKVALVLAFNVLVLFYKVTLGEGE 4688
Db 2169 -----SISFNLAFTNLA-----VALFYPFGD-DGDEGT 2196
QY 4689 GSLGDIAGGGSGAGSGDGSSEGEDDLEVVHIDEDFVMEHVIRMAAVLHSI 4748
Db 2197 LSPFLSVLW-----TAVACTSMLEFFSPKVGIRPFLVSI 2232
QY 4749 VSLAILIGYHLKV-PLAIFKREKETARKLEFDGLYIARQPEDDLKSHWDLVISAJSF 4807
Db 2233 MLRSI-----YTIGLPTLLGNAULCNKIVF-----LV---SP 2264
QY 4808 PNYWYDKFKVKVRAKYSTYFDSISNMLGMEKTSFSAQEBEGSKGLIHYIINIDWRYQ 4867
Db 2265 VGN-----RGFTFRGY-----2275
QY 4868 VMKAGVTITDNGSLYSLWFSVSMGNF--NNFFFAHLDDVAGFKTLRTILQSVTHNGK 4926
Db 2276 ----RAVILDMAFYHVAVYLVCMGLGFVHEFFYFSLFLDLVYREBTLNVIKSVTRNGR 2331
QY 4927 QLVLTVMLLTIIVYIVTIAFNFFKRYVVOED-----4959
Db 2332 SIILTAVLAILLVLESIGLFLKDDFTMEVDRLKNRTPVTGSHQVPTMTLITMWEACA 2391
QY 4960 -----DEVNRNCHMLTCTFVFNLYKGVAGGGIGDELPPPDGDS- 4999
Db 2392 KENCSPITASNTADEYEDGIERTCDTLMLCIVTVLNOGLRNGGVDGLVRPSKDEPL 2451
QY 5000 EVYRIIFDSFFFIIVAILLOGLIIDAPELRDQLESVEDMESNCFIGINKDYPD 5059
Db 2452 FAARVYVYDLFFVIVIIIVNLNIFGVIIIDTFADLRSEKQKKEILKTKTCICGLERKDP 2511
QY 5060 KVPHGFDTHVOREHNLANYMFFLHMLINKPDTYTGQETVYVMVYTORCWDFFP 5113
Db 2512 NKTVSFEHIKSEHNWHYLYFVLVKVDPTGYTGPESYVAQMIVKRLNDFP 2565
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## RESULT 4

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US-11-090-997-870
; Sequence 870, Application US/11090997
; Publication No. US20060216722A1
; GENERAL INFORMATION:
; APPLICANT: Betscholtz, Christer et. al.
; TITLE OF INVENTION: Glomerular Expression Profiling
; FILE REFERENCE: 04-1059
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; CURRENT APPLICATION NUMBER: US/11/090,997
; CURRENT FILING DATE: 2005-03-25
; NUMBER OF SEQ ID NOS: 2985
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 870
; LENGTH: 3913
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-090-997-870
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Query Match 1.1%; Score 304.5; DB 7; Length 3913;
Best Local Similarity 18.0%; Pred. No. 6.6e-09;
Matches 594; Conservative 446; Mismatches 1161; Indels 1101; Gaps 138;

QY 1800 AAHALCTHVDQKQL--LYAIQSQYM-----SQPL---RQGFYDLLIALHL 1839
Db 48 AHHDL--NIDSQCNEMVINSQSVESIVIPESITMRLTHSGEITSHQGF-----SVEL 100
QY 1840 ESH-ATTWEACNE-----FVIPLGPELKALYEBP---DMGHSLSRLQTESVRPOMKMTD 1890
Db 101 ESEISTTADDCSSEVNGCSFVMTGKPTNLLREBEFGVDDSYSEQAQDSPTHEMMESE 160
QY 1891 IASITEISNLYSPYFPLEVA-----REF-----VMOALAEAVE 1924
Db 161 LAGQHEIEELNRELEEMRVTYGTGLQLOQEFEEAAIKORDGIITQLPANLQOARREKDE 220
QY 1925 T-----NOVHNRDPVGGSNENLFLPLIKLVDRLLLVGMWRDDEVKL 1966
Db 221 TWREPLEUTEOSQKLIQFOQLQASETLRNTHSTASTADILLOAKQOILTHQOOLEEQHL 280
QY 1967 L-----IMTNPETWDPSPDKGDEHRKGL-----LHMMAEAGAK 2001
Db 281 LEDYKKKEDFTMQISFLQEKIKVYEMEQDKKVENSKKEEIQEKETIIEELNTKIIEBK 340
QY 2002 LQMCYLLOHLNDIQLRHVEAIIAPAFDVGDLQDQLRRYTEIKQSDLPSPAIAKKTRE 2061
Db 341 -----KTELKDK-----LTADKLGLGEQEIYQKQKQETKNMKLELTNSKQERQ 386
QY 2062 FRCPREOMNAILSF-----KHLREEDKENCPCGBELIARWNEFDHDLMA 2106
Db 387 SSEEIKQMGIVBELQKKNHKDSQFETDIVORMEQETORKL---EQLRAELDEMYGQIV 443
QY 2107 HVSLHALQEPDAAENQEPKAPGAFGLYNI-----2138
Db 444 QMKQELIQRHMA---QMEEMKTRHKGEMENALRSYSNITVNEQDIKMMVAINELNIKLO 500
QY 2139 --NTVKE--LEBEAKAIEPPPKTPEEKPRKVLQTI-----VNWAEISOIETPKLVREM 2189
Db 501 DTNSQKELKEELGLILE--EKALQQLQEDLVEELSFSREQIQRARQTIAEQESKINEA 558
QY 2190 FSLIVROYDAVGEILIRALE-----KTYVINAKTKLDVAEMVMVGLSOTRALLPVQMS 2240
Db 559 HKSJSTVEDLKAIEIVSASESKKELEKHAEVNTYKIKLEWLE-----KEKNVLDNRMAE 613
QY 2241 QEEBELMKRLWKLVNNHTFFQHPDLIRVLR-----VHENYMAVMNTLGRRAQASDA- 2294
Db 614 SQEAELERL-----TQLLSHEEELSKLEDIEHRINIEKLDNGLHIYKQIDGL 667
QY 2295 -OPSGPVAEDSKEDTSHEMVAVACCRFLCYFCRTGRONQKAMPDHPFLLENSILSR 2353
Db 668 QNEMSQIETMQFBKDN-----LITKQKQ-----LILEISKLDIQ 703
QY 2354 PSL--RGSTPLDVAYSSIMMENTELALAREHYLEKIAVYLSRCGLQSNSELVEKGYPDLG 2411
Db 704 QSLVNSKSEEMTLQINELQKEIEI---LRQBEKKEGTLEQVEQLQLKTELEKQMKKE 760
QY 2412 WD-----PVEGERYDLFRFCVWVNGESVEENANL 2441
Db 761 NDLQKPAQLAEANSILKDEKKTLEDMLKIHTFVPSQEBRLIFLDSIKSKSDSVWEKE-- 818
QY 2442 VIRLLIRPECLGPALRGEGELLKAIIVDANKMSERIAADRKLKREMEQGVDFHSHPLPE 2501
Db 819 -IEILIE-----ENEDLKQCCIQLNEEIEK--ORNTFSFAKNFEVNY----- 858
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Db 2502 LELTCYQKIQD--MOEQQFETEMLOKKIVNLOKIVBEKVAALVSQI-----QL 2550
Qy 4475 LVVRYIFGVLLGLMRGPOTDEPPPEEKEKIGOLRRHLLATOSSRHLPALPADDTGQ 4534
Db 2551 EAVOEY-----AKFCQDNQTISSPERTNIQNLNQLR-----DELGS 2588
Qy 4535 MQVSAGLIDITKEDNGQIQVKPHSPSTSPSSGEEAEVSPDESADHTEQRPSPSLIDL 4594
Db 2589 -DISALTRLISELESQVEM-----HTSLILEKEQVIAEKNVLE--KEKKLLEQLKL 2639
Qy 4595 GGEQAKQOQERMEAAQAQAAMSIAEASKAVOG-----PAPSALSQVLSQVTR 4646
Db 2640 EGNEKKQREKQKRSQPDVEVLKTTTLELFSHNEESGFNEALRAESVATKAELASYKE 2699
Qy 4647 RA 4648
Db 2700 KA 2701

RESULT 5
US-11-090-997-876
; Sequence 876, Application US/11090997
; Publication No. US20060216722A1
; GENERAL INFORMATION:
; APPLICANT: Betscholtz, Christer et. al.
; TITLE OF INVENTION: Glomerular Expression Profiling
; FILE REFERENCE: 04-1059
; CURRENT APPLICATION NUMBER: US/11/090,997
; CURRENT FILING DATE: 2005-03-25
; NUMBER OF SEQ ID NOS: 2985
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 876
; LENGTH: 3842
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-090-997-876

Query Match 1.1%; Score 301.5; DB 7; Length 3842;
Best Local Similarity 17.9%; Pred. No. 9.8e-09;
Matches 592; Conservative 458; Mismatches 1161; Indels 1089; Gaps 140;

Qy 1800 AAHALCTHVDQKQL--LYAIOSQYM-----SGPL---RQGFVLLIALHL 1839
Db 48 AHHDU--NIDQSQCNEMYNINSQVSVIPESTIMRHLHSGEITSHEQGF-----SVEL 100
Qy 1840 ESH-ATTMEACKNE-----FVPLGPELKALYEEP---DMGHSLSLQTESVRPQMKWTD 1890
Db 101 ESEISTTADDCSSEVNGCSFVMRTGKPTNLLREBEFGVDDSYEQQAQDSPTHEMSE 160
Qy 1891 IASITEISNLSYPFPLEVA-----REF-----VMOALAEAVE 1924
Db 161 LAGQHEIEBELNRELEEMRVYGTGEOLOQEFEEAIAIKORDGIITOLTANLQQAAREKDE 220
Qy 1925 T-----NOVHNRDPVGGSNENLFLPLIKLVDRLLLVGMWRDDEVEKL 1966
Db 221 TWREBLELETSQSKLOIQFOQLOQASETLNTHSTSTADLLQAKQOILTHQOOLEEQDHL 280
Qy 1967 L-----IMTNPETWDPSPDEKGEHRKGL-----LHMKAEGAK 2001
Db 281 LEDYQKKEDFTMQISFLQEKIKVYEMEQDKKVENSNKEEIQEKETIIEELNTKIIEBK 340
Qy 2002 LQMCYLLQHLNDIQLHRVVEALIAFAHDFVGLQTDQLRRYTEIKQSDLPNSAAKKTRE 2061
Db 341 -----KTELEKDK--LTTADKLLGELQEQVQKQNEIKMKLELNTNSKQERQ 386
Qy 2062 FRCPPEQNNALISF-----KHLEEDKENCCPGELIARMNEFHDTLMA 2106
Db 387 SSEEIKQLMGTVEELOKRNHKSQFETDIVQRMEOETQKLV---EQLRAELDEMYGQOIV 443
Qy 2107 HVSLHALQEPDAENQEPKAPGAFGLNII----- 2138
Db 444 QMKQELIRQHMA--QMEEMKTRHKGEMENALRSYNTIVNEDQIKLMMVAINELNIKLO 500

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Qy 2139 --NTVKE--LEEAKAIEBPCKTPEKFRKVLQTI-----VNABESQIETPKLVREM 2189
Db 501 DTNSQREKLEELGLILE--EKALORQLEDLVEELSFSEQIQORARQTTAEQESKLENEA 558
Qy 2190 FSLIVROYDAVGEILRALE-----KTYVINAKTKLDVAEMWVGLSQRALLPVOMS 2240
Db 559 HKSLSLTVEDLKAEIVSASESRKSELELKEAEVNTYKIKLEMLE-----KKNQAVLDRMAE 613
Qy 2241 QEEBELMRKELMWLVNNHTFQHPDLIRVLR-----VHENVMAVMNMTLGRRAQAQSDA- 2294
Db 614 SQAELELR-----TQLLFSHEEELSKLEDLEIEHRINIEKLDNLGHYKQIDGL 667
Qy 2295 -QPSQVABDSKESKOTSHEMVACCRFLCYFCRTGQONQKAMPDHPDFLENNIILSR 2353
Db 668 QNEMSQIETMQPEKDN-----LITKQNO-----LILEISKLDLQ 703
Qy 2354 PSL--RGSTPLDVAYSSIMMENTELALAREHYLEKIAVILSRCLQSNSLSEVKGYPDLG 2411
Db 704 QSLVNSKSEBMTLQINELQKEIEI--LRQBEKEKGTLEQVQELQKLELLEKQMEKE 760
Qy 2412 WD-----PVEGERYLDLFLRFVVMNGESVEENANL 2441
Db 761 NDLOEKAQLEAENSILKDEKKTLEDMLKHTPVSQEEERLIFLDSIKSKDSVWEKE-- 818
Qy 2442 VIRLLIRPECLGALRGEGLLKAIVDANKMSERADRKRKUREMOEGDVNFHPLPE 2501
Db 819 -IEILIE-----ENEDLKQOCIQLENEIEK--QRNTFSFAEKNFVNY----- 858
Qy 2502 SDEDEDYIDGAAILNFYCTIVLLGRCAPDAGVIALGKN--ESLRARAILSLRVLPLEDQ 2560
Db 859 QELOEEY-----ACLLKVKDDLED-----SKNQELEYSKKLKALNEELHLQ 900
Qy 2561 GVLSLRLFTLNNPAAAGEERPKSDMPGSLIPGHKQVGLFLE--RVYGIETQELFKYKLEEA 2618
Db 901 RI-----NPTTVK-----MKSSVDEDKTFAETLENGEVVEKDTTELMEK--LEVT 945
Qy 2619 FLPLDRAATMLDRNDGCESDMALSMNR-----YIGNSI-----LPLLI 2656
Db 946 KREKLELSQRL-----SDLSEQLKQKHGIBISPLNEEVSKLQBEQVSLRCRELEIII 998
Qy 2657 KHAYFYNEAEN-----YASLLDRTL-----HTVYRLSKN-----R 2686
Db 999 NH-----NRAENVQSCDTQVSSLLDGVVTMTSRGAGSVSKYKNSFGESKIMVEDKVSFE 1054
Qy 2687 MLTKG-----QREAVSDFLVALTS-----AMOPSMLLKLLRKLTVDSKLSBYTTVALRL 2737
Db 1055 NMTVGEESKQQLLIDLHLPSVTKESSLRATQPSSENDKLOKELNVLKSEOND-----LRQ 1109
Qy 2738 TLHYERCAKYVGSTGAGQAFGASDBEKRITMMLFSNIFDSLSKMDYEPBLFGKALPCL 2797
Db 1110 MEAQRICLSLVYSTHVDQVREYMEKDKALCSLKEELIIPAEEKIK----- 1156
Qy 2798 IAGCALPPDYSLSKNVDDDEFYG--KEQAAGDLDPQDPDPQINTSSVALNND-----LNTI 2852
Db 1157 -----ELQKIHOLEQTMKTQBTGDEGKPLH--LLIGKLQKAVSECSYFLQTL 1203
Qy 2853 VQKSEHYHDWA-----SRKTENGWVYGEHSDSQKTHPRKLPYNMNDYKERYKE--- 2905
Db 1204 CSVLGEYTPPAKCEVNAEDKENSQDY-----ISENEDPELODYR-----YEVQDFQENWH 1254
Qy 2906 ---PVRESLKALLAI-----GWSVHSEVDIPSNRSMRROKSGGRPPE 2948
Db 1255 TLLNKVTEYNKLLVLQTLRLSKINGQQQTDGKMLSFGEENLPKEETEPLSIHQ----- 1307
Qy 2949 IVTDSATPFDYNPHVDMTNLTLSREMOMAEALADNAHDIAWAKKKEELVNGGGIHPQ 3008
Db 1308 -----MTNL-----EDIDVNHKSK----- 1321
Qy 3009 LVPVDLLTDKEXKDRERSQEFKLYQYQGYKLRHPSKAPQSDTEQTTGTGVAIELRFPAYS 3068
Db 1322 ---LSSQDLKLEKTLQEQVQBE-----LSSLSSLOQLKETEQNYEAIEH----- 1363

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Qy 3069 LLEKLIQYIDRATINMKLKPSTTFSRRSPKTS-----TRDIKFSKAVLPLME 3118  
Db 1364 CLQRKQAVSESTVPPSLPVDVSVITSDAORTWPGSCVKKNIDGTIEFSGE----- 1416  
Qy 3119 KYFSTHRNYFATATANNVGAASLKEKEMVAALFCKLASLLRSALAAFGPDVRIITVRCL 3178  
Db 1417 -----PGVKEETNIV---KLEKQVQEQLEEEVAKVIVSMSIAFAQQTTEL----- 1458  
Qy 3179 QVLVKGIDAKSLVKNCPEFIRTSMLTFFNNVADVGHITIMNLDQKVAHLRGTHLKTSTS 3238  
Db 1459 -----SRISGGKE-----NTASSKQAH----- 1475  
Qy 3239 LGYINGVLLPILTAKFPHLANCE-----YGADLLDEIQVASYKMLGSLYALGTIDTASLTHD 3294  
Db 1476 -----AVCQEQHYFNMKLSODOI-----GFQTFETVD 1504  
Qy 3295 RYKLKTEIERHKPALGSCGAFSTFPVAFLEPHLNKHNOFSLINRIADHSL-BAQDIMQ 3353  
Db 1505 VKFK-----BEFKP-----LSKELGEGKEILLNSDPDHPIDESKD--- 1540  
Qy 3354 KMEQCMPTLETILGEVQFVESDKTYNEAPHIIDVLPILCSYLPFWAOGPDNVTPTGG 3413  
Db 1541 -----CVLTIS-----BEMFSKDKTIFVRSIHDEI-----SVSSMDA 1573  
Qy 3414 NHVTMTVAEHNQOLLKNVLKLIKIGNENAPWTRITATYTOQIIINSSEBELLRDSFLPL 3473  
Db 1574 SRQLMLNEEQLEDNRQ---ELVROYEQHQATELLRQAHMRQERQEDQEQLEIKRL 1630  
Qy 3474 AERVKRT---DNMFKEE-----SLRGFIK-----SST-----DDTS 3503  
Db 1631 NRQJQAQSSDNEMLVSEERVLLEALKQLSLAGREKLCCELRNSSTQTQNGENOG 1690  
Qy 3504 QVESIQEDMQL-----LVRDIYS-----FYPLLIKVDLQRNHLRNVP 3545  
Db 1691 EVEBQTFKEKELDRKPEDVPPEILSNERYALQKANNRLKILLEW-----KTTAAV 1742  
Qy 3546 ABELYNHVAEFTNWSQYFLKEEQNFISANEIDNVLNPTATRVATVD-GTQGG 3604  
Db 1743 BETIGRHLGILDRSSQ---SSASLIWRSEAE---ASVSKCVHEBTRVDESIPSYS 1796  
Qy 3605 GKKKKHKRDKKDKQVQASLWACLKRLPVCLNLPAGRE-----QEL-----VQH 3652  
Db 1797 GSDMPRDINMWSKVTEGTELS-----QRLVRSG---FAGTEIDPENEELMLNISRLOA 1849  
Qy 3653 CKDRFLKMSQ-----DVAEFAKTQL---TLDPKIDPADEMSWOHYLYSLGSKSKSNIT 3705  
Db 1850 AVEKLEAISTSSQLEHAKVTQTELMRESPROQEATESLKQCEULRERLHEESRAREQ 1909  
Qy 3706 VETAENKAK-IIDTVERIVMSKVLFGMLMIDHPQOMKKNVRSVVSIOBKRAVIACFR 3764  
Db 1910 LAVELSKAEGVIDG---YADEKTLFER-----QIOEKTDIIDRLE 1946  
Qy 3765 QTSLSLSPRHACNIPARTYVELMLEENIGOEVM-----EDLTSQFE 3808  
Db 1947 QELLACNR-----LQLEAEQOQOEERELLRSQKEAMKABAGPVEQQLLOETE 1996  
Qy 3809 DAELKSDVVEEGKPPDLTQLVTTFCRGAMTERSALQEDPLYSVAHIIAKSCGEBEE 3868  
Db 1997 KLMKELEVOQAEK-----VRDDLQKQVKALEID----- 2026  
Qy 3869 EGGEBEGGGEAEABEGRASI-----HEQSEMKQ-----KLLFHOA---RLADRGVAEM 3916  
Db 2027 -----VEEQVSRFIELEQEKNTLMDLRQONQALEKLEKRFLEQAIIDREHERDVFQ 2082  
Qy 3917 VLLHISASKGLPSMWKTKLQGISILRGGNIDIQMGMLNHLKDKDVGFTTSIAGLMNS 3976  
Db 2083 EIQKL-----EQQLKVPFRFOPISEHQTRVEQ-LANHLKEKTD-----KCSLELLS 2128  
Qy 3977 CSVLDDAFERNKTAEGVLGLEGAGGKKNHDAE-----FTCALFRFIQLTCEGHNLDWQ 4032  
Db 2129 KEQLORDIQERNEEIKL-----EFRVRELEQALLVSADTFQKVE-----DRK 2171  
Qy 4033 NYLRQTAGNTTNNVICTVDYLLRLQESIMDFVWHYSSKELIDPAGKANFFKAGVASQ 4092

Db 2172 HFCAVEAKPELSLEV-----QLOAERDAID-----RKEKITNLEEQLEQFR-----EE 2215  
Qy 4093 VFNLTLEVTIQGPCTQNOQALAHSLRWDAVGFLFLFSHMQDKLSKHSQV---DLLKELL 4149  
Db 2216 LENKNEEQVQ-----LHMQLBTQKKESTTRLOEBOENK 2249  
Qy 4150 NLOKDMIPMMLSMLEGNVNVGTIGKQWDTLVESASNNVELILKYFDMFLKLKDLTSSASF 4209  
Db 2250 LFKDDMEKLGIAIKESDAM-----STQDQHVLFKGAQIOEKEV----- 2289  
Qy 4210 QETDANNDGWLPKDFKMEQOKSYTPB-----BIEFLLA---COETN 4250  
Db 2290 -EIDQLEQ-----VTKLQQLKITTDNKVIEEKNEILRDLETQIECLMSQOEVCYRN 2341  
Qy 4251 HDGKLDYIG-FCDRFHEPAKEIGFNLAULLTNLSEH-----MNPENRIARPLET 4298  
Db 2342 REBEEIQLENEVIEKLQOELANIGQKTSMAHSLSEADSLKHQLDVVVIAEKLALEQOVET 2401  
Qy 4299 AGSVLNYFPFLGRIGIMGSKRIERYFEIKESNIEQWKEKPO-IKESKBAFFYSIVTEG 4357  
Db 2402 ANEEMTFMKNVLKETNFK--MNQLTQELFSLKRER-ESVEKIQSIPENS-----VNVVAIDH 2454  
Qy 4358 GDKKLEAFVNFCEDAIFEMTHASGLMAASEESVGGTQKREASYMTMGDDDDERAGKD-P 4416  
Db 2455 LSKDKELEVLVLTEDALKSLENTQYFKSFEENGKGSIIINLETLQLQ---ESTVSAKDL 2511  
Qy 4417 FRGLQSVKDGATAFSSLSPSNIKAKIADMQQMPAEALAVGFFKMFYLYLYGYGVLV 4476  
Db 2512 LTQCYKQIKD--MQEQGFETEMLKQKIVNLOKIVEEKVAAALVSQI-----OLEA 2560  
Qy 4477 VRYIFGVLLGLMRGPOTDEPPPEETEEKIGOLRHLRLATQSSRHLPALPPADDTGQM 4536  
Db 2561 VQBY-----AKFQDQNTISSPERTNIQNLNLE-----DELGS-D 2597  
Qy 4537 VSAFGLDITKEDNGQIQVQKPHSPSTSPSSGAEVSPDESADHTEEQRPSPSLDILGG 4596  
Db 2598 ISALTURISELESQVEM-----HTSLILEKEQVIAEKNVLE--KEKKLELQKLEGG 2649  
Qy 4597 EQAKQOQERMEAAQAQAAMSIAEASKKAVOG-----PAPSALSOVDLSQYTRRA 4648  
Db 2650 NEKKQREKEKRSQPDVEVLKTTTFLFHSNEESGFFNEALRAESVATRAELASYKEKA 2709

## RESULT 6

US-11-090-997-872  
; Sequence 872, Application US/11090997  
; Publication No. US20060216722A1  
; GENERAL INFORMATION:  
; APPLICANT: Betscholtz, Christer et. al.  
; TITLE OF INVENTION: Glomerular Expression Profiling  
; FILE REFERENCE: 04-1059  
; CURRENT APPLICATION NUMBER: US/11/090,997  
; CURRENT FILING DATE: 2005-03-25  
; NUMBER OF SEQ ID NOS: 2985  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 872  
; LENGTH: 3896  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-090-997-872

Query Match 1.1%; Score 301.5; DB 7; Length 3896;  
Best Local Similarity 17.9%; Pred. No. 1e-08;  
Matches 592; Conservative 458; Mismatches 1161; Indels 1089; Gaps 140;

Qy 1800 AAHALCTHYDOKL--LYALQSQYM-----SGPL---RQCFYDLIIAHL 1839  
Db 48 AHDDL--NIDQSCNEMYINSORVESTVPIESTIMTLHSGETSHSEQGF-----SVEL 100  
Qy 1840 ESH-ATTMEACKNE-----FVPIPLGPPELKALYEEP---DMGHSLSRLSQTSEVFPQMOWTD 1890  
Db 101 ESIISTADDCSESVNGCSFVMTKPTNLLREEEFGVDDSYSEQGAQDSPTTHLEMMESE 160





Db	1910	LAVLSKAEGVIGD- : : : : : : : : YADEKTLPER-----QIOEKTDIDRLR	1946
Qy	3765	QTSLSHPRIHRACNIFARTYYELWLBENICQEWI- : : : : : : : : -----EDLTQSFE	3808
Db	1947	QELLCASNR-----LQELAEAQOIQEERELLRSRKEAMKAEAGPVEQQLQETE	1996
Qy	3809	DAELUKSDVVEGBKPDPLQLVTTTCRGAMTERS GALQEDPLMYSAHIIAKSCGBEEE	3868
Db	1997	KLMEKELEVOCQAEK- : : : : : : : : -----VRDLOKQVKALEID-----	2026
Qy	3869	EGGSEEBEGGEAEAEDEGRASI-----HEQEMEQ-----KLILFHOA-----RLADRGVAEM	3916
Db	2027	-----VEQVSRFIELEGBKNTLMDLRQOQALEKQLEKRWKFLDEQAI DREHERDVFOQ	2082
Qy	3917	VLLHISASKGLPSEVMVWKTQLQGISILRGGNIDIOMGMJNLHKDKDVDPFTTSIAGLMNS	3976
Db	2083	EIQKL-----EQQLKWPFRQPISEHQTRVEQV-LANHLKEKTD-----KCSSELLS	2128
Qy	3977	CSVLDDLAFBRTNKAEGLVGLEGCAAGKNHDAE-----FTCALFRFIQLTCEGHNDWQ	4032
Db	2129	KEQLOQDIQENKEIEKL-----EFVRLEUQALLVSATFOKVE-----DRK	2171
Qy	4033	NYLRTQAGNTTTVMNVICTVDYLLRQESIMDFYHYSKSELIDPAGKANFFKAIGVASQ	4092
Db	2172	HFGAVEAKPELSLEV-----QLQAEARDAID-----RKEKEITNLBEQLQEFR-----EE	2215
Qy	4093	VFNTLTEVIQGPCTQNOQALAHSLRWDAVGGFLFSSHMQDKLSKHSQV-----DLLKELL	4149
Db	2216	LENKNEEVQO-----VTKLQQQLKITTDNKNVIBEKNELIRDLEQTOICLMSDQECVKRN	2249
Qy	4150	NLOKDMIPMLSMLEGNVNGTIGCKQMVDTLVESASNVELILKYDFMFLKKLKOLTSASF	4209
Db	2250	LFKDDMEKLGIAIKESDAM-----STQOQHVLFQKFAQIOIEKEV-----	2289
Qy	4210	QEIDANNDGWVLPKDFKEKMEQKSQTYPE-----ETEFLLA-----CCETN	4250
Db	2290	-EIDQLNEQ-----VTKLQQQLKITTDNKNVIBEKNELIRDLEQTOICLMSDQECVKRN	2341
Qy	4251	HDGKLDYIG-FCDRFHEPAKEIGFNLAVLLTNISEH-----MPNEPRLARFLET	4298
Db	2342	REEIEQNEVIEKQLOQLANIGOKTSMNAHLSSEADSLKHQJVDVVIABKLALEQQOQVET	2401
Qy	4299	AGSVLNTFEPPLGRIEIMGSKRIERYVYFIKESNIEQWEKQP-IKESKRAFFYSIVTEG	4357
Db	2402	ANEEMTFMKNVLYKETNFK--MNQLTOELFSLKRER-ESVEKIOSIPENS-----VNVAIDH	2454
Qy	4358	GDKEKLEAFYNFCEDALFEMTHASGLMAAEEESVGGTKNBEASWYMGDDDDDERAGKD-P	4416
Db	2455	LSKQDPELVVLTEDALKUSENQTYFKSPENGKGSIIINLETRLUQJ-----ESTVSAKOLE	2511
Qy	4417	FRRLQSVKQGVATAFSSLSPSNTKAKIADMQMPAEALAVGFFKMFYYFLVYLGYGVLV	4476
Db	2512	LTQCYKQIKD--MQEQOFETEMLOKKIVNLQKIVEEKVAALVSQI-----QLEA	2560
Qy	4477	VVRVIFGVLLGMKGPOTPDEPPPTBEEKIGQLRHLLLATQSSRHLPALPPADDTCMQQ	4536
Db	2561	VQEY-----AKFCODNOTISSEPRTNIQNLQRE-----DELGS-D	2597
Qy	4537	VSAFGLDITKEDNGIOVKPHESPSTSTPSSGBEAESVPDESADHTEORPPSLDILGG	4596
Db	2598	ISAUTLRISELSESVQVEM-----HTSLILEKEQVEIAEKNVLB--KEKKLELLOKLEGG	2649
Qy	4597	EQAKQOAKQERMAEQAAQQAAMSAIEAESKKAVOG-----PAPSALSQVDSLQSYTRRA	4648
Db	2650	NEKKOREKEKKRSPODYVELVKTITTELFHNSNEESGFFNEALRAEASVATKAELASYPEKA	2709

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; APPLICANT: Betsholtz, Christer et. al.
; TITLE OF INVENTION: Glomerular Expression Profiling
; FILE REFERENCE: 04-1059
; CURRENT APPLICATION NUMBER: US/11/090,997
; CURRENT FILING DATE: 2005-03-25
; NUMBER OF SEQ ID NOS: 2985
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 868
; LENGTH: 3907
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-090-997-868

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Db 2458 LSKDKPELVVLTEDALKSLNQTYFKSPFENGKSGSIINLETRLQLL---ESTVSAXDLE 2514
Qy 4417 FRRLQSVKGVATAFSLSPSNITAKIADMQMPAPLAVFFKMPFYLYLYGYGLV 4476
Db 2515 LTQCVKQIKD--MQEQGFETEMLQKIVNLQKIVEEKVAAALVSI-----QLEA 2563
Qy 4477 VVRIFGVLGLMRGPQTDPEPPPTBEKIGQLRHLLATQSSRHLPALPPADDTQM 4536
Db 2564 VQEQ-----AKFQDNQNTISSEPTNIQNLQRE-----DELGS-D 2600
Qy 4537 VSAFGLDTKEDNGIOVKPHESPSTSPSSGEBAEVSPDSADHTBEORPPSLIDLGG 4596
Db 2601 ISALTIRISELSQVEM-----HTSLLEKEQVEIAEKVLE--KEKKLLELOKLEG 2652
Qy 4597 EQAKQOQERMEAAQAQAQAASIAEASKKAVOG-----PAPSAQSVDLSQYTRR 4648
Db 2653 NEKQREKEKRSQDVEVLTKTTTTLFHSNEESGFFNELEALRAESVATRAELASYKEKA 2712

RESULT 8
US-10-505-928-325
; Sequence 325, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 325
; LENGTH: 3113
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-505-928-325

Query Match 1.1%, Score 283; DB 6; Length 3113;
Best Local Similarity 18.0%; Pred. No. 9,5e-08;
Matches 636; Conservative 474; Mismatches 1205; Indels 1220; Gaps 148;

Qy 1762 BEDRCIDLEPIEMDKLLSFHSHTLTLYAALCYOSNVRAAHALCTHVDQKOLLYAIO 1821
Db 68 ENQRLMEICESLEKTK-----QKISHEL--QVKESQV-----NF 99

Qy 1822 MSGPLRQGFYDLLTALHLESHATTMEACKNE-----FVIPL 1857
Db 100 QEGQLNSG-----KKQIEKLEQLCKRCKSELERSQQAQASADVSLNCPNTPQKIF 153

Qy 1858 GP-----ELKALY-----BEPDMGHSLRSIQTESVR---PQMKWT--DIA--ESI 1895
Db 154 TPSQYYSKSYEDLEKYNKEVEERKLEAEVKALQAKKASQTLPOATMNRHDIARHQAS 213

Qy 1896 TEI-----SNLYSPYFPLEVAREFVM-----QALABAVETQVHNHRDPVGGSGNEN 1940
Db 214 SSVFSWQOEKTPSHLSSNSQRTPIRRDPSSAFSGEQEVTPSRSTLQIGKRDANSFPDN 273

Qy 1941 LFLPLIKLVDRLLLVGMWRDEVEKLLIMTNPETWDFSPDKEGKDEHRKGLLHMKMAEGA 2000
Db 274 SSSP--HLLDQL----- 283

Qy 2001 KLQCYLLQHLNDIQLR---HRVEAIIAFAHDFVGDLTQDRLRYTEIKQSDLPSSA 2057
Db 284 KAQQLRANKINELELRLOQHEKE-----MKGVNKFQEL--QLQLEKAKV-- 327

Qy 2058 KTRFRCPPREQMNAILSFKHEEDKENCPCGBELIARMNEFHTLMAHVSLLHALQEPD 2117
Db 328 -----ELIEKEVLNCRBELVTRTTAQYDQASTKYTAL----- 360

Qy 2118 AAEVQEPKAPGAKGLNIINTVKELEEEAKAIEEPPKTPPEEKFKVL----- 2167
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Db 361 -----BQKLK-----KLTEDLSQQRQVABARSARCSLEQIKIKEKEFEQELSROORSQ 410
Qy 2168 -----IQIIVNABESQIETPKLVREMPFLLVROYDAVGELIRALEKTYIVINAKTKL 2223
Db 411 DQECIQMKARLTQELQ-----QAKNMHNVLQAECLKLTSVKQQLENN--LEEFQKLCRAE 464
Qy 2224 MWVGLSQIRALLPVQMSQBEELMRK--RLWKLVNNHTFFQHPDLIRVLRVHENVMAVMN 2282
Db 465 QAFQASQIK-----ENELRRSMEEMKKN-----LLKSHSEQAKREVC 503
Qy 2283 TLGRRQAQSDAQSPSSQPVAEKDSKEKDTSHSMVAVACCRFLCYFCRTGRQONKAMFDF 2342
Db 504 HLEAELKNIKQCLNQSNQNFQAEEMKAKNTSQETML-----RDLQEKINQO--- 547
Qy 2343 LLENSNILLRPSLRGSLTDLVDVAYSSLMENTEIA---LALREHYLEKIAIYVLSRCGL 2399
Db 548 --ENSLTTL-----EKLKLAVALDEKQDCSQDILLKKREHHIEQLNDKLSKTEKESK 596
Qy 2400 S-----ELVEKGYPDLGWDPEGEVYLDLFLFCVW-----VNGESVEENA----- 2439
Db 597 ALLSALLEKKKEY-----ELKEEKL-----FSCWKSNEKLLTOMESEKENLOS 646
Qy 2440 -----NLVIRLLIRPECLGPALRGEGEGLLKAIVDANKMGERIADRRKLR 2485
Db 647 ETCLKTQOIKSHEVNERVRTLEMDRENLSVEIRN-----LHNVLDSKSVE---VET 698
Qy 2486 EMQOEGVNPFS-----HPL-----PESDEDEDYIDTGA 2514
Db 699 YMBLQQAEPFSDQKHQKIEIENMCLKTSQLTQGVEDLEHKLQLLSNEIMDKRCYQDL 758
Qy 2515 ILNPFYCTLVDLLGRCAPDAGVIA----- 2537
Db 759 -----YESLRDLK--SKDASLVNEDHQRSLAFDQOPAMHHSFANIGGSGNP 812
Qy 2538 --LGKNESLRARAILRSLVPLEDQGLVLSURFTLNNPAAAGEERPKSPMPSGLIPGHK 2595
Db 813 CRLEAQSPKNSAILQNRVD-----SLEFSLES-----QKQNSDL-----QK 853
Qy 2596 GLF-----LERYGIEQIQLFYKLEBEAFPLDLRAATMLDR----- 2631
Db 854 ELVQIKGEIEENLMKAEQMHQSFAETSRQISKLEQDTSAHQNVVAETLSALENKEKEL 913
Qy 2632 --NDGCSDMALSMNRYIGNSILPLLIKHAIFYNEAENYASLLDATHVTVRVLSKNRMLT 2689
Db 914 LLMKDVETEQAETQELKKSNNHLEDSLKELOLSET---LSLEKKENSSIIISLNKR 970
Qy 2690 KQREAVSDFLVALTSAMQPSMLLK-----LRLKLTVDVSKLS--EYTTVALRLLTHYE 2742
Db 971 LTQENGTLKEINASLNQEKNNLIQKSPSPANYIDEREKSISELSDQYKQEKLIILL--- 1026
Qy 2743 RCAYKYGSTGAGQAFGASSDBEKRLTMMLPSNIFDSL-----SKMDYEPFLFGKA-L 2796
Db 1027 RCBEETGNAYEDLSQYKAAQKNSKLECLL--NECTSLCENRKNELQLEAFKAEHQEF 1084
Qy 2797 LIAIGCALPPDYSL-----SKNYDDDFYKQEAAGDLDNPDYDPPQIPQINTSSVA 2844
Db 1085 LTKLAFABERNQNLMLLETTVQOALRSEMTDNQNSKSEAG--LQKEIMTLKEEQNK 1140
Qy 2845 LNNDLNTIVQK-----FSEHYHDAMASRKIENGWYVGEWGSQSKTHP 2887
Db 1141 MQKEVNDLLQENELQMKVMKTKHECQNLSEPIRNSVKERESERNQCNFKPQMDLVEKEI 1200
Qy 2888 RLKPYN-----MLND-----YEKERYKEPVRESLKALLAIGWSVEHSEVDIPSN 2934
Db 1201 SLDSYNAQLVQLEAMLRNKLKLOESEKECECLOHELQITRG-----DLETSNLQ 1250
Qy 2935 SMRRQSGSGRPPPIVTDSATPDYPNPHVDMTNLTLISREMNMAERLADNAHDIWAKKK 2994
Db 1251 DMOSEQISGLKDCBI--DAEEKYISGPHLESTS-----QNDNAH----- 1287
Qy 2995 KEELVTNGGGTHPOLVPVYDILLTDKEKKDRERSQEFLLKYQYQYKYLHRPSKAPQSD 3054
Db 1288 -----LQCSLQTTMKNLELEKICEI---LQAEKYELVTELNDRSRSECIT 1329
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; SEQ ID NO 10
; LENGTH: 3811
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-090-997-10

Query Match      0.9%; Score 253.5; DB 7; Length 3811;
Best Local Similarity 17.0%; Pred. No. 9.6e-06;
Matches 660; Conservative 560; Mismatches 1411; Indels 1245; Gaps 157;

1249 QPIFENTDEMDTRIDVT-----RIPAGSDTPPCLKISHTTETMEKANWPELRSLP 1301
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
542 QTIAEQENRLESEARSKSLSTVEDLKAEIVAASESKELELXHEAETNYKIKLEMLEKE-- 599
Qy      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1302 VICNEFID-----EAEKARWVEIKRQOI-LMKEAVEAQMPAHIQIWRSGFTMN 1352
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
600 ---KNAVLDRAESQEAELERLTQLLFHSHEELSCLKEDLEVEHRNIEK-----LK 649
Qy      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1353 DIKGLHYEDNQFELPSSKMKELPSPRPKSGSMTRGVTON-----YNNLQPGQVNG- 1403
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
650 DNLGIHYKQIQIDGLQENMRKQMSMQCETDNL-----ITQNLILENSJKLRDLQELVNSK 706
Qy      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1404 -----MHRSTSAEMAKYDLGAQGLTPDDKDKRGKSPKPRSKRGSSDRAKSRKS 1456
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
707 SEEMNLQINELQKEIEILKQBEKEKGTLEQVE-----LQLKTEQLEKQLEKED 757
Qy      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1457 KTPDPFS--DTEVSPERGARRP-NPQIKV-SQANQRYNGMVARPSRTNLYGSQVGLNMA- 1511
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
758 DLQEKCAQLDAENNLKEEKRVLEDKLMYSPSQEERSIAVDPSTSKSADSRMQKEVAM 817
Qy      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1512 --TPTDRKQ---MTTSTLAQSAETVGNIEIPAECCLKLINEFYGVRIYPGQDPTHY 1565
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
818 LRKETEDLQOQCLYLNIEEIKQRTNFAPEAKNFVNYQELQREYTCILKI----- 867
Qy      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1566 IGWTTQVHLHSKDPNOSKVTKSSVIITDDYD---RVVENVRQSCYVMRADELYNEWA 1622
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
868 -----RDLLEATQTKQAL-----EYESKLRALE-----EELLSKRG 899
Qy      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1623 EATAKASQGMF-----IGCSVDTSSTGVSFTCEGKDTSPKFMPEPETKLPFAIFVEAT 1676
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
900 PAAPKGKSSGIFPSETLEIGEVVEKDTTEL---MEKLEVTREKLELSEK-----V 950
Qy      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1677 SKEILOELGRSATSPLSAAVLPTSCKHVIPOPPRLKVCQCLKPHQWAR----- 1726
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
951 SEQLKQTH-----CTINSLSAEV-----RALKQBEQLLRCGLELLANPGSTENA 1000
Qy      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1727 -VPNQSQVHAL--KLSDIRGWSMLCEDAVSMLALHIPEEDRCIDILEPIEMDKLLSFHS 1783
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1001 PVQSSSYQAGLVMGKVGDSGG-----SISKISKDLAESK-----PMIEDKIPFES 1047
Qy      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1784 HTLLTYAALCYQSNYRAAHALCTHVDQQLLYAIQSQVMGSLRGPGFYDLLIALHLSHA 1843
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1048 GREQLLLPTRAQKPSHATVPECESEKQQLQELHALKAEQDLDLRLQWEAQRICLFVYVSTHA 1107
Qy      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1844 TTMEACKNEFVILPGPELKALIEYBDMCHSLSRSLQTESVRPQMKMTDIASITISNLYS 1903
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1108 DQVRA-----HMEKREALCSLKDELISAQKKID-----ELHKQHQ 1145
Qy      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1904 PYF-----PLEVAREFVMQALAEAVETNQVHNRPDPVGGSNENLFLPLIKLVDR 1952
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1146 COLQNFKIQTGDEPLQVLIBERLOQAVSEK-----FHISKTLNNVFECYTP----- 1193
Qy      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1953 LLVGMWRDEDEVEKLLIMT-----NPTWDPSPDKGDKDEHRKGLLHMKAEGAKLQMCYLL 2008
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1194 -LKCEMNEEKENSGVYTSQNSPELQRYEVQDFQESQMVLGKVTTECKRLS--GLQ 1250
Qy      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
2009 QHLNDIQLRHVRVIAIIAPAHDFVGLQTDQLR-----RYTEIK-QSDLPSPAIAKTR 2060
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1251 TRLGKIHEQQTGDGVALFEFAEQAAEBEAGLLSGCSQSALQSTDVLSKVSSSLPA 1310
Qy      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
2061 EFRCPPEOMNAILSFK-HLEEDKENCPCGEELIARNEPHDTLMAHVSILHALQEPDAA 2119
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1311 ECERQVQLQSPVAAGQLQLTETETANHRAETESLQORLEAVSE-----APVQPSLS 1361
Qy      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
2120 ENQPEAKPGCAFCKLY-----NIINTVK-----ELEBEAKAI-----EPPPKTPEKFR 2164
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1362 IDSVFPGSGAQRPVYVCGSCLRECVGTAKFSDFEVRQETNMVNLMEKQYQERLEBEIA 1421
Qy      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
2165 KVLQIQTIVNWAESQIE-----T 2182
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1422 KVIIVMSIAFAQQTETLSRLSEGKENTIQSEQAHTLCSQNKHQLNDITSQSOVQLQTFEAT 1481
Qy      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
2183 PKLVREMFSLLRQ-----YD-----AVGELIRALEKTYVINAKT 2217
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1482 DKNFKKEFPKPLSKELGEYRKAVPLSSHDDLDLDLKSEHGLAISEEIFSDETFIVRKSM 1541
Qy      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
2218 KLDVAEMWVGLSQRALLPVQMSQEBEELMRKLWKLNNHTFFQHPDLRLVLRVHENVM 2277
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1542 HDEVLSSMDTSS-QLILNEQLEDMRQELVRQ-----YEEHQOQATEMLR----- 1584
Qy      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
2278 AVMMNTLGRRAQQAQSDAQSSQPAEDSKEK---DTSH-----EMVVA 2317
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1585 QAHMQMERQOREQEQLEBEIKRLNQLAQSSIDTEHVYSERERVLLBELEALKQLPLA 1644
Qy      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
2318 CCRFLCYFCRTGRQNKAMPDHFDFLENSNILLSRPSLRGSTPLDVAYSLSMENTELAL 2377
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1645 GRKELC--CELRRSSTQTDGHDQVEVEQTL---KDKTLERSPEDALLDRNLSERYAL 1699
Qy      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
2378 ALREHYLEKIAVYLSR-----CGL-----QSNSELVEKGYPDLG---WDP 2414
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1700 KKANNRLKILLEVVKTSAAEETIGHVLGILDRSKGQTASSLLWRSSADASATTCAP 1759
Qy      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
2415 VEGERYLD-----FLRFCVWNGESVEENANLIRLIRPECLGPALRGEGEG 2463
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1760 EDCARAMDSSI PSYPGTATATHDSIW--SKVTBEGAELSQRLV--RSGFAGPVIDPENEE 1815
Qy      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
2464 LKKAIVDANKMSRIADRRKLRMEWQEGDVNFHSLPESDE--DEDVIDTGAAILNFYCT 2521
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1816 LM-----LNISSRLQAAVEKLEAISETNTQLEHAKVTQTELMRESPROQEATESLHC- 1869
Qy      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
2522 LVDLLGRCAPDAGVIALGKNESIRARAILRSVLPLEDLQGLVLSRFTLNNPAAGEERPKS 2581
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1870 LEELRERL-----QESRAREQL-----ABEUNKA 1894
Qy      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
2582 DMPGSLIPGHKQSVGLFLERVYGIETQELFYKLEEAFLPDLRAATMLDNDGCESDMAL 2641
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1895 E---SWIDGVSDEKTLFERQIQ--EKTDIIHLEQEVL-----CNMNLQELSESQOR- 1941
Qy      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
2642 SMNRYIGNSLPLLIKHAVPYNEAENYASLLDATHVTYFLSKNRMULTKQOREAV----- 2696
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1942 -----RVEEERQLLCQREAMRAEAG 1962
Qy      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
2697 ---SDFLVALTSAMQPSM-----LLKLLRKLTVDVSKLSEYTTVALRLLTLHY 2741
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1963 FVEQQFLQETEKLMKEKLELVQCOAEKVRGDLQKVKALEIDVEE-----QVSRFIELEQ 2016
Qy      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
2742 ERCAKYVSTGACQAGAFGASSDEEKRLTMMLFNSIFDSLKMDYEPPELFGKALPCIIAIG 2801
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
2017 EKNAELTDLRQSQAL-----EKQLEKM----- 2039
Qy      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
2802 CALPPDYSLSKNYDDDEFYKGEQAAGLDNPDQDPQINTSSVALNNDLNTIVOKFSHYH 2861
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
2040 -----RKFLDE-----QAID-----REHER 2054
Qy      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
2862 DAWAS--RKLENGWVYGEHSDSQKTHPRLPKPNMLNDYKERYKEPVRESLKALLAIGW 2919
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
2055 DVFQEQIQKLEH-----QLKAVPRIQPVSEHQAREVEQUTNLHKEKTRCSELLL 2104
Qy      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
2920 SVHSEVDIPSNKRSMRQSKGGRPPETVDSATPF-----DYNPHFVDMNTLTLREM 2975
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
2105 SKQLQRDIQERNEEIEKLECRVRELEQALLA-SAEFPKVEDQKRGSAVEADPELSLEV 2163
Qy      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
2976 QNMAERLADNAHIWAKKKKEELVTNGGGHPQLVPYVDLLTDKBEKKKDRSSQBFKYLQ 3035
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
2164 QLQVER-----DATDRKQKE--ITN---LEEQLQEQF---RELEKNKNDEQVLLMQLE 2208
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Db 3384 NWEAGLSTQQAQTADYTAERLSVLCNWFANLQPEGVSLSHRDDIYSFLINDQVSSA 3443  
Qy 4172 IGKQWDTLVESASNVILKYFDMFLKLDLTSSAQFQEDANNDGQVLPKDPKEMEQ 4231  
Db 3444 I---KTRRLAIAIAGIQLYI-----NRALNRIEPNARADVSTRQFTDWTV 3486  
Qy 4232 QKSTPEIEFLACCETNHHGKLDYIGFCDRFPHEPAKEIGFN--LAVLLTNLSEHPNE 4289  
Db 3487 NNRV-----STWGGVSRVLYPENYIDPTQIGQTRMDELLENIS-----Q 3528  
Qy 4290 PRLARFLETAGSVLNYPFPFGRTEIMGGSKRIERVYFEIKESNIEQWPKQIKESKRAF 4349  
Db 3529 SKLSR-----DTVEDAFKTYLTRTETVADLVKVSAYHDNVNSNTGLTFWFGQTRNLPEY 3583  
Qy 4350 FYSIV---TEGGD-----KE--KLEAFNFCEDAI 4374  
Db 3584 YWCNVDISRMQAGELAAANAKWETKIDTAVNPKDAI 3620

RESULT 11  
US-11-056-355B-86482  
; Sequence 86482, Application US/11056355B  
; Publication No. US20060150283A1  
; GENERAL INFORMATION:  
; APPLICANT: Brover, Vyacheslav  
; APPLICANT: Alexandrov, Nikolai  
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding  
; TITLE OF INVENTION: Polypeptides Encoded Thereby  
; FILE REFERENCE: 2750-1590PUS2  
; CURRENT APPLICATION NUMBER: US/11/056.355B  
; CURRENT FILING DATE: 2005-02-14  
; PRIOR APPLICATION NUMBER: 60/544,190  
; PRIOR FILING DATE: 2004-02-13  
; NUMBER OF SEQ ID NOS: 119966  
; SEQ ID NO 86482  
; LENGTH: 1703  
; TYPE: prt  
; ORGANISM: Arabidopsis thaliana  
; FEATURE:  
; NAME/KEY: peptide  
; LOCATION: (1)..(1703)  
; OTHER INFORMATION: Ceres Seq. ID no. 12690877  
US-11-056-355B-86482

Query Match 0.8%; Score 219; DB 7; Length 1703;  
Best Local Similarity 18.9%; Pred. No. 0.00031;  
Matches 273; Conservative 246; Mismatches 481; Indels 446; Gaps 69;

Qy 3083 NMKLLKPSSTTPSRSSPKTSTR-----DIKFFSKAVLPMLMEKYFSTHRNYFIAVAT 3133  
Db 121 NIAFMEDPQSVSSGKGFKTAKARKGLNFNNVDGKEINAKVLSESER-ASKAAEAIKAD 179  
Qy 3134 ATNVVGAASLKEKWVAALF---CKLASLSRLAAGFPDVRITVRCQLVLKIGIDAKSL 3190  
Db 180 ALSKVQA-----EKEASLQAQPNLEKUNLSESVRAQEDSRVLIE-----RATRAAE 229  
Qy 3191 VKNCPEFI-----RTSMLTF--FNNVADVVGHTIMNLQDGKYAHLGRTHLKTSTSLG 3240  
Db 230 VETLRESLSKVEKESLSLQYQQCLQNIAD-----LEDRLSLA 268  
Qy 3241 YINGVLLPILTAKEFDHLANCEYGADLLDEITQVASYKMLGSLYALGTADSLTHDRKYLKT 3300  
Db 269 QKE-----AGEVDERANRAEAETLALKQSLVSS-----ETDKEAALVQYQQCLKT 313  
Qy 3301 EIERHKPALGSLGAFSSTFFVALEPHLNKHNFSLNRIADLSLEAQDIMQKWEQMP 3360  
Db 314 -----ISNLEERLHKAEDSRLTN-----QRAENAE 340  
Qy 3361 TLETILGEVDQFVSDKTYN-EAPHIIDVVLPLCLSYLPFWMAQG-----PDNVTP 3410  
Db 341 EVESLKKQKVSKLIEENAEYELQYQQCLDTIADL---KLKLPHAQEETQRLSREIEDGVAK 397

Qy 3411 TGCNHHVTWTAEHWNOLLKNVLKLIKNIIGNENAPWMTRIATVTQIIINSSEBELLRDSF 3470  
Db 398 LKFAEBKCVVLSRNQNLHSELGDLKLGNO-----SHELTEK-- 436  
Qy 3471 LPLAEBVRKRTDMNFH--KEESLRGFIKST--DDTSQVESQIQEDMQLLVRIYSYPL 3526  
Db 437 -----QKELGRGLWTCVQEENLR-FWEAETAFTQLQHLHSQSEELSTLLELQNRSQI 488  
Qy 3527 LIKYVDLQ-RNHVLRNNVPEAEELYNHVABIFNWSQSYFLKEEQNFISAN-----EI 3579  
Db 489 L---KOMEARNLQBEVQEAQKQSLNELNLSAASIKLSQBEVSKLRETQKLEAEV 545  
Qy 3580 DNMVIMPTATRVATVTDGTPQGGKKKKKRRDKRDKDEVOASLWACLKRLLLDVGL 3639  
Db 546 ELRVDQNALQQBIYCLKEELSQIG---KKHQ-----SMVEQVELVGL 585  
Qy 3640 N--LFAGREQELVQHCCKDRFLKMSQBDVAEFAKTQTLTPDKIDPADEMSQWHLVSKLG 3697  
Db 586 HPESFGSSVKELQE--ENSKLKEIRERESIE--KTALI--EKLEMEKLVQKNLLE--N 637  
Qy 3698 SKSKSNITVETAEAKAKIIDDTVERIVAMSKVLFGLH-----MIDHPQQMSKN----- 3745  
Db 638 SISDLNAELETIRGKLKTLLE---EASMSLAEBEKSGLHSEKMDLISRLOSATENSKKLSEE 694  
Qy 3746 -----VYRSVVSIOKRAVIACFRQTSLSHSLPRHRACNIFARTYYELWLEENIQGEV 3798  
Db 695 NMVLENSLFNANVELELK-----SKLKSJ--BESCHLLNDDKTTLTSESLLSHI 744  
Qy 3799 -----MIEDUTQSFEDEALKKSDVBEGEKPDLTQTLVTTFCRGAMTERSGALQE-DPLY 3852  
Db 745 DTWRKRIEDLEK-EHAELKVK-VLE-----LATERESSLOKIBELG 783  
Qy 3853 MSVAHIIAKSCGEEBEGGEEBEGGEEA---FAEDEGRASIHIEQMEKOKLFLPHQARLA 3909  
Db 784 VS---LNAKDCYASVFQFSESRMNGMESTIHLQDENQCRVREYQVELDRA--HDAHI- 837  
Qy 3910 DRGVAEMVLLHISAKGLPSEPMVKTLQIGI---SILRGNNIDIQMG--MLNHL---KDK 3961  
Db 838 -----EIIVL-----QKLDWLKSSSLIAENQDIKASKLLEKLVSELEE 879  
Qy 3962 KDVFFTSIAGLNSCSVLDDAFERNTKAE---GLGVGLEGAAGEKNMHDABFTCALFR 4018  
Db 880 ENIGKQVQIDSSINCILRTGIYQVLMKLEIIPGIGSGDENSQRDQNMHD-----ILN 933  
Qy 4019 FIQLTCEGHNLDWQNYL---RTOAGNTTTVNVVICTVDYLLRLQESIMDYPWYSSKELI 4075  
Db 934 RLE-----DMQTMLLSIRDENQHSAINLVL--IEFLRLKLS----- 968  
Qy 4076 DPAGKANFFKAIGVASQVFNLTTEVIQGPCTQNOQALAHSLRLWDVAGGFLFLFSHMQDKL 4135  
Db 969 -----EAVGIETEK-KILEEBLESQC---QQLSFSR--DETQKLIFVNGELTKV 1012  
Qy 4136 SKHSSQVDDL-----KELLNLQKDMIPMLSMLEGNVYVNGTIGQMVDTLVESASNV 4187  
Db 1013 NOGVNREKVLWVEIEDFHRQVLQRDDY-----TILQDGNK 1049  
Qy 4188 ELILKVPDMLKLDLTSSASFOEIDANDNGWVLPKDPFKEMEQOKSYTPEEFILACC 4247  
Db 1050 TLDEKAY-----LTKSTL-----QLEEKCKLEDDISLLS-- 1080  
Qy 4248 ETNHDGKLDYIGFCDRFPHEPAKEIGFNLAULLTNLSEHPNEPRLARFLTAGSVLVNFE 4307  
Db 1081 ETIYQS-----NLIITLSEDV-----ILSKLSAMKLINE 1108  
Qy 4308 PFLGRIEIMGG--SKRIERYVFIKESNIBQWEPQIKESKRAFFYSI----- 4353  
Db 1109 D-LDRLSIVKCLEEEVRELGDKLSADIANFOLQVVLEKSNAEILLSARGANVHLEHEIA 1167  
Qy 4354 -VTEGGDKEKLEA--FWNFCEDAIFEMTHA-SGLMAASESVGCTKNREASVYMWGDDDD 4409  
Db 1168 NVKVOKEKELLEAMLTISIMQNEKSELSKAVEGLECRYKEAKAIEDRDQVLRKRGDYD 1227  
Qy 4410 ERAGKD 4415



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; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 86480
; LENGTH: 1744
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(1744)
; OTHER INFORMATION: Ceres Seq. ID no. 12690875
US-11-056-355B-86480

Query Match      0.8%; Score 219; DB 7; Length 1744;
Best Local Similarity 18.9%; Pred. No. 0.00032;
Matches 273; Conservative 246; Mismatches 481; Indels 446; Gaps 69;

Qy 3083 NMKLLKPTTFSRSSSFKTSTR-----DIKFFSKAVLPLMEKYFSTHRNFIYAVAT 3133
Db 162 NIAFMEDPQSVSSGKGFATARKGLNPNVVDGKEINAKVLSSESR-ASKABEIVALKD 220
Qy 3134 ATNNVGAASLKEKEMVAALF---CKLASLLRSRLAAFGPDVRIIVRCLQVLVKGIDAKSL 3190
Db 221 ALSKVQA-----EKEASLAQPDONLEKLSNLESEVSRAQEDSRVLJE-----RATRAEAE 270
Qy 3191 VNCPEFI-----RTSMLTF--FNNVADVGHITMNLQDGKYAHLRGLHKLTKSTSLG 3240
Db 271 VETLRESLSKVEKESLSLQYQOCLQNIAD-----LDRISLA 309
Qy 3241 YINGVLLPILTAKEPHLANCEYAGADLLLDLQVASYKMLGSLYALGTDASITDRKYLKT 3300
Db 310 QKE-----AGEVDERANRAEAEETLAKQSLVSS-----ETDKAALVQYQCLKT 354
Qy 3301 EIERHKPALGCLGAFSTFPVAFLEPHLNKHNFSLNRIADHLSLEAQDIMQWECMP 3360
Db 355 -----ISNLEERLHKAEDSRLTN-----QRAENAE 381
Qy 3361 TLETILGEVDQFVSDKTYN-EAPHIDVILPLCSVLPFWAAG-----PDNVT 3410
Db 382 EVESLQKQVKSLIBENAEYELQYQCLDTIADL---KLKLPHAQEETQRLSREIEDGVAK 438
Qy 3411 TGGNHVTMTVAEHMNLKNVLLKIKKNIGNENAPWMTRIATYQQIINSBELLRDSF 3470
Db 439 LKFAEKCVCVLERSNQNLHSELGDLEKLGQ-----SHELTEK-- 477
Qy 3471 LPLAERVKRRTDNMFH--KEESLRGFIKSST--DSTSQVESQIQEDWQLLVRIYFYPL 3526
Db 478 -----QKELGRMTVCQOENLR-FMEAEATFQTLQOLHQSQOEBLSTLAEIQNRSQI 529
Qy 3527 LIKYVDLQ-RNHWLRNNVPAAEELYNHVAEIFNTWSKSYPLKEEQNFISAN-----EI 3579
Db 530 L---KDMERNNGLEEVQAEAKDQSKSLNELNLSAASIKSLQSEVSKLRETIQKLEAEV 586
Qy 3580 DNMLVIMPTARRVTAVTDGTPQGGKKKKKGRDKRDKQKQVQASLMVACLKELLVGL 3639
Db 587 ELRVDQRNALQOEYCYCLKEELSQTG---KKGQ-----SMVEQVELVGL 626
Qy 3640 N--LPAGREQELVQHCDFRFLKMSQEDVAFKATQTLTPKIDPADMSQHWLYSKLG 3697
Db 627 HPESFGSVSKLEQ--ENSKLKEIRERESIE--KTALI--EKLEWMEKLVQKNLLS--N 678
Qy 3698 SKSKSNITVETAENAKIIDTVERIVAMSKVLFGH-----MIDHPQOQMSKN----- 3745
Db 679 SISDLNAELETIRGLKLTLE---EASMSLAEEKSLGHSKDKMLISRLQSATENSXKLSEE 735
Qy 3746 -----VYRSVSTQKRAVIACFRQTSLSLSPRHACNIFARTYYELWLEENIGOE 3798
Db 736 NMVLENSLFNANVELELK-----SKLSL--EESCHULNDKTKTLTSESSLSLHI 785
Qy 3799 ----MIEDLQSPEDAECLKSDVVEGEKPDPLTQLTTPFCGAMTERSGALOE-DPLY 3852
Db 786 DTMKRLEDLEK--EHAELKYK-VLE-----LATERESSLQKIBELG 824
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Qy 3853 MSVAHIIIAKSCGEEEBEGGEGGEA---BAEDEGRASIIHEQEMEKOKLLPFOARLA 3909
Db 825 VS---LNAKDCFYASVQFSESQRMGWESTIHHLODENQCRVREYQVELDRA--HDAHI- 878
Qy 3910 DRGVAEMVLLHISASKGLPSEVMYKTLQLGI---SILRGGNIDIQMG--MLNHL---KDK 3961
Db 879 -----EIIVL-----QKCLQDWLEKSSSLIAENQDIKEASKLLEKLVSELEE 920
Qy 3962 KOVGFTSTAGLMNCSVLDLDAFERNTKAE---GLGVGLEGAAGEKNMMDAEFTCALFR 4018
Db 921 ENICKQVQIDSSINCILRTGIYQVLMKLEIIPGIGSGDENSQRDNMHD-----ILN 974
Qy 4019 FIQLTCEGHNLDWQNYL---RTOAGNTTTVVVICTVYLLRLQESIMDFVWYSSKELI 4075
Db 975 RL8-----DMQTMLLSTRDENQHSATENLVL--IEFLRQLKS----- 1009
Qy 4076 DPAGKANFFKAIGASQVFNLTTEVIQGPCTONQQAALAHSLRDWAVGGFLFLFSHMMDKL 4135
Db 1010 -----EAVGIETEK-KILSEELSQC---QQLSPSR--DETQKLIFVNGELTTKV 1053
Qy 4136 SKHSSQVDLL-----KELLNLQKDMIPMLMSLMEGNVVGTTIGKQMYDTLVESASNV 4187
Db 1054 NOGVNREKVLWVEIEDFHRQVLQLRDDY-----TILQGDNNK 1090
Qy 4188 ELTLKYDFMPLKLDLTSSASFQEI DANNDGWVLPKDFKEKMEQOKSYTPEETEFLLACC 4247
Db 1091 TLDEKAY-----ITKSTL-----QLEEKCKLEDDISLLLS-- 1121
Qy 4248 ETNHDGKLDYIGCDRPFHEPAKEIGFNLAIVLLTNLSHMPNEPRLARFLETAGSVLNYFE 4307
Db 1122 ETIYQS-----NLIILEDV-----ILEKLSGAMKLINE 1149
Qy 4308 PFGRIEIMGG--SKRIERVVFEIKSNIBQWEKPKQIKSKRAFFYSI----- 4353
Db 1150 D-LDRLSIVKCKLEEEVRELGDKLKSADIANFOLQVVVLEKSNABLSSANSVHLEHIA 1208
Qy 4354 -VTEGGDKKLEA--FVNFCEDAIFEMTHA-SGLMAASBESVGGTKNREASVYVMGDDDD 4409
Db 1209 NVKQVQEKELLEAMLMISIMQNEKSELSKAVEGLECRYEKAIEEDRDQVLRGDDYD 1268
Qy 4410 ERAGKD 4415
Db 1269 EQVKKN 1274

RESULT 14
US-10-953-349-9275
; Sequence 9275, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 9275
; LENGTH: 3429
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
US-10-953-349-9275

Query Match      0.8%; Score 208.5; DB 6; Length 3429;
Best Local Similarity 18.4%; Pred. No. 0.0051;
Matches 332; Conservative 246; Mismatches 628; Indels 601; Gaps 77;

Qy 1060 TGCQHEALLLEASKQKQADRTTYRAEKYAVSSGKTYFEFEILTATGPRVYGAHADMAPG 1119
Db 1865 TVETHKAEDSGSLKQCALYNLSKADK--LVSDIPHVPVPGDLTTSGSV---ANKVDIG 1918
Qy 1120 MMLGQDENSWAFDGYNEEKYVSGNTESFGKQWAGVDVVGVLIDLIDTISFSLNGELIMD 1179
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Db 1919 SSKVAENELV-----KIPGDDVSSVQLSLGNLTAKSSL-EKCTADQLLEKLSQ 1970  
Qy 1180 ALGGTTTFADVGDNFVPACTLGVQKARLTGVQDVNTLYKFTTCLGLEGYEPFCVNM-- 1237  
Db 1971 E--GETTPAS-DGE-----TCHLAETASSLSVVRSEPTASATTA-----EPLPTDKLE 2017  
Qy 1238 -----KRDVTHYTKDQ-----PIFENTDEMIDTRIDVTRIPAGSDTPPC 1277  
Db 2018 KNISFQDEVKTLNGDKREAILLSSEEQTVNSKIETNSELOASRTD----- 2064  
Qy 1278 LKISNTPFTMKANWEFLURLSLPVIChNEFDIEAKARWVEIKDRQIILMKEAVEAQM 1337  
Db 2065 -EVPHVDSKSDVA-----NQTVKE-DEAKHSVEI-----QSSMLE----- 2098  
Qy 1338 PAHIQIMRSGTMDIKGLHYE-----DNQBELPSSKMKRLPSRPPKSGMTRGV 1388  
Db 2099 PDELPNAGQKSHSIDQLPLVLVTNENAMSLDDXDYDPIKSADIEQDP-----ESV 2152  
Qy 1389 TIQYNNLQPGQVNGMHRSTSEA-----EMAKYDLGAQGLTPDDKKDKRGRSPFKPF 1440  
Db 2153 FVQGVGRPKVGTADTQMETNDNAKLLVGCSESEKEKTLQSLIPGDDADTE-QDPEESV 2211  
Qy 1441 RSKRG-----ESSDRASRKSCTPDPPFSDTEVSPE-----RG 1472  
Db 2212 SDQRPKVSAYTQMEDTDEAKLLMGCSVESEKEKTLQSHIPGDDADTEKNPEESVSQ 2271  
Qy 1473 ARRPPOIKVQANQRYNGWNPASRTNLYGQVGLNMPATQDRKQMTTSLAQASAT 1532  
Db 2272 VDRP-----KVGTTDTQME-----DTNDAKLLVGCSESEKEK 2305  
Qy 1533 VGNEIFDAECLLINEFYGVGRIYPGQDPTHVIGWVTTQYHLHSDKFNQSVTKSSVII 1592  
Db 2306 -----TLQSHIPGDDADTEQNPESVS 2328  
Qy 1593 TDDYDRVENVARQSCYMRADLYNEVMAEATAKASQGMFIGCSVDTS----- 1642  
Db 2329 QGVNRPKVGNTQ--MEDTDE-----AK-----VLVGCSESEKEKTLQSHI 2370  
Qy 1643 -----TGSVFTCEGKDTSPFKWE--PETKLPFAIFVEATSKELIQLGRSA 1689  
Db 2371 PGDDADTEQNPESVSFNDRPKDGTADTHMEDIDDAKLLVGCSESEKE----- 2420  
Qy 1690 TSLPLSAAVLPTSDKHVIFQFPRLKVQCLKPHQWARVPNQSLQVHA--LKLSDIRGWSM 1747  
Db 2421 -----KSLQSH-----MFSDDAVLHAPFENTKDSKGDLD 2449  
Qy 1748 LCEDAVSMLALHIPER-----DRCIDIILEPIEMDKLLSFHSHTLTLYAA 1791  
Db 2450 HGESLVSCPTMEVMEQKGFETHARTDSGGIDRGNEVSENMSDGVKMNISVQVP--- 2505  
Qy 1792 LCYQSNYRAHALCTHVDQKQ--LLYAIOSQW-----SGPLRGFYDLLIALHLESH 1842  
Db 2506 -----DASHDLNVSQDQTDIPLVGGIDPEHQVNDVPASP--HGAAPNIVIFQSEGH 2556  
Qy 1843 -----ATTWEACKNEFVPLGPPELKALVEEPMGMHSLRSLOTESVRPOMKMTDTA 1892  
Db 2557 LPSFILPDDVAGQLESNDKENTNISSE-----QVPDVSHDLKVSDQDQTDIPVGGI-VP 2610  
Qy 1893 ESITENSLNYSPPFLPEVAREFWQALAEAVETNVQHNDRDPVGGSENLFLPLIKLVDRL 1952  
Db 2611 ENLQEIADV--PASPHGVVPDVV-----SQSEEIQSFSILPDD-- 2647  
Qy 1953 LLVGMMDREDEKLLIM-----TNPETWDPSPFKEGKDEHRKGLLHMMAE----- 1998  
Db 2648 -VPGQDDGCKEKMWTQNNNTSIDIGTSKTCQPSSTQPEDENRNSLSHCPEPSVWEQ 2706  
Qy 1999 -GAKLQWCYLLQHLNDIQLHRVREAIIPAHDFVGLDQDQ-----LRYETIKQSDLS 2052  
Db 2707 ROSRDQVC-----IGSVE--SQVEISSAILENRSADIQPPQSILVDQKDIESKEPGIES 2759  
Qy 2053 A-VAACKTREFRCPPR---EQNNAILSFKHLEBEDKENCPCGBELIARMEFHTLMAHV 2108

Db 2760 ADVSLHQLADIQABEPSNLVDQMDI-----EESKE-----PGTESADV 2796  
Qy 2109 SLHAL-----QEPDAENQEP-----EAKPGAGFKLYNIINTVKEL 2144  
Db 2797 SLHQLADIQPGSILVDQMDTEKSEKPGTESADVSLHQLADIQPGP-SILVDQMDTEKSK 2855  
Qy 2145 EEEAKAIBEPKPKTPEEKFRKVLQTIQVNWAEESQIETPKLVREMFSLVRYQDAVGELI 2204  
Db 2856 EPAVKQNIQEDKQSHVETAGSELVDVSAECSTEPQVQLPPSPBPVGMHVLHGLASKSEIV 2915  
Qy 2205 -----RALEKTYVINAKTKLDVAMVMVGLSQRALLPVQM-----SQBE 2243  
Db 2916 AEGTDFSSLPKTEENAKSQLADTEPSSSLTAQVKNIQEDQVETAGCFVSVVSTCSTEP 2975  
Qy 2244 EELMRKLWLKLVNHNHTFFQHPDLIRLVRVHENVAMVMTLGRRAQAQSDAQPSOPVA- 2302  
Db 2976 QVQLPPSAEPVVAEGTEPSSILMTGVDNSHLMTGVDNAKTHLA---DVPVSSSPTTM 3031  
Qy 2303 EDSKEKOTSHEMVWVACCRFLCYFCRTGRQONKAMPDFHDFLLENSNILLRPSLR---GS 2359  
Db 3032 EKNTEAQDQDQVTTGGCGLV-----DVLTECS-----SEPQLQPPSA 3069  
Qy 2360 TPLDVAYSSLMNTFLA-LALREHYLEKIAVYLSRCGLQSNSELVEKGYDGLWDPV--- 2415  
Db 3070 EPV-----ISEGTELATPLTEE--ENADSOLANIEPSSPVVVEKKNIEAQDQVKTA 3121  
Qy 2416 -----EGERYLDFLFCVWYNGESVEENANLVIRLLIRRPCC 2452  
Db 3122 GCELSTVSCSSEPQVHLPPSAEPDGD-----IHVHLKETEKESMVV----- 3163  
Qy 2453 LGPALRGEGEGLLKA--IVDANKMSERIADRRKUREMEQEGDVNFSPH--LPESDEDEY 2508  
Db 3164 -----VGEGTAPPSPPLVTEGNABSQADTEP-----FTSPTVVEKNIKDQSQ 3207  
Qy 2509 IDTGAAILNFYCTLDLLGRCAPDAGVIALGKNESLRARAILRSLVP-LEDLQGVLSLRF 2567  
Db 3208 VETTG-----CGLVDDSTGCSSEPOV-----QLPPSAEPMEGGCDL--- 3243  
Qy 2568 TLNPPAAGEERPKSDMPGLIPGHKQSVGLFRLVRYGIETQELFYKLLEAEFLPOLRAAT 2627  
Db 3244 -INVPSGCGSTEPQIQLSSAEP--EGMHIIHLEAMNSET-----VVTGSELPSLSPMT 3295  
Qy 2628 MLDRNDG 2634  
Db 3296 EDENADG 3302

RESULT 15

US-10-953-349-9274  
; Sequence 9274, Application US/10953349  
; Publication No. US20060107345A1  
; GENERAL INFORMATION:  
; APPLICANT: ALEXANDROV, Nikolai et al.  
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
; TITLE OF INVENTION: ENCODED THERBY  
; FILE REFERENCE: 2750-1579PUS2  
; CURRENT APPLICATION NUMBER: US/10/953,349  
; CURRENT FILING DATE: 2004-09-30  
; NUMBER OF SEQ ID NOS: 40252  
; SOFTWARE: Patent in version 3.3  
; SEQ ID NO 9274  
; LENGTH: 3438  
; TYPE: PRT  
; ORGANISM: Arabidopsis thaliana  
US-10-953-349-9274

Query Match 0.8%; Score 208.5; DB 6; Length 3438;  
Best Local Similarity 18.4%; Pred. No. 0.0051;  
Matches 332; Conservative 246; Mismatches 628; Indels 601; Gaps 77;  
Qy 1060 TGEQHEALLLEASKQKQADFRTRYRAKNYAVSSGKWFYFEFLTAGPMRVGAHADMAPG 1119  
Db 1874 TVETHKAEDSSGLKNQELYNLSKADK--LVSDIHPHPVPGDLTTSQSV-----ANKQVDIG 1927

Qy	1120	MLLQDQDENS	WAFDGYNEBEKYVSGNTE	SFGKQWAGVDVGVFLDLIDIKTISFSLNGEL	MD	1179
Db	1928	SSKVAENELV	-----KIPG	GDVSSVQLSGLNLTAKSSL- EKTADQLLGEKLSQ		1979
Qy	1180	ALGETTTFAD	VOGNFNFPACTILGVQKARLTYGQDVNTLKYFTTCGLQEGVEPFCVM	--	1237	
Db	1980	E--GETTPAS	-DGE-----TCHLAE	ETASSIVSRSEPTASASTA-----EPLT	DKLE	2026
Qy	1238	-----KRDV	THWYTKDQ-----PIFENT	DEMIDTRIDVTRIPAGSDTPPC		1277
Db	2027	KNISFQDEV	KLNGDKKEAILLSEEBQTNVNSKLETNSEELOASRTD	-----	2073	
Qy	1278	LKISHNTFET	MEKANWFLRLSLPVI	CHNEFIDAEAKRARRWEIKDRQQILMKEAVEAQM		1337
Db	2074	-EVPHVGDKS	VDVA-----NOTVKE	-DEAKHSVEI-----QSSMLE	-----	2107
Qy	1338	PAHIDQIMR	SGFTMNDIKGLHYE-----DNQE	ELPSKMKRLPSRPRKGSMTGRV		1388
Db	2108	PDELNPAGQ	KGHSSIDLOPLVLVTSNENAMSLDDKOYDPI	SKSADI	EQDP-----EESV	2161
Qy	1389	TIQYNNNL	QPQVNGMHRSTSEA-----EMAKYD	LGAGLTPDDKKDKGRGSRPFKF		1440
Db	2162	FVQGVGRPK	VGTAQTOMEDTNDAKLLVCCSVSESEKEKT	LOSLIPGDDADTE-QDP	ESV	2220
Qy	1441	RSKRG-----ESDRA	KRSKTPDPFSDTEVSPE-----RG		1472	
Db	2221	SDQRPKVS	AYTOMEDTDEAKLLMGCSVESEKEKT	LQSHIPGDDADTEKNP	ESVSVOG	2280
Qy	1473	ARRPNQIKY	SOANQRNGMWARSPRINLYCSQVGLNMAPTDQR	KOMTSTTLAQSATET		1532
Db	2281	VDRP-----KVGT	TDTOME-----DTNDAKLLVGC	SVASEBEKE		2314
Qy	1533	VGNEIFDAE	CLKLINEFYGVRIYPGDPTHVYIGWTTVOYHL	SHSKDFNQS	KVTKSSVII	1592
Db	2315	-----	-----TLOSHIP	PGDDADTEQNP	EEVS	2337
Qy	1593	TDDYDRV	VENVNRQSCVMRADELINYMBAEATKAGASQGM	FIGCSVDTS-----	1642	
Db	2338	QGVNRPKV	GNANTQ-----MEDTDE-----AK	-----VLVGC	SVSEBEKTLQSHI	2379
Qy	1643	-----TGSVS	FTCEGKOTSFPKME--PETKL	FPAI	FVEATSKELQIELGRSA	1689
Db	2380	PGDDADTEQ	NPESVSFNDPRPKOGTADTHMEDIDDAKLLVGC	SVSESEKE-----	2429	
Qy	1690	TSLPLSAA	VLPTSDKHVIQPPPRLKVCQCLPHQWARVP	NQSLQVHA--LKLSDIRGWSM		1747
Db	2430	-----	-----KSLQSH-----MPSDDA	VLHAPFENTKDSKGGDL	2458	
Qy	1748	LCEDAVSM	LALHIPEE-----DRCIDILE	PIEMDKLLSPHSHTLTYAA		1791
Db	2459	HGESLVSC	PTMEVMEQGFSETHARTDSOGIDRGNEVSNM	DGVKMTSSVOQP----	2514	
Qy	1792	LCYQSNYRA	AHALCTHYDQKQ--LLYAI	QSOYM-----SGPLRQCFYDL	LALHLESH	1842
Db	2515	-----DASH	LVNSQDQTDIPLVGGIDPEHVOENVDV	PASP--HGAA	NNIVIFQSEGH	2565
Qy	1843	-----ATTME	ACKNEFVIFLGPPELKALYEEPDMGHSLRS	LQTESVRPQMKMTDIA		1892
Db	2566	LSPSILPDD	VAGQLESNDEKTNISSE-----QVPD	VSHDLKVSQDQTDI	PPVGGI--VP	2619
Qy	1893	ESITEI	NLVSPPYPLEVAREFVMOALAEAVETNQV	HNRPDPVGSNENLFLPLIKLVDRL		1952
Db	2620	ENLQEI	VDV--PASPHGV	VPDVV-----SQSEI	QSPSLTPDD--	2656
Qy	1953	LLVGMRDE	DEVEKLLIM-----TNPET	MDPSPDKCKGDBHRKGLLHMKAEE	-----	1998
Db	2657	-VPQCPDD	GNCEKMDTQNNTSIDIGITSGKTCQPSSTQ	PEDENRNL	SLHCEPSEVVEQ	2715
Qy	1999	-GAKLQWCY	LLQHLNDIQLRHRVBEAIIAFAHDFV	CDLQTOQ-----LRRYTEIK	QSOLDPS	2052
Db	2716	RDSRDQVC	-----TGSVE--SQVRS	IAILENRADIQPPQSILV	DQKJTEESKEPIES	2768

Qy	2053	A-VAAKTTRFRCP	PR	---	EOMNA	ILSF	KHL	BEED	KENC	PC	GB	ELI	ARN	VE	HD	TL	MA	UV	2100																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																							
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Db	2806	SLH	Q	L	A	D	I	Q	P	G	S	I	L	V	D	Q	M	T	E	K	S	E	P	G	T	E	S	A	D	V	S	L	H	Q	L	A	D	I	Q	P	G	---	S	I	L	V	D	Q	M	T	E	K	S	E	P	G	T	E	S	A	D	V	S	L	H	Q	L	A	D	I	Q	P	G	---	S	I	L	V	D	Q	M	T	E	K	S	E	P	G	T	E	S	A	D	V	S	L	H	Q	L	A	D	I	Q	P	G	---	S	I	L	V	D	Q	M	T	E	K	S	E	P	G	T	E	S	A	D	V	S	L	H	Q	L	A	D	I	Q	P	G	---	S	I	L	V	D	Q	M	T	E	K	S	E	P	G	T	E	S	A	D	V	S	L	H	Q	L	A	D	I	Q	P	G	---	S	I	L	V	D	Q	M	T	E	K	S	E	P	G	T	E	S	A	D	V	S	L	H	Q	L	A	D	I	Q	P	G	---	S	I	L	V	D	Q	M	T	E	K	S	E	P	G	T	E	S	A	D	V	S	L	H	Q	L	A	D	I	Q	P	G	---	S	I	L	V	D	Q	M	T	E	K	S	E	P	G	T	E	S	A	D	V	S	L	H	Q	L	A	D	I	Q	P	G	---	S	I	L	V	D	Q	M	T	E	K	S	E	P	G	T	E	S	A	D	V	S	L	H	Q	L	A	D	I	Q	P	G	---	S	I	L	V	D	Q	M	T	E	K	S	E	P	G	T	E	S	A	D	V	S	L	H	Q	L	A	D	I	Q	P	G	---	S	I	L	V	D	Q	M	T	E	K	S	E	P	G	T	E	S	A	D	V	S	L	H	Q	L	A	D	I	Q	P	G	---	S	I	L	V	D	Q	M	T	E	K	S	E	P	G	T	E	S	A	D	V	S	L	H	Q	L	A	D	I	Q	P	G	---	S	I	L	V	D	Q	M	T	E	K	S	E	P	G	T	E	S	A	D	V	S	L	H	Q	L	A	D	I	Q	P	G	---	S	I	L	V	D	Q	M	T	E	K	S	E	P	G	T	E	S	A	D	V	S	L	H	Q	L	A	D	I	Q	P	G	---	S	I	L	V	D	Q	M	T	E	K	S	E	P	G	T	E	S	A	D	V	S	L	H	Q	L	A	D	I	Q	P	G	---	S	I	L	V	D	Q	M	T	E	K	S	E	P	G	T	E	S	A	D	V	S	L	H	Q	L	A	D	I	Q	P	G	---	S	I	L	V	D	Q	M	T	E	K	S	E	P	G	T	E	S	A	D	V	S	L	H	Q	L	A	D	I	Q	P	G	---	S	I	L	V	D	Q	M	T	E	K	S	E	P	G	T	E	S	A	D	V	S	L	H	Q	L	A	D	I	Q	P	G	---	S	I	L	V	D	Q	M	T	E	K	S	E	P	G	T	E	S	A	D	V	S	L	H	Q	L	A	D	I	Q	P	G	---	S	I	L	V	D	Q	M	T	E	K	S	E	P	G	T	E

Search completed: October 7, 2006, 00:10:38  
Job time : 164 secs



GenCore version 5.1.9  
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OM nucleic - nucleic search, using sw model

Run on: October 10, 2006, 15:44:08 ; Search time 854 Seconds  
(without alignments)  
10954.970 Million cell updates/sec

Title: US-10-668-767-1\_COPY\_1\_5000

Perfect score: 5000

Sequence: 1 ctgaattcgaattcccatc.....ggtgaccaccagctaccact 5000

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents, NA:\*

- 1: /EMC\_Celerra\_SIDS3/ptodata/2/ina/1 COMB.seq.\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/2/ina/5 COMB.seq.\*
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- 9: /EMC\_Celerra\_SIDS3/ptodata/2/ina/RE COMB.seq.\*
- 10: /EMC\_Celerra\_SIDS3/ptodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description
1	869.4	17.4	15378	US-08-785-420-1 Sequence 1, Appli
2	840.8	16.8	4078	US-09-016-434-1154 Sequence 1154, Ap
3	809	16.2	15572	US-09-424-783-1 Sequence 1, Appli
4	65.6	1.3	1050	US-08-480-481-4 Sequence 4, Appli
5	64	1.3	1050	US-08-480-481-3 Sequence 3, Appli
6	53.6	1.1	1598	US-08-785-420-3 Sequence 31, Appli
7	51.6	1.0	7218	US-08-232-463-14 Sequence 14, Appli
8	51	1.0	900	US-08-480-481-6 Sequence 6, Appli
9	40.8	0.8	1334	US-09-668-097A-35 Sequence 35, Appli
10	39.4	0.8	294	US-09-252-991A-11838 Sequence 13, Appli
11	38.6	0.8	1768	US-09-485-529-13 Sequence 14, Appli
12	38.6	0.8	2125	US-09-485-529-14 Sequence 5066, Ap
13	38.2	0.8	1290	US-09-902-540-5006 Sequence 1036, Ap
14	38.2	0.8	12950	US-09-902-540-1036 Sequence 8976, Ap
15	37.6	0.8	399	US-09-621-976-8976 Sequence 31, Appli
16	37.6	0.8	1738	US-10-164-595-31 Sequence 15141, A
17	37.2	0.7	34534	US-09-949-016-15141 Sequence 18033, A
18	37	0.7	474	US-09-621-976-18033 Sequence 310, App
19	36.8	0.7	711	US-09-574-300-310 Sequence 8406, Ap
20	36.8	0.7	1599	US-09-902-540-8406 Sequence 882, App
21	36.8	0.7	7581	US-09-902-540-882 Sequence 1424, Ap
22	36.6	0.7	1750	US-10-104-047-1424 Sequence 306, App
23	36.4	0.7	650	US-09-533-559-306

Sequence 160, App  
Sequence 15, Appli  
Sequence 14999, A  
Sequence 15000, A  
Sequence 6077, Ap  
Sequence 6158, Ap  
Sequence 1, Appli  
Sequence 11354, A  
Sequence 11295, A  
Sequence 11374, A  
Sequence 6576, Ap  
Sequence 464, App  
Sequence 482, App  
Sequence 14172, A  
Sequence 7810, Ap  
Sequence 22, Appli  
Sequence 7948, Ap  
Sequence 1, Appli  
Sequence 2, Appli  
Sequence 7533, Ap  
Sequence 53, Appli  
Sequence 53, Appli

ALIGNMENTS

RESULT 1

US-08-785-420-1  
; Sequence 1, Application US/08785420  
; Patent No. 6001976  
; GENERAL INFORMATION:  
; APPLICANT: MacLennan, David H  
; APPLICANT: O'Brien, Peter J.  
; TITLE OF INVENTION: DIAGNOSIS FOR PORCINE MALIGNANT  
; TITLE OF INVENTION: HYPERTHERMIA  
; NUMBER OF SEQUENCES: 3  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Bell, Seltzer, Park & Gibson  
; STREET: P.O. Drawer 34009  
; CITY: Charlotte,  
; STATE: No. 6001976th Carolina 28234  
; COUNTRY: U.S.A.  
; ZIP: 28234  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/785,420  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/249,388  
; FILING DATE:  
; APPLICATION NUMBER: US 08/030,159  
; FILING DATE: 15-MAR-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Layton, Jr., Samuel G.  
; REGISTRATION NUMBER: 22807  
; REFERENCE/DOCKET NUMBER: 3477-73  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 704-377-1561  
; TELEFAX: 704-334-2014  
; TELEX: 57-5102  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15378 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)

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; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; IMMEDIATE SOURCE:
; CLONE: Porcine RYR1 Gene
; POSITION IN GENOME:
; UNITS: bp
US-08-785-420-1

Query Match      17.4%; Score 869.4; DB 3; Length 15378;
Best Local Similarity 55.3%; Pred. No. 4.6e-261;
Matches 2099; Conservative 0; Mismatches 1591; Indels 105; Gaps 17;

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QY 329 TGCAACGCTACGGTCTCAAGGAGCAGCTCAAGCTCTGCTGGCGCGGAGGCTTCGGC 376
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QY 199 TGCAACGCTACGGTCTCAAGGAGCAGCTCAAGCTCTGCTGGCGCGGAGGCTTCGGC 258
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QY 1151 CAGAAATGAGCTGATTAGTTAGCAGAGAGAAACCCACACAGCTTCTGTGCTTCTGCG 1210
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Qy 2462 CCGGTCAATAGGACTCATGCTGAAGAGCCTTATATTAGGAAAGGTGACGTGATAGTTGT 2521  
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Qy 2642 CTGAGTTGTCGGTTCCTCTGGCGGGAGAACACGGTGAACCTCCGTAACGGCTCCAGAA 2701  
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Db 2548 GGCTACGCCCTTGGCCAGAGCTGTCTCCACAGAGAGCACTCCGTCTGGAACCCATC 2607  
Qy 2762 TTCTACTTCGCAACCTGTCCAAAGCGG-----CCTTGGTGGACCCCGCTAGTACAG 2815  
Db 2608 AAGGAGTATCGCGAGAAGGGCCCGGGGACCCACCTGGTGGGGCCCGACGCGCTGCCTC 2667  
Qy 2816 GACGATACGGCTTTGTGCTTACGCTGTGATACTTTACAGATTAATCTGCTGCATACAT 2875  
Db 2668 TCACACACGACTTTGTGCTGCTGCGGTGGACACTGTCCAGATGTTCTGCTCTCCCAT 2727  
Qy 2876 GTGGAACAAATCAGACAGAAGTACTGAAATATTTCAAGAAATGTGGGCTATGAATAAG 2935  
Db 2728 CTGGAGCGTATCCGGAGAGCTGCGAGAGACATCCATGAACTCTGGCGCTGACGGCG 2787  
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Db 3088 CGGCTGGCGGAGAACCGGCACAACTGTGTGGGCGGAGACCGAGTGGCCCGAGGCTGGAGC 3147  
Qy 3293 TACGGAATTAATGAGGACTTCGGACATGATGATGATGATGATGATGATGATGATGATGATG 3352  
Db 3148 TACAGTGTGTGAGGACATCCAGCGCGCGCCGCAACCCCTCGCTCGCTCGCTCGCTCGCTG 3207

Qy 3353 GTTGACGATCCCATCAAGAAAGGCCAACAGGACACAGCCTCGGAGACTGTGAGACCCCTG 3412  
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Qy 3413 CTGGTCTACGGGTATATGCTGGACCCGCTTACTGGGAGCAGCATGAAGCACTCTTGTGTG 3472  
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Qy 3473 GAAGCGTCAAAACAGAAAGCAAGCGGACTTCAGAAATACACCGGCTGAGAAACATATGCC 3532  
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Db 3613 TTCAAGCTCAACGGCGAGGCTCTCATGTCCGACTTCGGGCTCTGAAACCGCTTCGGGAT 3672  
Qy 3833 GTCCAG--GTTGACAACTTTGTACCTGCTTGCACGCTTGTGTGCGGCAAAAAGCCAGG 3889  
Db 3673 ATCAGGTTGGGATGCTTCTCCGCTCTGAGCTTGGAGACCTGGCCAGGTGGGCCAC 3732  
Qy 3890 TTAACATACGCTCAGGAGCTGAACACGCTGAAATACCTTCAACATGTGGTGTGAGAG 3949  
Db 3733 CTGAACCTGGGCCAGGATGTGAGCTCCCTCGGTTCTTTGCCATCTCGGCGCTCCAGGAA 3792  
Qy 3950 GGATATGAACCAATCTGTGTCAATATGAAGAGAGAGCTGACTCAGTGTACACCAAGAC 4009  
Db 3793 GGTTTGAGCCTATCGCCATCAACATGAGCGCTCCCGTCTCACTCTGTTTTCAGCAAAAGC 3852  
Qy 4010 CAGCGATCTTCGAG 4024  
Db 3853 CTTCCCGAGTTTGAG 3867

## RESULT 2

US-09-016-434-1154  
; Sequence 1154, Application US/09016434  
; Patent No. 6500938  
; GENERAL INFORMATION:  
; APPLICANT: Janice Au-Young  
; APPLICANT: Jeffrey J. Seilhamer  
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING  
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION  
; NUMBER OF SEQUENCES: 1490  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
; STREET: 3174 PORTER DRIVE  
; CITY: PALO ALTO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
; CURRENT APPLICATION DATA:

```
; APPLICATION NUMBER: US/09/016.434
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1154:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4078 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g1526977
; US-09-016-434-1154

Query Match 16.8%; Score 840.8; DB 3; Length 4078;
Best Local Similarity 55.0%; Pred. No. 1.7e-252; Indels 101; Gaps 19;
Matches 2105; Conservative 0; Mismatches 1622;

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Qy 460 GCTTTCAGTAGAGCTTTACAGGATGGTAAACAGCTGCGGATCTGAACTG----- 512
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Qy 337 CCTCTCTGTGCGGGCGCTGCGAGGATGCTGGCTAAACCGTGGAGAAATCAGAAAGGCA 396
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Qy 811 TGGTGTATGTCCTCAGGTTGCTGTCATGGACATGGAACGAGTGTCTCATCTGCTCCCTTCAGG 870
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970 TTGGACAAAGGATGGGGGCAAAATATCGTAGTCTTACAAAGAGGTTTCACTGATGTCCTCA 1029
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871 AGAACATGTTGAAGACGACGCGGAGAACTGTTTATTATGAAGTGGCGCTGTGTCTGTTCA 930
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1051 AGCAAAACCTTCTACTCATGACAAAGAGAAAGCTGATGTAATAATCAACAGCATTTAC 1110
Qy 1210 CTTGCCCAGGAGAGGATGATCAGAAACAGTGTGTAGAGACAAGGACTTGGAGTTCAT 1269
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Qy 1390 GAAGCAAGCGATTTCTCCAGAGAAAGGCAAGATGGACGATGGCTCGACCTCTCCAGGTC 1449
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1288 TAAG---GCTATTATGCATCATGAAGGCCACATGGATGATGGCATAAAGTTTGTGAGATC 1344
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1465 TATAGAGTCG-----TAAGCCTAAGTCTGCGAGATCTCATTTGGCTACTTCCACCCCC 1518
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2707 CTCGCCGCTGGTAGTCTCTCTCCGCGCAGAGATCCTCAGCTGGAGCCGTG----- 2761  
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2941 ASCAGCTGGATGTAGCGGACACAGAGAAAGACTTGCACAAAGATCCACCCCTGCTCGT 3000  
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3061 ACTCAAGACTATCTGGCTCTGGGCTACTACTAT---CAGCTTAGATAAGCCTCCAGCAG 3117  
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3118 CATCCGCAAGTTCGCTGCTGCCCAATGAACCTTTTCATGCAAGTCCAGCGGTACAAGCCAGC 3177

2998 CAAGGTGAAAAAATGAAGCTACCCCAAGATTACCAGCTGACAAAGTGGATACAAAGCCTGC 3057  
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3058 CCCTATGACCTGAGCTTTTATCAAACTCACCCCATCGCAAGAACAAATGTTGGACAAGTT 3117  
3238 GGTGAGAACACCAACCTTTGGGCGAGGAGAGATACAGAGGATGAGATGATGATGATGATGATGAT 3297  
3118 GGCAGAAAATGCAATATGTTGGGCGCGGATCGAATCCGGAGGCTGGAATTTATG 3177  
3298 ACTTAATGAGGACTCGGACATGCTATCCCGCCTGCTGTCATACCCGAAGTTGA 3357  
3178 CATCAACAGACGCTAAGAACAGAAATCTCTGCTGTTTCCCTACATCTCTCTGGA 3237  
3358 CGATGCCATCAAGAAAGCCCAACAGGACACAGCCTCGGAGACTGTGAGGACCTCTGCTG 3417  
3238 TGACCGAACCAAGAAATCCCAACAGGACAGCCTCGGAGGCTGTGGCAGCCTGCTGCTGG 3297  
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3298 GTACGGCTACAACTTGAAGCAC-----AGATCAAGATCATGACGACGAGCCGAAGT 3351  
3478 GTCAAAACAGAAAGCCGACTTTCAGAACATACCGGCTGAGAAAGTATGCGTCTGAG 3537  
3352 GTGACGCGCACCGGGGAAAGGTTCCGAATCTTCCGTGCCGAGAAAGCTATGCAAGTGA 3411  
3538 CTCTGGAAGTGTACTTTCGAGTTTGAAGTCTTAAACGCTGAGCTATGAGGGTGGGCTG 3597  
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3598 GGCTCAGCTGATATGGACCAAGAAATGATCTCGGACAAAGACGAGAACTCTTGGGCTTT 3657  
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3589 GCAAGCAGCGCATGTCGTGGGGTGTATGGTTGATGATGATGATGATGATGATGATGATGATGAT 3648  
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3838 GGGTGACAA---CTTTGTACCTGCTTGCACGCTTGGTGTGCGCCCAAAAGCCAGTTAAC 3894  
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3895 ATACGGTCAGGACGTTGAACACGCTGAATACTTCAACATGTGTCTGCGAGGAGGATA 3954  
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4074 CTGGTTTCAGATACACTCCATCCCTCAAGATTTCCCAACACAGTTTG 4121  
3945 GCACCATAGACAGTTTCCCATGTTTAAAGGTCACTCAGAAAGTCTTTTG 3992

## RESULT 3

US-09-424-783-1  
; Sequence 1, Application US/09424783  
; Patent No. 6780608  
; GENERAL INFORMATION:  
; APPLICANT: Hakamata, Yasuhiro

APPLICANT:	Nishimura, Seichiro
APPLICANT:	Barsoumian, Edward Leon
TITLE OF INVENTION:	Human Type 3 Ryanodine Receptor Protein
TITLE OF INVENTION:	and DNA Molecules Coding Therefor
FILE REFERENCE:	0652.2000000
CURRENT APPLICATION NUMBER:	US/09/424,783
CURRENT FILING DATE:	1999-12-01
PRIOR APPLICATION NUMBER:	PCT/EP98/02926
PRIOR FILING DATE:	1998-05-18
PRIOR APPLICATION NUMBER:	DE 197 22 317.6
PRIOR FILING DATE:	1997-05-28
NUMBER OF SEQ ID NOS:	11
SOFTWARE:	Patentin version 3.1
SEQ ID NO 1	
LENGTH:	15572
TYPE:	DNA
ORGANISM:	Homo sapiens
US-09-424-783-1	
Query Match	16.2%; Score 809; DB 3; Length 15572;
Best Local Similarity	54.4%; Pred. No. 4.5e-242;
Matches 2112; Conservative	0; Mismatches 1665; Indels 104; Gaps 20;
Qy	346 GAGGGTGTGCTGCTGCGAGTCTCGGCAACCGGCACCTGCTTCCTGAGATAATTGC 405
Db	188 GAAGTTCTGCTGCGCAGCCGAGGACTTGGGAATCGCCTGTGCTTCTTGGAAACCCACTTC 247
Qy	406 CGA---CAAGAAACATACCCTGATCTGTCGACGTGTGTCTCATCGAAACAGGCGCT 462
Db	248 AGAAGCCAAATACATCTCTCAGATCTCTGGCTGCAATTTTGTGTCGAAACAGTCCCT 307
Qy	463 TTCAGTAAAGAGCTTTACAGGAGTTGGTAAACAGCTCGCGGATCTGAAACTCGGAAAGAAAA 522
Db	308 ATCTGTACAGAGCCCTGCAGGAATGCTTGCCAACACAGG-----TGAAATGCGG 358
Qy	523 CTTAGGTAAAGGTACCGGTTCTGGTTATCGTACGTAACGTAATGCTATTCTTTT 582
Db	359 CGAAGGGCAGCAACAAGAGGTGGCCACAGGACCCCTGTATACGGCCATCGAGTTCTCT 418
Qy	583 GCGACATCTTAAACAGTCATATGTAACCTGGCTGCTGTCACATCATATCCCAAG---GA 639
Db	419 GAGGCATCTTTACGGGAATGATATCAATGTTGACTACATCAAGATCCACAGACAGA 478
Qy	640 TAAGCTGGCCCTTTGACGTGGGTCTGCAACAGCACTCCCAAGGTGAAGCCCTGCTGGTGGAC 699
Db	479 CAAACTTGGCTTTGATGTAGTCTACGGGAACATGCCACAGGAAAGCCCTGTTGGTGGAC 538
Qy	700 CTTGCATCTGCGCAGCAAAACAGAGATCCGAGGGCGAGAGGTGCGAGTCGAGATGACTT 759
Db	539 TATACATCTCTCTTCCAAAACAGAGGTCCGAGGAGAGAAAAGTTCGAATTTGGCATGACCT 598
Qy	760 GATTCTAGTCTCCGTGGCCATTGAGAGATCTTGCACACACAGAAACAGAAAGTATC 819
Db	599 CATCCTCGTCAGCGGTGCTCTGAAAGATACCTTCATCTCTCAGTATCAATTGGTAACAT 658
Qy	820 GATAGTGAACCGCTCGTTCCACGTGACGCACATGCTCGGTACAGCCCTATGCTACTGGTAT 879
Db	659 ACAAGTGGATGCTCTTATATGCAACACCTGGAATGTACATCC-----TACGTGCTC 712
Qy	880 ATCAGAGATGAAGTATATGGGCTATGTTTCGGAGGTGATGTGCTCAGGTTCTTCCATGG 939
Db	713 AGGAAGTAGCATCGAAGAAGGATACCTACTTGGTGGGCATGTAGTAGCTCTTTTCCATGG 772
Qy	940 AGGTGACGAGTGTCTCATATACCTAGCACATTTGGACAAAGGATGGGGGGCAAAATATCGT 999
Db	773 TCATGATGAATGTTTTCAGTATACCATCTTACAGACAGAAATGATTTCCAGCACAGGAGAT 832
Qy	1000 AGTCTCAAAAGGAGGTTTCAGTATGTCCTCAAGCCCGTCTCTATGGCGCCCTGGAGCTGGC 1059
Db	833 ATTCTACGAGCTGGGGAGCTGGGACTCGAGCCAGGTCTCTTTGGAGAGTGGAAACCCCT 892
Qy	1060 TAGAACCAAGTGGGCGGAGGTTTCATTAACTGTGTAACATCTCTATAGGATTCGGACAT 1119

Qy	2194	AGATCAGGTATCTAGTTCGGTCCGAACATCTTCTGTGGGCCGAGTAGAAGGGTTCGGCAGT	2255
Db	1994	TAACGATGTAACAGTATCCGGCCAAACATCTTCTTGGGAGTCCGCGAGGGCTCAGCCCA	2053
Qy	2254	GTACCGCAAAATGGTACTTTCAGAGTGACTATGGACCACATAGAGAAGACC---ACACATAT	2310
Db	2054	GTACAAGAAGTGGTACTTTCAGCTGATATATCGACCAAGTGGACCCCTTCTCAACACGAGA	2113
Qy	2311	GATGCCACATCTACGCATAGGATGGGCTAAACATCTCTGGTTATGTCCCATACCCGGGTGG	2370
Db	2114	GCCACACATCTCGGGTGGGCTCTTCTTCAGGCTATGCCCATACCCAGAGG	2173
Qy	2371	TGTTGAGAAGTGGGGAGGTTAACCGCTGGGAGACGACTGTACTCTGTACGGGTTTGATGG	2430
Db	2174	TGGAGAAGGATGGGAGGCAATGGTGTGGTGAAGACCTGTACTCTCTATGGCTTTTGATGG	2233
Qy	2431	CGCCTACTCTGGTCCGGCGGAGGAAGACCCCGGTCAATAGGACTCATGTCTGAAGAGCC	2490
Db	2234	ACTTCACTTTGGTCAGCGCGGA-----TACCCAGAGCTGTGGCTTCATCAACACGACCC	2289
Qy	2491	TTATATTAGAAAGGTACGCTGATAGGTTGTGCAATTGGACCTGACGCTACCCATCATCAA	2550
Db	2290	TCCTGAGATCGGATGACGTGGTTAAGTGTCTGCTGGACCTCGGGGTGCCAGCATCTC	2349
Qy	2551	CTTCATGTTCAACGGAGTGGGGTGG-ACGGGATCTTTCAACAACTTCAATCTCGGAAGGCA	2609
Db	2350	ATTCCGCATCAATGGCGAGCCCGTGCAGGGGATGTTTGGAGAACTTCAACACAGACGGGC	2409
Qy	2610	TGTTCTTCCCGGTACATCAGCTGCTCTAGTAAGCTGAGTTGTCGGTTCCTGCTCGGCGGAG	2669
Db	2410	TCTTCTTCCCTGTGATGAGCTTTTCAGCAGGTTCAAGTACGTTTCTCTGATGGGTGGAC	2469
Qy	2670	AACACGGTATAGACTCCGGTACGCGCTCCAGAAAGCTACTCCCGCTGGTGGAGTCTCTCC	2729
Db	2470	GTCATGGAGAGTTTAAGTTCCTGCTCCCTCTGGCTATGCCCTTGCTATGAAGCCTTAC	2529
Qy	2730	TGCCCGACGAGATCCTCAGCCTGAGCGGTGC-----TTCCTACTTCGGCAACCTGTCCA	2783
Db	2530	TTCCAAAGAGAAGATGAGATTTGAGGCTGTCAAGAATAATAAACGTTGATGCTGATGGCA	2589
Qy	2784	AGCGGCTTGGCTGGACCCCGCTAGTCAGAGCAGATACGGCTTTTGTGCCCTACGCTG	2843
Db	2590	TTAGAGATCTCTTGGGTACACCAGTTCCTCTCCAAGCTCTTTCATCCCATGCCCG	2649
Qy	2844	TTGATACTTTACAGATTACTCTGCCTACATATGTGGAACAAATACAGAGCAAGCTAGCTG	2903
Db	2650	TAGACACAGTCAGGTTATTTTGGCCACTCACCTTAGAAAAGATCCGAGACAGACTAGCTG	2709
Qy	2904	AAATATTACAGAAATGTGGCTATGAATAAGATCGAAGCAGGCTGGATGTACGGCGACC	2963
Db	2710	AAAAATCTCCATGAGCTTTGGGGAAATGAATAAAATAGAACTTTGGCTGGACTTTTCGGCAAGA	2769
Qy	2964	AGAGAAGAGCTTGCACAAGATCCACCCCTGCTCTGTCGCTTCGACGCACTCCCGCCCG	3023
Db	2770	TACGAGATGACAATAAAGACAACACCTTGCCTTGTGGAGTTTCAAAGCTCCAGAAA	2829
Qy	3024	CTGAGAAACGATACGATATACAACTTCTGTGCAGACACTCAAGACTATCCTGGCTCTGG	3083
Db	2830	CTGAGAAGAACTATAAACCCTGCAAAATGTCAACTGAAAACCTTAAAAACCTCTTGACCCCTGG	2889
Qy	3084	GCTACTACATCAGCTTAGATTAAGC-----CTCCAGACCGCATCCGCAACGTTCTGTGCCCA	3140
Db	2890	GTTGCCACATTTGCTCATGTTTAAACCAGCTGCTGAGGAGGATCTCAAGAAGGTCAAACTGC	2949
Qy	3141	ATGAACCTTTTCATGCGAGTCCAAACGGCTACAAGCCAGCAACCACTCGACTCGAGTGTGTCA	3200
Db	2950	CCAAAACATATATGATGTCCAAACGGCTATAAGCCAGCCCTTTTGGATTTGTCTGATGTGA	3009
Qy	3201	CCCTGACACCCAGATGGAATGAGCTAGTAGGCCAGTGGGTGAGAACACCCCAACACCTTTT	3260
Db	3010	AGCTGTTACCTTCCTCAAGAAATTTTATGTGATAAGCTTGCAGAAAAATGCAACAATGTTT	3069

Qy	3261	GGGCCAGGAGAGGATACACACGGATGGACTTACCGGACTTAATGAGGACTCGGCATGC	33232
Db	3070	GGGCNAAGACAGAAATAAAACAAGGATGGACCTATGGCATCCAAACGAGATTTTGAAGAACA	31299
Qy	3321	ATCGATCCCGCACCTGGTGCCCATACCCGAAGGTTGACAGATGCGCATCAAGAAAGCCCAACA	3380
Db	3130	AAAGAAATCCCGTCTGGTGCCCATATGCCATTACTGGATGAGCGTACCAAGAAGTCAAACA	3189
Qy	3381	GGGACAGACGCTCGGAGACTGTGAGGACCCCTGCTGGTCTACGGGTATATGCTGGACCCGC	3440
Db	3190	GGGACAGCCTGCGGGAAGCTGTGCGCACTTTTGTGGTTACGGGTATAACATTGAGCCAT	3249
Qy	3441	CTACTGGGAGCAGCATGAAGCACTCTTGTGGAGGCTCAAAACAGAACGACGCGACT	3500
Db	3250	C-----AGACCAAGAACTAGCTGACTCGGCTGTGGAGNAGGTCAGCATAGACAAGA	3300
Qy	3501	TCAGAACATACCGCGCTGAGAAGAACTATGCCGTGACTCTCGGAAGTGTGACTTCCAGT	3560
Db	3301	TCCGATTTTCCGGGTAGAGCGATCTTATCCAGTGAGATCTGGANAAGTGGTATTTTGAGT	3360
Qy	3561	TTGAGATCTTAAACGCTGGACCTATGAGGCTCGGCTGGGCTCACGCTGATATGGCACCCAG	3620
Db	3361	TTGAAGTGGTGACTGGAGGAGACATCGAGTCTGGCTGGCGGAGGCCAGGCTGTCAGCCTG	3420
Qy	3621	GAATGATGCTCGGACAAAGACAGAACTCTCTGGGCTTTTGATGTTACATGAGGAAAAAG	3680
Db	3421	ATGTCGAGCTGGGGCCCGATGACCAAGCCCTTTGTGTTGAAGCAACAGCGGGCCAGCGTT	3480
Qy	3681	TGTACAGCGGTAAACACTGAGTCTTTCCGCAAGCAATGGGCTGTTGGTGACGTAGTGGGGG	3740
Db	3481	GGCATCAAGG---AAGTGGGTATTTTGGGCGTACCTGGCAGCCAGGGGATGTGTCGAT	3537
Qy	3741	TGTTCTTAGATCTCATTTGATAAGACGATAAGTTTCTCACTCAACGGTGAAGTGTGTTGATGG	3800
Db	3538	GTATGATTAACCTGGATGATGCTTCAATGATCTTCACACTGAATGGGGAGCTGCTGATCA	3597
Qy	3801	ATGCTCTTGGCGAGAGACTACGTTTCTGATGTCCAGGGTGACAA---CTTTGTACTCG	3857
Db	3598	CCAAACAAAGGCTCTGAACCTTGCCCTTCGCTGACTACGAGATTGGAATGGGCTTCGTGCCCA	3657
Qy	3858	CTTGACGCTGGGTGCGGCCAAAGCCAGGTTTAAATACCGTTCAGGACGTTGAACACGC	3917
Db	3658	TCTGCTGTGGGTCTATCTTCAGATCGGCCGATGAATCTCGGACAGATGCCAGTACTCT	3717
Qy	3918	TGAAATACTTCACAACTGTGGTCTGCAGGAGGATATGAACCAATCTGTGTCATATGA	3977
Db	3718	TCAAGTTTATACCATGTGGGTCTCCAAGAGGCTTTGAGCCCTTTTGTCTGCTCAACATGA	3777
Qy	3978	AGAGAGCTGACTCACTGTGTACCAAAAGACAGCCGATCTTCGAGAAATCGGATGAGA	4037
Db	3778	ACAGAGATGTGCTATGTGGTTTCAGCAAGGCGCTCCCGACGTTTGTCAA---CGTGCCAA	3834
Qy	4038	TGATCGACACAGAAATAGATGTGACAGGATACCGAGCTGGTTTCAGATACACCTCCATGCC	4097
Db	3835	AGGATCATCCACACATAGAGGTCAATGAGGATTTGATGGCAACATGGACAGCCCTCCGTGTC	3894
Qy	4098	TCAAGATTTTCCCAACACCGTTTTCAGAC---GATGGAGAAAGCTTAACCTGGAGTCTTTC	4154
Db	3895	TCAAGGTGACCATTAAGACATTTGGCACACAGATAGCAATGCCACATGATCTATTGCC	3954
Qy	4155	GTCTCTCACTGCCCTGTCACTGCGCATTAACGAGTTTCATTGAC	4195
Db	3955	GCTTGAGCATGCGCTGTGGATGGCCACTCTCTCTTCAGTCACTC	3995

RESULT 4  
US-08-480-481-4  
; Sequence 4, Application US/08480481  
; Patent No. 5639614  
; GENERAL INFORMATION:  
; APPLICANT: Sen, Luyi  
; APPLICANT: Phillipson, Kenneth D  
; APPLICANT: Lugsis, Aldons J.



## TITLE OF INVENTION: GENE MUTATION IN PATIENTS WITH IDIOPATHIC DILATED CARD

NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Knobbe, Martens, Olson & Bear  
STREET: 620 Newport Center Drive 16th Floor  
CITY: Newport Beach  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 92660  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/480,481  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Altman, Daniel E  
REGISTRATION NUMBER: 34,115  
REFERENCE/DOCKET NUMBER: UCLA012.001A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 714-760-0404  
TELEFAX: 714-760-9502  
TELEX:  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1050 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: Genomic DNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
FEATURE:  
NAME/KEY: Other  
LOCATION: 380...380  
OTHER INFORMATION: Position distinguishes idiopathic  
OTHER INFORMATION: dilated cardiomyopathy  
NAME/KEY: Other  
LOCATION: 776...776  
OTHER INFORMATION: Position distinguishes idiopathic  
OTHER INFORMATION: dilated cardiomyopathy  
NAME/KEY: Other  
LOCATION: 1...1  
OTHER INFORMATION: Position 1 corresponds to  
OTHER INFORMATION: 7987 of the rabbit cDNA homolog  
US-08-480-481-4

Query Match 1.3%; Score 65.6; DB 2; Length 1050;  
Best Local Similarity 48.2%; Pred. No. 2.8e-09;  
Matches 237; Conservative 0; Mismatches 234; Indels 21; Gaps 1;  
Qy 2828 TTGTGCTACGCTGTGTGATACCTTACAGATTACTCTGCTACATATGTGGACAAATC 2887  
Db 118 TTTAACCCCAACCTGTGTGATACCTCAATATATAATTTCTGAGAGTTGGAAATCTTC 177  
Qy 2888 AGAGACAGCTAGCTGAAATATTACGAAATGTGGCTATGAATAAGATCGAAGCAGGC 2947  
Db 178 ATTAACAATATGAGAACATCTTCATGACAAATGGTCAATGGCAAGTTAGCAATGGA 237  
Qy 2948 TGGATGTACGGCGACCGAGAGAGACTTGCACAAAGATCCACCCCTGCTGTCCTTC 3007  
Db 238 TGGATTTATGAGAAATATATTACAGACTCTCCCAAGATTCAACCTTGTGTAACCATAT 297  
Qy 3008 GAGGACTCCCGCGCTGAGAAACGATACATATACAACTTGTGTGCGACACTCAAG 3067

Db 298 ABACTATTATCTGAAAGGAAAAAATTTATCGCTGGCCAAATCAAAGAATCTCTCAA 357  
Qy 3068 ACTATCTCTGCTCTGGCTACTACAT-----CAGCTTAGATAAG 3106  
Db 358 ACTATGTGGCTTTGGGTTTGAAGAATTTGAAGAACCCTCCAGAGGAGACACGATGGCCCTT 417  
Qy 3107 CTCCAGCAGCATCGCAACGTTTCTGCTGCCCAATGAACCTTTTCATGTCAGTCCCAACGGC 3166  
Db 418 TATAACCGAACTCGTGTATTTCTCAGAACAGCCAGGTTTCTGTAGATGCTGCCCATGGT 477  
Qy 3167 TACAAGCCAGCACCACCTCGACCTGAGTGTGTCACTGACCCCAAGATGGATGAGCTA 3226  
Db 478 TATAGTCCCGAGCCATTGACATGAGCAATGTTTACACTATCCAGAGACCTGCACTATG 537  
Qy 3227 GTAGGCCAGCTGCTGAGAACACCCCAACCTTTGGCCAGGAGAGATACAGCAGGA 3286  
Db 538 GCAGAAATGATGCTGTAACACTATATACATATGGGCAAGAAAAAGAACTGGAGTTG 597  
Qy 3287 TGGACTTACGGA 3298  
Db 598 GAGCTAAAGGA 609

## RESULT 5

US-08-480-481-3  
Sequence 3, Application US/08480481  
Patent No. 5639614  
GENERAL INFORMATION:  
APPLICANT: Sen, Luyi  
APPLICANT: Philipson, Kenneth D.  
APPLICANT: Luisi, Aldons J.  
TITLE OF INVENTION: GENE MUTATION IN PATIENTS WITH IDIOPATHIC DILATED CARD  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Knobbe, Martens, Olson & Bear  
STREET: 620 Newport Center Drive 16th Floor  
CITY: Newport Beach  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 92660  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/480,481  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Altman, Daniel E  
REGISTRATION NUMBER: 34,115  
REFERENCE/DOCKET NUMBER: UCLA012.001A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 714-760-0404  
TELEFAX: 714-760-9502  
TELEX:  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1050 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: Genomic DNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
FEATURE:  
NAME/KEY: Other

[illegible]



Db 305 TTTCTGTAGTGTGCCCATGTTTATAGTCTCCCGAGCCATTGACATGAGCAATGTTTACAC 364  
Qy 3204 TGACACCAAGATGGATGAGCTAGTAGGCCAGCTGGCTGAGAACACCCACAACTTTGGG 3263  
Db 365 TATCAGAGACTGCTATGCTATGCGAGAAATGATGGCTGAAAATATCATTAACATATGGG 424  
Qy 3264 CCAGGAGAGATACAGCAGGAGTGGACTTACGGA 3298  
Db 425 CAAGAAAAGAACTGGAGTTGGAGTCTAAAGGA 459

## RESULT 9

US-09-668-097A-35

; Sequence 35, Application US/09668097A

; Patent No. 667398

; GENERAL INFORMATION:

; APPLICANT: Cahoon, Edgar B.

; APPLICANT: Cahoon, Rebecca E.

; APPLICANT: Klein, Ted

; APPLICANT: Shen, Jennie

; TITLE OF INVENTION: Plant Lipases

; FILE REFERENCE: B1401 US NA

; CURRENT APPLICATION NUMBER: US/09/668,097A

; PRIOR FILING DATE: 2000-09-22

; PRIOR APPLICATION NUMBER: 60/157309

; PRIOR FILING DATE: 1999-10-01

; NUMBER OF SEQ ID NOS: 41

; SOFTWARE: Microsoft Office 97

; SEQ ID NO 35

; LENGTH: 1334

; TYPE: DNA

; ORGANISM: Triticum aestivum

US-09-668-097A-35

Query Match 0.8%; Score 40.8; DB 3; Length 1334;  
Best Local Similarity 58.1%; Pred. No. 0.21;  
Matches 72; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

Qy 1864 CAACACAGCACTGCGCGCAGTTGCGGAACCTGCAACCGTTCAACTGGCTGTTCTCGCG 1923  
Db 728 CAACGCGCGCACTACGACCACTAGCGTCTGAAGCGGTTCAACGCGCTGTGCGCCG 787  
Qy 1924 CTTGGCTCGAGGCTCGCGGAGGCGACCGGATGCTGCAAGTGTGCACTGCACTCT 1983  
Db 788 CCACAACTCGTGTCTCCAGAGCAAGTGACCAAGCTGAGGCGCAAGTACCCCTAGCCAA 847  
Qy 1984 CATC 1987  
Db 848 GATC 851

## RESULT 10

US-09-252-991A-11838

; Sequence 11838, Application US/09252991A

; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 11838

; LENGTH: 294

; TYPE: DNA

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-11838

Query Match 0.8%; Score 39.4; DB 3; Length 294;  
Best Local Similarity 52.8%; Pred. No. 0.19;  
Matches 85; Conservative 0; Mismatches 76; Indels 0; Gaps 0;

Qy 3280 GCAGGGATGACCTTACGAGCTTAATGAGGACTCGGACATGCATCGATCCCGCACCTGGT 3339  
Db 84 GCAGCAGCACCTTACGAGCCCAACCCGGAATCGAATCGCTCGCCAGCAGCTACGTGGA 143  
Qy 3340 GCCATACCCGAAGTTGACGATGCCATCAAGAAGGCCAACAGGAGACACAGCTTCGAGAC 3399  
Db 144 AGGGCGCTGGACATGCCCGGGTGATCTACAAGACCGACTGTGGAGCGCTGTGGGAT 203  
Qy 3400 TGTGAGGAGCCCTGCTGTGTGTACGGGTATATGCTGGACCCGC 3440  
Db 204 CGTCCCGCGCGCTGTGTCTACGAGGACTCGCAGGGCGAGC 244

## RESULT 11

US-09-485-529-13

; Sequence 13, Application US/09485529

; Patent No. 6762348

; GENERAL INFORMATION:

; APPLICANT: Harberd, Nicholas P

; APPLICANT: Richards, Donald E

; APPLICANT: Peng, Jinrong

; TITLE OF INVENTION: Genetic Control of Plant Growth and Development

; FILE REFERENCE: 620-91

; CURRENT APPLICATION NUMBER: US/09/485,529

; PRIOR FILING DATE: 2000-03-01

; PRIOR APPLICATION NUMBER: PCT/GB98/02383

; PRIOR FILING DATE: 1998-08-07

; PRIOR APPLICATION NUMBER: GB 9717192.0

; PRIOR FILING DATE: 1997-08-13

; NUMBER OF SEQ ID NOS: 108

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 13

; LENGTH: 1768

; TYPE: DNA

; ORGANISM: Triticum aestivum

US-09-485-529-13

Query Match 0.8%; Score 38.6; DB 3; Length 1768;  
Best Local Similarity 47.6%; Pred. No. 1.2;  
Matches 147; Conservative 0; Mismatches 159; Indels 3; Gaps 1;

Qy 1873 GAACCTGCGCGCAGTTGCGGAACCTGCAACCGGTTCAACTGGCTGTTCTCGCGCTCGGCTC 1932  
Db 573 GAAGTCCGCCAGTTGCGGCACACCATCCGGTGCATTCAGTACCGCGCTCGTCCG 632  
Qy 1933 GCAGGCTCGGGCGAGGCGACCGGCATGCTCGAGCTGCTGCACTTCATCGACTC 1992  
Db 633 ---CGCCACGCTCGGGACCTGGAGCCGTTTCATCTGCAGCGGAGGAGGAGCC 689  
Qy 1993 GCCTGAAGCGCTCAATATGATGAGGAGCGAACAATAAAGTATATCTCTTATTAGA 2052  
Db 690 GAACGAGGAGCCGAGGTAATCGCGTCAACTAGTCTTCGAGATGCACCGGCTGCTCGC 749  
Qy 2053 AAAGCAGGCGCGACCCCTAAAGTACTAGATGCTATGTTCACTCTCGCTCGGTAACGG 2112  
Db 750 GCAGCCCGCGCCCTTGAGAAAGGTCCTGGGACCGCTGCGCCCGTGGCGCCAGGATCGT 809  
Qy 2113 CGTCCGCTGCGCTCGTTCACAGAAACATCTGGGACTATTTGCTGCCCGCAAGAACCT 2172  
Db 810 CACGCTGTTGAGCAGGAGGCGGATCACTCCGGCACATCTCTGGAGCGCTTCACCGA 869  
Qy 2173 GTTCTGCA 2181  
Db 870 GTCTTGCA 878

## RESULT 12

US-09-485-529-14

; Sequence 14, Application US/09485529

```
; Patent No. 6762348
; GENERAL INFORMATION:
; APPLICANT: Harberd, Nicholas P
; APPLICANT: Richards, Donald E
; APPLICANT: Peng, Jinrong
; TITLE OF INVENTION: Genetic Control of Plant Growth and Development
; FILE REFERENCE: 620-91
; CURRENT APPLICATION NUMBER: US/09/485,529
; CURRENT FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: PCT/GB98/02383
; PRIOR FILING DATE: 1998-08-07
; PRIOR APPLICATION NUMBER: GB 9717192.0
; PRIOR FILING DATE: 1997-08-13
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 2125
; TYPE: DNA
; ORGANISM: Triticum aestivum
; US-09-485-529-14

Query Match      0.8%; Score 38.6; DB 3; Length 2125;
Best Local Similarity 47.6%; Pred. No. 1.4;
Matches 147; Conservative 0; Mismatches 159; Indels 3; Gaps 1;

Qy 1873 GAATCGCGCGAGTTCGGGAACCTCGAACCAGTTCAACTGGCTGTCTCGCGCCTCGGCTC 1932
Db 1194 GAAGCTCGCCAGTTTCGGGCACACCATCCGGCTCGACTTCAGTACCGCGCCCTCGTCGC 1253
Qy 1933 GCAGCGCTCGGGCGAGGCGACCGCATGCTCGAGCTGTGTGACATCTCTCATCGACTC 1992
Db 1254 ---GCCACAGCTCGGAGACCTGGAGCCGTTTCATCTCGAGCGCGGAGGCGGAGNAGACC 1310
Qy 1993 GCCTGAAGCGCTCAATATGATAGGGGACGAACACATAAAGTGAATATCTCTATTAGA 2052
Db 1311 GAACGAGGAGCGCGAGGTAAATCGCGTCAACTAGTCTTCGAGATGACCGGCTGTCTCGC 1370
Qy 2053 AAACGAGGAGCGGACCCCTAAAGTACTAGATGTGTCTATGTTCACTCTCGCTCGTAACGG 2112
Db 1371 GCAGCCCGCGCCCTTGAGAAAGTCTTGGGACACGTCGCGCGCGTGTGGCCCGCAGGATCGT 1430
Qy 2113 CGTCGCGTGGCTCGTCACAGAAACATCTGGAGCTATTGTCTGCCCGGCAAGAACCT 2172
Db 1431 CACGCTGTGAGGAGGAGGCGGAATCAACTCCGGCACATCTCTGGACCGCTTCAACCGA 1490
Qy 2173 GTTGCTGCA 2181
Db 1491 GTCTCTGCA 1499

RESULT 13
US-09-502-540-5006
; Sequence 5006, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/502,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 5006
; LENGTH: 1290
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
; US-09-502-540-5006

Query Match      0.8%; Score 38.2; DB 3; Length 1290;
Best Local Similarity 47.6%; Pred. No. 1.4;
Matches 147; Conservative 0; Mismatches 159; Indels 3; Gaps 1;
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Best Local Similarity 56.4%; Pred. No. 1.3;
Matches 92; Conservative 0; Mismatches 68; Indels 3; Gaps 1;

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Db 906 CAACACAGAACTGAGCGCGTTTCAGCGGCAACGAGTACCGGGTGGGCACGCTGTCTCGCCAG 965
Qy 1924 CCTCGGCTCGCAGCGCTCGGGCGAGGGCACCGGCATGCTCGAGTGTCTGCACTGCACTCCT 1983
Db 966 CGGCTCTTACCAGGCC---GGCGAGGCCACCGGTCAACGGAGCTGTCTGTGGCGGCAT 1022
Qy 1984 CATCGACTCGCCTGAAGCGCTCAATATGATGAGGGACGAACAC 2026
Db 1023 CGTCCGCTCGTACACAGCAGCAGACGACGACGCCCGGCTC 1065

RESULT 14
US-09-902-540-1036
; Sequence 1036, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1036
; LENGTH: 12950
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
; NAME/KEY: unsure
; LOCATION: (1)..(12950)
; OTHER INFORMATION: unsure at all n locations
; US-09-902-540-1036

Query Match      0.8%; Score 38.2; DB 3; Length 12950;
Best Local Similarity 56.4%; Pred. No. 7.1;
Matches 92; Conservative 0; Mismatches 68; Indels 3; Gaps 1;

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Qy 1924 CCTCGGCTCGCAGCGCTCGGGCGAGGGCACCGGCATGCTCGAGTGTCTGCACTGCACTCCT 1983
Db 1367 CGGCTCTTACCAGGCC---GGCGAGGCCACCGGTCAACGGAGCTGTCTGTGGCGGCAT 1423
Qy 1984 CATCGACTCGCCTGAAGCGCTCAATATGATGAGGGACGAACAC 2026
Db 1424 CGTCCGCTCGTACACAGCAGCAGACGACGACGCCCGGCTC 1466

RESULT 15
US-09-621-976-8976
; Sequence 8976, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
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; SEQ ID NO 8976
; LENGTH: 399
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-8976

Query Match      0.8%; Score 37.8; DB 3; Length 399;
Best Local Similarity 10.5%; Pred. No. 0.75;
Matches 24; Conservative 114; Mismatches 91; Indels 0; Gaps 0;

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Qy 4176 GCCATAACGAGTTCATTGACGAGCGACGAAAAAGGACGCGCTGGGTGAGAAATCAAGGACC 4235
Db 90 SWMTYMTRRWRYRYRKACTKWPAAGCWGKAGWAWYAKWYMWAWRPTAMKYWAMKS 149
Qy 4236 GCCAACGGATCTTAATGAAAGAGCGACTTGAAGCTCAGATGTCCGCCATATTTGACGAGA 4295
Db 150 KRSRRRRRAWYAWMYMMARRTTMGMRASCYRGAYMASAGWYMMYMMYMMRRKWMYSAGW 209
Qy 4296 TCATGAGAGCGGTTTCACCATGAACGATATTAAAGGTTTGCACCTACGA 4344
Db 210 SMREKWTTRRACYSYCSWSSYCNWGAAGKMMYWKTSRWSYWSYRCTKYRR 258

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GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

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Perfect score: 5000

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Total number of hits satisfying chosen parameters: 37784340

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Listing first 45 summaries

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16: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11D\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	5000	100.0	15679	US-10-668-767-1	Sequence 1, Appli
2	4570.8	91.4	15429	US-10-668-767-143	Sequence 143, App
3	4501.6	90.0	15405	US-10-668-767-129	Sequence 129, App
4	4472.8	89.5	15387	US-10-668-767-127	Sequence 127, App
5	4288.8	85.8	15303	US-10-668-767-145	Sequence 145, App
6	2185.8	43.7	16363	US-10-668-767-9	Sequence 9, Appli
7	2158.2	43.2	15606	US-11-097-143-22562	Sequence 22562, A
8	2078.2	41.6	15413	US-10-668-767-7	Sequence 7, Appli
9	1846	36.9	15845	US-10-668-767-3	Sequence 3, Appli
10	1835.2	36.7	15315	US-10-668-767-5	Sequence 5, Appli
11	1455.8	29.1	24236	US-11-097-143-22561	Sequence 22561, A
12	840.8	16.8	4078	US-10-305-720-1154	Sequence 1154, Ap
13	840.8	16.8	14302	US-10-276-774-552	Sequence 552, App
14	840.8	16.8	15731	US-10-887-553A-490	Sequence 490, App
15	831.4	16.6	15359	US-10-276-774-500	Sequence 500, App
16	831.4	16.6	15359	US-10-887-553A-489	Sequence 489, App
17	831.4	16.6	15359	US-10-450-763-4960	Sequence 4960, Ap

Sequence 48, Appli  
Sequence 491, App  
Sequence 1500, Ap  
Sequence 12305, A  
Sequence 2337, A  
Sequence 5796, Ap  
Sequence 17, Appli  
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Sequence 18, Appli  
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821.4 16.4 15564 15 US-11-000-688-1500  
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809 16.2 15820 10 US-10-450-763-23337  
801.2 16.0 15453 9 US-10-723-860-5796  
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686.8 13.7 3168 15 US-11-044-111-18  
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130.6 2.6 636 15 US-11-044-111-19  
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86.4 1.7 643 6 US-10-027-632-51124  
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86.4 1.7 1800 10 US-10-450-763-23334  
71.6 1.4 595 12 US-10-301-480-261241  
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#### ALIGNMENTS

#### RESULT 1

US-10-668-767-1  
; Sequence 1, Application US/10668767  
; Publication No. US20040171114A1  
; GENERAL INFORMATION:  
; APPLICANT: Caspar, Timothy  
; APPLICANT: Cordova, Daniel  
; APPLICANT: Gutteridge, Steven  
; APPLICANT: Rauh, James  
; APPLICANT: Smith, Rejane  
; APPLICANT: Tao, Yong  
; APPLICANT: Wu, Lihong  
; TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors  
; FILE REFERENCE: B01533 US NA  
; CURRENT APPLICATION NUMBER: US/10/668,767  
; CURRENT FILING DATE: 2003-09-23  
; PRIOR APPLICATION NUMBER: 60/412,795  
; PRIOR FILING DATE: 2002-09-23  
; PRIOR APPLICATION NUMBER: 60/427,324  
; PRIOR FILING DATE: 2002-11-18  
; NUMBER OF SEQ ID NOS: 149  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 15679  
; TYPE: DNA  
; ORGANISM: Heliothis virescens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (251)..(15676)  
; OTHER INFORMATION:  
; FEATURE:  
; NAME/KEY: misc.feature  
; LOCATION: (5515)  
; OTHER INFORMATION: n = c or g  
; FEATURE:  
; NAME/KEY: misc.feature  
; LOCATION: (13000)  
; OTHER INFORMATION: n = a or t  
US-10-668-767-1

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Best Local Similarity		100.0%;	Pred. No. 0;		
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Qy	61	TTATGGGACGTGTGATTATTTCCGAATTTAGAAATCATTTAGTGTGTGTGAACCGTTAAAAATG	120		
Db	61	TTATGGGACGTGTGATTATTTCCGAATTTAGAAATCATTTAGTGTGTGTGAACCGTTAAAAATG	120		
Qy	121	TGTTAAACAGTCGCGTCAGCGCTTGATCCAGAAAAACCGATTTATTTGTGCGTTTGAACG	180		
Db	121	TGTTAAACAGTCGCGTCAGCGCTTGATCCAGAAAAACCGATTTATTTGTGCGTTTGAACG	180		
Qy	181	CATGTGTGATGCATTTTCGAGTGTATGGCAACCGTTGCAGTAAGGCACCTGACGCTACTG	240		
Db	181	CATGTGTGATGCATTTTCGAGTGTATGGCAACCGTTGCAGTAAGGCACCTGACGCTACTG	240		
Qy	241	AGAAATCAAAGATGGCGAAGCAGAGGGGGGAGCAAGCGAGCAAGATCATGTTTCAATCTT	300		
Db	241	AGAAATCAAAGATGGCGAAGCAGAGGGGGGAGCAAGCGAGCAAGATCATGTTTCAATCTT	300		
Qy	301	CGGTACGGAAAGACATGGTGTGCATGTCGTCACAGCGACAGGAGGGGTGTCCTGGC	360		
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Db	361	TGCCGAAGGTCTCGGCCAACCGGCACCTGCTTCCTGGAGAANTATGCCCACAAAGACATACC	420		
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Qy	481	GGAGTTGGTAAACAGCTCGGGATCTGAAACTGGGAAAGAAACTTAGGTAAAGTACCGG	540		
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Db	781	TGAGAGATCTTGCACACACGAAGAGACGAAGTATCGATAGTGAACCGCTGTTTCCA	840		
Qy	841	CGTGACGCACCTGGTCCGTACAGCCCTATGGTACTGTTATTCGAGGATGAAGTATGTGGG	900		
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Qy	901	CTATGTGTTCGGAGGTGATGTCTCAGGTTCCTCCATGGAGGTGACGAGTGTCTCACTAT	960		
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Qy	961	ACCTAGACATTTGGACAAAGGATGGGGGGCAAAATATCGTAGTCTACAAAGGAGTTTCAGT	1020		
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Qy	1021	GATGTCTCAAGCCCGTTCTCTATTCGGCGCTGGAGCTGGCTAGAACCAAGTGGGCGGAGG	1080		



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Qy 4321 CGATATTAAAGGTTTGCACTACGAAGCAATCAGGAAGAGTTGCCAGCTCCAGATGAA 4380
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Db |||||
Qy 4381 GCGCTGCTCTCAAGGCCACCAAGGATCCATGACAAAGAGGTGTACTATACAAA 4440
Db |||||
Qy 4381 GCGCTGCTCTCAAGGCCACCAAGGATCCATGACAAAGAGGTGTACTATACAAA 4440
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Qy 4441 TTACAATAATTGCAACAGGCCAAGTCAACGGGATGACCGGTGCGACCAAGTGA 4500
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Qy 4501 AATGCCAAGTATGACTTTGGGAGCGCAAGTTTCAACGCTGATGATGAAGAGGCAAGAG 4560
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Qy 4501 AATGCCAAGTATGACTTTGGGAGCGCAAGTTTCAACGCTGATGATGAAGAGGCAAGAG 4560
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RESULT 2

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US-10-668-767-143
; Sequence 143, Application US/10668767
; Publication No. US2004017114A1
; GENERAL INFORMATION:
; APPLICANT: Caspar, Timothy
; APPLICANT: Cordova, Daniel
; APPLICANT: Gutteridge, Steven
; APPLICANT: Rauh, James
; APPLICANT: Smith, Rejane
; APPLICANT: Tao, Yong
; APPLICANT: Wu, Lihong
; TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors
; FILE REFERENCE: B1533 US NA
; CURRENT APPLICATION NUMBER: US/10/668,767
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: 60/412,795
; PRIOR FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: 60/427,324
; PRIOR FILING DATE: 2002-11-18
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 143
; LENGTH: 15429

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; TYPE: DNA
; ORGANISM: Heliothis virescens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(15429)
; OTHER INFORMATION:
; FEATURE:
; OTHER INFORMATION: pXL-Hv3
US-10-668-767-143

Query Match      91.4%; Score 4570.8; DB 8; Length 15429;
Best Local Similarity 97.6%; Pred. No. 0;
Matches 4638; Conservative 0; Mismatches 112; Indels 0; Gaps 0;

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Db 1 ATGCGCGAAGCAGAGGGGGAGCAAGCGAGCAGAGATGATGTTTCAATCTTCGCTACCGAA 60
Qy 311 GACATGCTGTGCATGTCTGCACAGCGACAGAGGAGAGGGTGTGCCTGGCTGCCGAAGGT 370
Db 61 GACATGCTGTGCCTGTCTGCACAGCGACAGAGGAGAGGGTGTGCCTGGCTGCCGAAGGT 120
Qy 371 CTCGGCAACCGGCACCTGCTTCTCGAGAAATATTTGCCGACAAAGACATACCGCTGTACTG 430
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Qy 431 TCCAGTGTGTGTTTGTATCGAAACAGGCGCTTTCAGTAAGAGCTTTACAGGAGTTGGTA 490
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Qy 491 ACAGCTGCGGAGTCTGAAACTGGGAAAGAAACTTAGGTAAAGGTACCGGTCTCTGGTTAT 550
Db 241 ACAGCTGCGGCTTCTGAAACTGGGAAAGAAACTTAGGTAAAGGTACCGGTCTCTGGTTAT 300
Qy 551 CGTACGCTACTATACGCGCAATGCTATTTCTTCCGACATCTTAAAGTATGATGATGATGATG 610
Db 301 CGTACGCTACTATACGCGCAATGCTATTTCTTCCGACATCTTAAAGTATGATGATGATGATG 360
Qy 611 GCCTGCTGTCAACATCATCCAGGATTAAGCTGGCCTTTGACGTTGGGTCTGCAACAG 670
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Qy 671 CACTCCCAAGGTCAAGCTGCTGCTGAGACCTCTGATCTCCAGCAAAACAGAGATCCGAG 730
Db 421 CACTCCCAAGGTCAAGCTGCTGCTGAGACCTCTGATCTCCAGCAAAACAGAGATCCGAG 480
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Db 481 GGTGAGAAGGTGCGAGTCCGAGATGATGATTTCTAGTCTCCGTTGGCCATTTGAGAGATAC 540
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Qy 911 GGAGGTGATGTGCTCAGGTTCTTTCCATGGAGGTGACGAGTGTCTCACTATACCTTAGCACT 970
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Qy 1091 TGGTACCATCTATGAGGATTCGGCACATCATCACTGAGAGATATCTTGGAGTTAAACGAC 1150
Db 841 TGGTACCATCTATGAGGATTCGGCACATCATCACTGAGAGATATCTTGGAGTTAAACGAC 900

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Qy	1151	CAGAAATGAGCTGATTTAGTTAGCAGAGAGAACCCACAAAGCTTCTGTGCTTCTG	1210
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Qy	1211	CTGCGCCAGGAGAGGATGATCAGAAAGCAAGTGTGTAGAAAGCAAGGACTTGGAGGTCA	1270
Db	961	CTGCGTACAGGAGAGGAGTATCAGAAACAAAGTGTGTAGAAAGCAAGGACTTGGAGGTCA	1020
Qy	1271	GGCGGCCCATCATCAAGTACGGTACCTCCACCGTCAATTTGCGAGCATTCGGAGACTGGC	1330
Db	1021	GGCGGCCCATCATCAAGTACGGTACCTCCACCGTCAATTTGCGAGCATTCGGAGACTGGC	1080
Qy	1331	TTGTGGCTGTCTTATAAGTCTTACGAAACGAGAGAAAGCGTGGGTAAAGTAAAGAG	1390
Db	1081	TTGTGGCTGTCTTATAAGTCTTACGAAACGAGAGAAAGCGTGGGTAAAGTAAAGAG	1140
Qy	1391	AAGCAAGCGATTTCTCACAGAGAAAGGCAAGATGGACGATGGCTCGACCTTCCAGGTCA	1450
Db	1141	AAGCAAGCGATTTCTCACAGAGAAAGGCAAGATGGACGATGGCTCGACCTTCCAGGTCA	1200
Qy	1451	CAGAGGAAGAAATCTATGACTGCTCGAGTTATCAGGAAGTGTCTTCTGCTGTCTACTAAG	1510
Db	1201	CAGAGGAAGAAATCTATGACTGCTCGAGTTATCAGGAAGTGTCTTCTGCTGTCTACTAAG	1260
Qy	1511	TTTATCAATGGCTGGGAACTCTTCAAGAGAACCGTCTGATGCTCTTCTGCGTCA	1570
Db	1261	TTTATCAATGGCTGGGAACTCTTCAAGAGAACCGTCTGATGCTCTTCTGCGTCA	1320
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Db	1321	GTGAACCTGGGCGAGATGATGTGTCTTGAAGATCTCACAACTACTTGGCAGAGCC	1380
Qy	1631	GATGAGGATATGGAAACAGAAAGAAAGCAAAATTTCCGGCCCTCCGGAAACCGTCAAG	1690
Db	1381	GATGAGGATATGGAAACAGAAAGAAAGCAAAATTTCCGGCCCTCCGGAAACCGTCAAG	1440
Qy	1691	GACCTGTTCAGAGAGGAGGATCTGAACCTGATCTCGAGCTATAGACAAAGATCAAC	1750
Db	1441	GACCTGTTCAGAGAGGAGGATCTGAACCTGATCTCGAGCTATAGACAAAGATCAAC	1500
Qy	1751	FTCGTCAAGTCCAGGGGTTCTGGCTGATTCCTGGCGGGAGAGCAATCTGGAAGAGC	1810
Db	1501	GTCAATCAAGTCCAGGGGTTCTGGCTGATTCCTGGCGGGAGAGCAATCTGGAAGAGC	1560
Qy	1811	TGGGAAATGATATCTGGATATTTGATCAGTTGCTGGCGGCAATTAATAAGGCAACAC	1870
Db	1561	TGGGAAATGATATCTGGATATTTGATCAGTTGCTGGCGGCAATTAATAAGGCAACAC	1620
Qy	1871	ACGAATCGGCGGAGTTCGCGAACTCGAACCGGTTCACTGGCTGTTCTCGGCTCGGC	1930
Db	1621	ACGAATCGGCGGAGTTCGCGAACTCGAACCGGTTCACTGGCTGTTCTCGGCTCGGC	1680
Qy	1931	TCGCAAGGCTCGGCGAGGGACCGGATGCTCGACGCTGCTGCACTGCACTCTCATCGAC	1990
Db	1681	TCGCAAGGCTCGGCGAGGGACCGGATGCTCGACGCTGCTGCACTGCGTGTCTATCGAC	1740
Qy	1991	TCGCTGAGAGCGCTCAATATGATAGGAGCGAACACATATAAAGTGAATCTCTCTATTA	2050
Db	1741	TCGCTGAGAGCGCTCAATATGATAGGAGCGAACACATATAAAGTGAATCTCTCTATTA	1800
Qy	2051	GAAGAAGCAGGACCGGACCTTAAGTACTAGATGTGCTATGTTCACTCTGCGTGGTAAC	2110
Db	1801	GAAGAAGCAGGACCGGACCTTAAGTACTAGATGTGCTATGTTCACTCTGCGTGGTAAC	1860
Qy	2111	GGCGTGGGCTGGCTCGTCAAGAACCAATCTCGACTATTTGCTGCGCGGCAAGAAC	2170
Db	1861	GGCGTGGGCTGGCTCGTCAAGAACCAATCTCGACTATTTGCTGCGCGGCAAGAAC	1920
Qy	2171	CTGTTGCTGCAAACTCGCTTGTAGATCAAGTATCTAGTGTCCGTCGGAACATCTTCGTG	2230
Db	1921	CTGTTGCTGCAAACTCGCTTGTAGATCAAGTATCTAGTGTCCGTCGGAACATCTTCGTG	1980

Qy	2231	GGCGAGTAGAAGGGTCGGCAGTGTACCGCAAAATGGTACTTTCGAGGTGACTATGAGACCAC	2290
Db	1981	GGTCAAGTAGAAGGGTCGGCAGTGTACCGCAAAATGGTACTTTCGAGGTGACTATGAGACCAC	2040
Qy	2291	ATAGAGAAGACCAACACATATGATGCGCATACGATAGGATGGGCTAACACACTACTGGT	2350
Db	2041	ATAGAGAAGACCAACACATATGATGCGCATACGATAGGATGGGCTAACACACTACTGGC	2100
Qy	2351	TATGTCCTCATACCCGGTGGTGGAGAGTGGGGAGGTAAACCGCGTGGGAGAGACGACCTG	2410
Db	2101	TACGTCCCATACCCGGTGGTGGAGAGTGGGGAGGTAAACCGCGTGGGAGAGACGACCTG	2160
Qy	2411	TACTCTGACGGGTTGATGGCGCTTACTCTGTGTCGGCGGAGAGAACCCCGGTCAAT	2470
Db	2161	TACTCTGACGGGTTGATGGCGCTTACTCTGTGTCGGCGGAGAGAACCCCGGTCAAT	2220
Qy	2471	AGGACTCATGCTGAAGCCCTTATATTAGGAAGAGGTGACGTGATAGGTTGTCATGGAC	2530
Db	2221	AGGACTCATGCTGAAGCCCTTATATTAGGAAGAGGTGACGTGATAGGTTGTCATGGAC	2280
Qy	2531	CTGACGGTACCCATCATCAACTTCTCATGTTCAAACGGAGTGGGGTGAACGGGATCTCTCAC	2590
Db	2281	CTGACGGTACCCATCATCAACTTCTCATGTTCAAACGGAGTGGGGTGAACGGGATCTCTCAC	2340
Qy	2591	AACCTTCAATCTGGAAGGATGTTCTTCCGGTCTATCAGCTGCTCTAGTAAAGCTGAGTTGT	2650
Db	2341	AACCTTCAATCTGGAAGGATGTTCTTCCGGTCTATCAGCTGCTCTAGTAAAGCTGAGTTGT	2400
Qy	2651	CGGTTCTGTCGGCGGAGAAACAGCGTAGACTCTCGGTACCGGCTCCAGAGGCTACTTCC	2710
Db	2401	CGGTTCTGTCGGCGGAGAAACAGCGTAGACTCTCGGTACCGGCTCCAGAGGCTACTTCC	2460
Qy	2711	CCGCTGTGTGAGTCTCTCTGCGCAGCAGATCTCTCAGCTGGAGCCGCTCTTACTTTC	2770
Db	2461	CCGCTGTGTGAGTCTCTCTGCGCAGCAGATCTCTCAGCTGGAGCCGCTCTTACTTTC	2520
Qy	2771	GGCAACCTGTCCAAAGCGGGCTTGGCTGGACCCCGCTAGTACAGGACGATACGGCTTTT	2830
Db	2521	GGCAACCTGTCCAAAGCGGGCTTGGCTGGACCCCGCTAGTACAGGACGATACGGCTTTT	2580
Qy	2831	GTGCTACGCTGTTGATATCTTTACAGATTTACTCTGCTCTATATATGTTGGAACAAATCAGA	2890
Db	2581	GTGCTACGCTGTTGATATCTTTACAGATTTACTCTGCTCTATATATGTTGGAACAAATCAGA	2640
Qy	2891	GACAAGCTAGCTGAAATATTTACGAAATGTGGCTATGAATAAGATCGAAGCAGGCTGG	2950
Db	2641	GACAAGCTAGCTGAAATATTTACGAAATGTGGCTATGAATAAGATCGAAGCAGGCTGG	2700
Qy	2951	ATGTACGGCGACACAGAGAGAGACTTGCACAAGATCCACCCCTGCTCTGCTGCTTCGAG	3010
Db	2701	ATGTACGGCGACACAGAGAGAGACTTGCACAAGATCCACCCCTGCTCTGCTGCTTCGAG	2760
Qy	3011	CGACTCCCGCGCTGAGAAACGATACGATATACACTTGTCTGTGTCAGACACTCAAGACT	3070
Db	2761	CGCTCCCGCGCTGAGAAACGATACGATATACACTTGTCTGTGTCAGACACTCAAGACA	2820
Qy	3071	ATCTGCTCTGCGCTTACTATCAGCTTAGATAGCCCTCCAGCAGCATCCGCAACGTT	3130
Db	2821	ATCTGCTCTGCGCTTACTATCAGCTTAGATAGCCCTCCAGCAGCATCCGCAACGTT	2880
Qy	3131	CGTCTGCCCAATGAACCTTTTCATGCGTCCCAACCGGCTCAAGCCAGCACCCTCGACCTG	3190
Db	2881	CGTCTGCCCAACGAACTTTTCATGCGTCCCAACCGGCTCAAGCCAGCACCCTCGACCTG	2940
Qy	3191	AGTGTGTCACTCTGACACCCAAAGATGATGAGCTAGTAGGCCAGCTGGCTGAGAACACC	3250
Db	2941	GGTGTGTCACTCTGACACCCAAAGATGATGAGCTAGTAGGCCAGCTGGCTGAGAACACC	3000
Qy	3251	CACACCTTTGGCCAGGAGGAGATACAGCAGGGATGAGCTTACGGACTTAATGAGGAC	3310
Db	3001	CACACCTTTGGCCAGGAGGAGATACAGCAGGGATGAGCTTACGGACTTAATGAGGAC	3060
Qy	3311	TCGGACATGTCATCCGCTCCCGCACCTGTGTGCATACCCGAGAGGTTTGACGATCCATCAAG	3370

Db 3061 TCGACATGCATCCCGCCTCTGGTCCATACCCGGAAGGTTGACGATGCCATCAAG 3120  
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Db 4991 CAGTACCCT 5000  
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RESULT 3  
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; Sequence 129, Application US/10668767  
; Publication No. US20040171114A1  
; GENERAL INFORMATION:  
; APPLICANT: Caspar, Timothy  
; APPLICANT: Cordova, Daniel  
; APPLICANT: Gutteridge, Steven  
; APPLICANT: Rauh, James  
; APPLICANT: Smith, Rejane  
; APPLICANT: Tao, Yong  
; APPLICANT: Wu, Lihong  
; TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors  
; FILE REFERENCE: B51533 US NA  
; CURRENT APPLICATION NUMBER: US/10/668,767  
; CURRENT FILING DATE: 2003-09-23  
; PRIOR APPLICATION NUMBER: 60/412,795  
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; PRIOR APPLICATION NUMBER: 60/427,324  
; PRIOR FILING DATE: 2002-11-18  
; NUMBER OF SEQ ID NOS: 149  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 129  
; LENGTH: 15405  
; TYPE: DNA  
; ORGANISM: Heliothis virescens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(15402)  
; OTHER INFORMATION:

FEATURE:  
OTHER INFORMATION: pXL-HV2  
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Best Local Similarity 97.1%; Pred. No. 0;  
Matches 4614; Conservative 0; Mismatches 109; Indels 27; Gaps 2;

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QY 311 GACATGTTGTCATGTCGTGACAGCGACGAGAGAGGGTGTGCTCGCTGCCGAAGGT 370  
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DB 121 TTGGGCAACCGGCACTGCTTCTGTGAGAAATATTTGCCGACAGAAATACCCGCTGATCTG 180  
QY 431 TCGCAGTGTGTTTGTGTCATCGAACAGCGCTTTTCAGTAAGAGCTTTTACAGAGTTGGTA 490  
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DB 346 GCCTGCTGTCAACATCATCTCCAGGATGAGCTGGCTTTGAGCTGGGTCTGCAACAG 405  
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QY 1991 TCGCCTGAAGCGCTCAATATGATGAGGAGCAACACATATAAAGTGAATATCTCTATTA 2050  
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Db 2206 AGGACTCATGCTGAAGAGCCTTATATAGGAAGGTGACGTGATAGTGTGTGCGTTAGAC 2265  
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Db 2266 CTGACGCTACCCATCATCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTT 2325  
Qy 2591 AACTTCAATCTGGAAGGCATGTTCTTCCCGGTCACTAGCTGCTCTAGTAAAGCTGAGTTGT 2650  
Db 2326 AACTTCAATCTGGAAGGCATGTTCTTCCCGGTCACTAGCTGCTCTAGTAAATGAGTTGC 2385  
Qy 2651 CGGTTCTGCTGGCGGAGAACACGGTAGACTCCGGTACCGGCTCCAGAAAGGTACTCC 2710  
Db 2386 CGGTTCTGCTGGCGGGAACAATGGTAGACTCCGGTACCGGCTCCAGAAAGGTACTCC 2445  
Qy 2711 CCGCTGTGGAGTCTCTCTGCGCGCAGAGATCCTGAGCCTGGAGCGTCTTACTCTTC 2770  
Db 2446 CCGCTGTGGAGTCTCTCTGCGCGCAGAGATCCTGAGCCTGGAGCGTCTTACTCTTC 2505  
Qy 2771 GGCAACCTGTCCAAGCGGCTTGGCTGGACCCCGCTAGTACAGGACGATACGGCTTTT 2830  
Db 2506 GGCAACCTGTCCAAGCGGCTTGGCTGGAGCCCGCTAGTACAGGACGATACGGCTTTT 2565  
Qy 2831 GTGCTACGCTGTGTGATCTTTACAGATTACTCTGCTACATATGTGGAACAAATCAGA 2890  
Db 2566 GTGCTACGCTGTGTGATCTTTACAGATTACTCTGCTACATATGTGGAACAAATCAGA 2625  
Qy 2891 GACAGCTAGCTGAAATATTCAGAAATGTGGCTATGATAGATCGAAGCAGGCTGG 2950  
Db 2626 GACAAGCTAGCTGAAATATTCAGAAATGTGGCTATGATAGATCGAAGCAGGCTGG 2685  
Qy 2951 ATGTACGGCACGAGAGAAGACTTGCACAAGATCCACCCCTGCTCGTCCCTTCGAG 3010  
Db 2686 ATGTACGGCGATCAGAGAGAAGACTTGCACAAGATCCACCCCTGCTCGTCCCTTCGAG 2745  
Qy 3011 CGACTCCCGCCGCTGAGAAACGATACGATATACAACTTGTGTGACAGACACTCAAGACT 3070  
Db 2746 CGTCTCCCGCCGCTGAGAAACGATACGATATACAACTTGTGTGACAGACACTCAAGACA 2805  
Qy 3071 ATCTGGGCTCTGGGCTACTACATCAGCTTAGATAAGCTCCAGCACGATCCCGCAACGTT 3130  
Db 2806 ATCTGGGCTCTGGGCTACTACATCAGCTTAGATAAGCTCCAGCACGATCCCGCAACGTT 2865  
Qy 3131 CGTCTGCCCAATGAACCTTTTATCAGTCCAGTCCAAAGCTTACAGCCAGCACCTCGACCTG 3190  
Db 2866 CGTCTGCCCAACGAACTTTTATCAGTCCAGTCCAAAGCTTACAGCCAGCACCTCGACCTG 2925  
Qy 3191 AGTCTGTCACTCTGACACCCAGATGGATGAGCTAGTAGGCCAGCTGGCTGAGAACACC 3250  
Db 2926 AGTCTGTCACTCTGACACCCAGATGGATGAGCTAGTAGGCCAGCTGGCTGAGAACACC 2985  
Qy 3251 CACAACCTTTGGGCCAGGAGAGATACAGCAGGGATGGACTTACGACACTTATAGAGGAC 3310  
Db 2986 CACAACCTTTGGGCCAGGAGAGATACAGCAGGGATGGACTTACGACACTTATAGAGGAC 3045  
Qy 3311 TCGACATGATTCGATCCCGCACCTGTGTGCATACCCGAGGTTGACGATGCCATCAAG 3370  
Db 3046 TCGACATGATTCGATCCCGCACCTGTGTGCATACCCGAGGTTGACGATGCCATCAAG 3105  
Qy 3371 AAGGCCAACAGGACACAGCCTCGGAGACTGTGAGGACCCCTGCTGGTCTACGGGTATATG 3430  
Db 3106 AAGGCCAACAGGACACAGCCTCGGAGACTGTGAGGACCCCTGCTGGTCTACGGGTATATG 3165

Qy 3431 CTGGACCCCGCTACTCTGGGAGCAGCATGAAGCACTCTTGTGTGAAGCGTCAAAACAGAAG 3490  
Db 3166 CTGGACCCCGCTACTCTGGGAGCAGCATGAAGCACTCTTGTGTGAAGCGTCAAAACAGAAG 3225  
Qy 3491 CAAAGCGACTTTCAGAACATACCGCGCTGAGAGAACTATGCCCTCAGCTCTCGGAACTGG 3550  
Db 3226 CAAAGCGACTTTCAGAACATACCGCGCTGAGAGAACTATGCCCTCAGCTCTCGGAACTGG 3285  
Qy 3551 TACTTTCGAGTTTTCAGAACATACCGCGCTGAGAGAACTATGCCCTCAGCTCTCGGAACTGG 3610  
Db 3286 TACTTTCGAGTTTTCAGAACATACCGCGCTGAGAGAACTATGCCCTCAGCTCTCGGAACTGG 3345  
Qy 3611 ATGGCACCAAGGAATGATGCTCGGACCAAGACGAGAACTCTCTGGGCTTTTGTATGGTTACAAT 3670  
Db 3346 ATGGCACCAAGGAATGATGCTCGGACCAAGACGAGAACTCTCTGGGCTTTTGTATGGTTACAAT 3405  
Qy 3671 GAGGAAAAAGTGTACAGCGGTAACTACAGTCTTTTCGGCAAGCAANTGGGCTGTGTGTGAC 3730  
Db 3406 GAGGAAAAAGTGTACAGCGGTAACTACAGTCTTTTCGGCAAGCAANTGGGCTGTGTGTGAC 3465  
Qy 3731 GTAGTGGGGGTGTTCCCTAGATCTCATTGATAAGACGATAGTTTCTCAGCTCAACGGTGAG 3790  
Db 3466 GTAGTGGGGGTGTTCCCTAGATCTCATTGATAAGACGATAGTTTCTCAGCTCAACGGTGAG 3525  
Qy 3791 TTGTTGATGGATGCTCTTGGCGGAGAGACTACGTTTGTCTGATGTCAGGGTGACAACTTT 3850  
Db 3526 TTATTTGATGGATGCTCTTGGCGGAGAGACTACGTTTGTCTGATGTCAGGGTGACAACTTT 3585  
Qy 3851 GTACTGCTTGTGACGCTTGTGTCGCGCAAAAAGCAGGTTAACTACCGTCAAGGAGCTG 3910  
Db 3586 GTACTGCTTGTGACGCTTGTGTCGCGCAAAAAGCAGGTTAACTACCGTCAAGGAGCTA 3645  
Qy 3911 AACACCTGAAATACCTTCAACATCTGCTCTCAGGAGGATATGAACCACTTCTGTGTC 3970  
Db 3646 AACACCTGAAATACCTTCAACATCTGCTCTCAGGAGGATATGAACCACTTCTGTGTC 3705  
Qy 3971 AATATGAAGAGAGACGCTGACTCACTGGTACACCAAGACCCAGCCGATCTTCGAGAAATACG 4030  
Db 3706 AATATGAAGAGAGACGCTGACTCACTGGTACACCAAGACCCAGCCGATCTTCGAGAAATACG 3765  
Qy 4031 GATGAGATGATCGACACCGAATAGATGTGACCGAGATACCACTGGTTCCAGATACACCT 4090  
Db 3766 GATGAGATGATCGACACCGAATAGATGTGACCGAGTACCACTGGTTCCAGATACACCT 3825  
Qy 4091 CCATGGCTCAAGATTTCCCAACACGTTTGGACCGATGGAGAAAGCTAACTGGGAGTTC 4150  
Db 3826 CCATGGCTCAAGATTTCCCAACACGTTTGGACCGATGGAGAAAGCTAACTGGGAGTTC 3885  
Qy 4151 TTACGCTCTCTCACTGCTGCTCATCTGCCATAACGAGTTTCACTGACGAGGAGGAGGAGGAGG 4210  
Db 3886 TTACGCTCTCTCACTGCTGCTCATCTGCCATAACGAGTTTCACTGACGAGGAGGAGGAGGAGG 3945  
Qy 4211 AGCGTTGGGTAGAAATCAAGGACCGCAACCGGATCTTAATGAAGAGGAGGAGGAGGAGGAGG 4270  
Db 3946 AGCGTTGGGTAGAAATCAAGGACCGCAACAGATCTTAATGAAGAGGAGGAGGAGGAGGAGG 4005  
Qy 4271 CAGATGTCGCGCCATATTGACCGAGATCATGAGGCGGTTTCCACCAATGAAGAGGAGGAGGAGG 4330  
Db 4006 CAGATGTCGCGCCATATTGACCGAGATCATGAGGCGGTTTCCACCAATGAAGAGGAGGAGGAGG 4065  
Qy 4331 GGTTCGACCTTACCAAGACAAATCAGGAAGAGTTCGCCAGCTCCCAAGATGAAGAGGAGGAGGAGG 4390  
Db 4066 GGTTCGACCTTACCAAGACAAATCAGGAAGAGTTCGCCAGCTCCCAAGATGAAGAGGAGGAGGAGG 4125  
Qy 4391 TCAAGGCCACCAAGTAAAGGATCCATGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 4450  
Db 4126 TCAAGGCCACCAAGTAAAGGATCCATGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 4185  
Qy 4451 TTGCAACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 4510  
Db 4186 TTGCAACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 4245

QY 4511 TATGACTTGGGAGCCAAAGTTTGTGACGCTGATGATTAAGAGGACAAAGAGGGGACGATCG 4570  
 DB 4246 TATGACTTGGGAGCCAAAGTTTGTGACGCTGATGATTAAGAGGACAAAGAGGGGACGATCG 4305  
 QY 4571 CTTTCAAGTTCTTTCAGAGCAAGCGCGGCGGAGAGGAGTGTGCTGCTAAATCCCGTAAA 4630  
 DB 4306 CTTTCAAGTTCTTTCAGAGCAAGCGCGGCGGAGAGGAGTGTGCTGCTAAATCCCGTAAA 4365  
 QY 4631 TCCAAAACACAGACCCCTTTCAGTGATACCGAAGTATCACCAAGAACGTTGGTGTCTCGAAGG 4690  
 DB 4366 TCCAAAACCTCCAGATCCCTTTCAGCGATACCGAGGTATCACCAAGAACGTTGGTGTCTCGAAGG 4425  
 QY 4691 CTTAACCTTCAGATCAAGTGTACAGGCGCAATCAAGATATAACCGGATGAACGCGGT 4750  
 DB 4456 CTTAACCTTCAGATCAAGTGTACAGGCGCAATCAAGATATAACCGGATGAACGCGGT 4485  
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 DB 4486 CCTACGAGCAACCTGTATGGGAGCCAAAGTTTGTGAACTCGAACGCTCAGATGGG 4533  
 QY 4811 AGCGCCACGCAAGACAGGAAGCAGATGACACGACACTCTCGCGCAGTGGCTACGGAA 4870  
 DB 4534 AGCGCCACGCAAGACAGGAAGCAGATGACACGACACTCTCGCGCAGTGGCTACGGAA 4593  
 QY 4871 ACTGTGCGCAATGAGATCTTCGATCGAGAGTGTGTTGAAGCTCATCAATGAGTACTTTTAT 4930  
 DB 4594 ACTGTGCGCAATGAGATCTTCGATCGAGAGTGTGTTGAAGCTCATCAATGAGTACTTTTAT 4653  
 QY 4931 GGAGTCAGATCTACCGAGTCAAGACCCCAACCCCATGTATACGCTGGTGGTGAACCC 4990  
 DB 4654 GGAGTCAGATCTACCGAGTCAAGACCCCAACCCCATGTATACGCTGGTGGTGAACCC 4713  
 QY 4991 CAGTACCCT 5000  
 DB 4714 CAGTACCCT 4723

RESULT 4

US-10-668-767-127  
 ; Sequence 127, Application US/10668767  
 ; Publication No. US20040171114A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Caspar, Timothy  
 ; APPLICANT: Cordova, Daniel  
 ; APPLICANT: Gutteridge, Steven  
 ; APPLICANT: Rauh, James  
 ; APPLICANT: Smith, Rejane  
 ; APPLICANT: Tao, Yong  
 ; APPLICANT: Wu, Lihong  
 ; TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors  
 ; FILE REFERENCE: B01533 US NA  
 ; CURRENT APPLICATION NUMBER: US/10/668,767  
 ; CURRENT FILING DATE: 2003-09-23  
 ; PRIOR APPLICATION NUMBER: 60/412,795  
 ; PRIOR FILING DATE: 2002-09-23  
 ; PRIOR APPLICATION NUMBER: 60/427,324  
 ; PRIOR FILING DATE: 2002-11-18  
 ; NUMBER OF SEQ ID NOS: 149  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 127  
 ; LENGTH: 15387  
 ; TYPE: DNA  
 ; ORGANISM: Heliothis virescens  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (1)..(15384)  
 ; OTHER INFORMATION:  
 ; FEATURE:  
 ; OTHER INFORMATION: pXL-Hv7  
 US-10-668-767-127

Query Match 89.5%; Score 4472.8; DB 8; Length 15387;  
 Best Local Similarity 96.8%; Pred. No. 0;

Matches 4596; Conservative 0; Mismatches 127; Indels 27; Gaps 2;  
 QY 251 ATGCGGAAGCAGAGGGGGAGCAAGCAGCAAGATGATGTTTCAATCTTCGCGTACGAA 310  
 DB 1 ATGCGGAAGCAGAGGGGGAGCAAGCAGCAAGATGATGTTTCAATCTTCGCGTACGAA 60  
 QY 311 GACATGTTGTCATGTCGTGCACAGCAGAGAGAGGGTGTGCTGGCTGCCGAAGGT 370  
 DB 61 GACATGTTGTCATGTCGTGCACAGCAGAGAGAGGGTGTGCTGGCTGCCGAAGGT 120  
 QY 371 CTGCGCAACCGGCACTGCTTCTCGGAGAAATATTCGCCACAAGAAACATACCCCTGATCTG 430  
 DB 121 TTCCGCAACCGGCACTGCTTCTCGGAGAAATATTCGCCACAAGAAACATACCCCTGATCTG 180  
 QY 431 TCGCAGTGTGTGTTGTGTCATCGAACAGCGCTTTTCAGTAAAGAGCTTTACAGAGTGTGTA 490  
 DB 181 TCGCAGTGTGTGTTGTGTCATCGAACAGCGCTTTTCAGTAAAGAGCTTTACAGAGTGTGTA 240  
 QY 491 ACAGTCGGGATCTGAAACCTGGGAAAGAAACCTTAAAGGTACCGGTTCTGGTTAT 550  
 DB 241 ACAGTCGGGCTCTGAAACT-----GGTAAAGGTACCGGTTCTGGTTAT 285  
 QY 551 CGTACGCTACTATACGGCAATGCTATTCTTTGCGACATCTTAACAGTGATATGACCTG 610  
 DB 286 CGTACGCTACTATACGGCAATGCTATTCTTTGCGACATCTTAACAGTGATATGACCTG 345  
 QY 611 GCCTGCCTGTCAACATCATATCCAGGATAAGCTGGCCTTTGACGTGGGTCTGCAACAG 670  
 DB 346 GCCTGCCTGTCAACATCATATCCAGGATAAGCTGGCCTTTGACGTGGGTCTGCAACAG 405  
 QY 671 CACTCCCAAGGTGAAGCCTGCTGTGGAACCTGCTGTCGCAAGCAACAGAGATCCGAG 730  
 DB 406 CACTCCCAAGGTGAAGCCTGCTGTGGAACCTGCTGTCGCAAGCAACAGAGATCCGAG 465  
 QY 731 GCGAGAAAGGTGCGAGTCGGAGATGACTTGATTCTAGTCTCCGTGGCCATGAGAGTAC 790  
 DB 466 GGTGAGAAAGGTGCGAGTCGGAGTGAAGTGAATCTGCTCCGTGGCTACTGAGAGATAC 525  
 QY 791 TTGCACACAAAGAGAGAAAGTATCGATAGTGAACGGCTCGTTCCACGTGACGAC 850  
 DB 526 TTGCACACAAAGAGAGAAAGTATCGATAGTGAACGGCTCGTTCCACGTGACGAC 585  
 QY 851 TGGTCCGTACAGCCCTATGTTGATATCGAGGATGAAGTATGTCGGCTATGTTTC 910  
 DB 586 TGGTCCGTACAGCCCTATGTTGATATCGAGGATGAAGTATGTTAGGCTATGTTATTC 645  
 QY 911 GGAGTGATGTCCTCAGGTTCTTCATGGAGGTGACGAGTGTCTCATTACTACCTAGCCT 970  
 DB 646 GGAGTGATGTCCTCAGGTTCTTCATGGAGGTGACGAGTGTCTCATTACTACCTAGCCT 705  
 QY 971 TGGCAAAAGGATGGGGGCAAAATATCGTAGTCTACAAAGAGGTTTCAGTGTCTCAA 1030  
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 QY 1031 GCCCGTTCTCTATGGCGCTCGAGCTGGCTGAGAACCAAGTGGCGGCGAGGTTTCAATTAAC 1090  
 DB 766 GCCCGTTCTCTATGGCGCTCGAGCTGGCTGAGAACCAAGTGGCGGCGAGGTTTCAATTAAC 825  
 QY 1091 TGGTACCATCCTATGAGGATTCGGCACTACTCTGGAAGATATCTTGGAGTTAAACGAC 1150  
 DB 826 TGGTACCATCCTATGAGGATTCGGCACTACTCTGGAAGATATCTTGGAGTTAAACGAC 885  
 QY 1151 CAGATGAGCTGTTTATTTAGTTAGCAGAGAGAACCCCAACAGCTTCTGTCCTTCTGC 1210  
 DB 886 CAGATGAGCTGTTTATTTAGTTAGCAGAGAGAACCCCAACAGCTTCTGTCCTTCTGC 945  
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 DB 946 CTGCGCCAGGAGAGGATGATCAGAAAGCAAGTGTGTAGAGCAAGGACTTGGAGTCTATA 1005  
 QY 1271 GCGCGCCCATCATCAAGTACGGTGAATCCACCGTCAATGTGTCAGACATTCGAGACTGCG 1330  
 DB 1006 GCGCGCCCATCATCAAGTACGGTGAATCCACCGTCAATGTGTCAGACATTCGAGACTGCG 1065

QY	1331	TTGTGGCTGTCTTATAGTCTTACGAAACGAAGAAGAAAGCGGTGGTAAAGTAGAAGAG	1390
Db	1066	TTGTGGCTGTCTTATAAGTCTTACGAAACGAAGAAGAAAGGAGTGGGTAAAGTAGAAGAG	1125
QY	1391	AAGCAAGCGATTCTCCACAGGAGGAAGCAAGATGAGCATGGCTTCGACCTCTCCAGGTCA	1450
Db	1126	AAGCAAGCGATTCTCCACAGGAGGAAGCAAGATGAGCATGGCTTCGACCTCTCCAGGTCA	1185
QY	1451	CAGGAGAAGAACTATGACTGTCTCGAGTTATCAGGAAGTGTCTTTCGCTGTTCCTAAG	1510
Db	1186	CAGGAGAAGAACTATGAGTGTCTCGAGTTATCAGGAAGTGTCTTTCGCTGTTCCTAAG	1245
QY	1511	TTTATCAATGGCTGGGAAACTCTTCAAGAGAAACCGTGTCTCACTCGATGTTCTTCGGGTCA	1570
Db	1246	TTTATCAATGGCTGGGAAACTCTTCAAGAGAAACCGTGTCTCACTCGATGTTCTTCGGGTCA	1305
QY	1571	GTGAACCTGGGCGAGATGGTGTCTTGAAGATCTCACCAACTACTTTCGACAGCC	1630
Db	1306	GTGAACCTGGGCGAGATGGTGTCTCGAGATCTCATCACTACTTTCGACAGCC	1365
QY	1631	GATGAGGATATGGAACACGAAGAAAGCAAAACAAATTCGCGGCTTCGCAACCGGTCA	1690
Db	1366	GATGAGGATATGGAACACGAAGAAAGCAAAACAAATTCGCGGCACTCCGAAACCGGTCA	1425
QY	1691	GACCTGTCCNAGAGGAGGACTACTGAACTGTCTCGAAGTATAGACAGATCAAC	1750
Db	1426	GACCTGTTCNAGAGGAGGACTACTGAACTGTCTCGAAGTATAGACAGATCAAC	1485
QY	1751	GTGCTCAGCTCCAGGCGTCTCGCTGGTGGATTCCTGGCGGAGACGAATCTGGACAGAGC	1810
Db	1486	GTGCTCAGCTCCAGGCGTCTCGCTGGTGGATTCCTGGCGGAGACGAATCTGGACAGAGC	1545
QY	1811	TGGGAAATGATATCTGGATATTTGTATCAGTTGCTGGCGCAATPAATAAAGGCAACCAC	1870
Db	1546	TGGGAAATGATATCTGGATATTTGTATCAGTTGCTGGCGCAATPAATAAAGGCAACCAC	1605
QY	1871	ACGAACCTGGCGGAGTTTCGGAACTCGAAACCGGTTCACTGGCTGTTCTCGCGCTCGGC	1930
Db	1606	ACGAACCTGGCGGAGTTTCGGAACTCGAAACCGGCTCACTGGCTGTTCTCGCGCTCGGC	1665
QY	1931	TCGACGCTCGGCGAGGCGACCGGATGCTCGACGTGCTGCACTGCATCTCATCGAC	1990
Db	1666	TCGACGCTCGGCGAGGCGACCGGATGCTCGACGTGCTGCACTGCCTGCTGCTTTAGAC	1725
QY	1991	TCGCTCTGAAGCGCTCAATATGATGAGGAGCAACACATAAAGTGAATCTCTCTATTA	2050
Db	1726	TCGCTCTGAAGCTCTCAATATGATGAGGAGCAACACATAAAGTGAATCTCTCTATTA	1785
QY	2051	GAAAGCACGGAACCGGACCTTAAAGTACTAGATGTGTCTATGTTCACTCTGGTGGTAAAC	2110
Db	1786	GAAAGCATGCGGCGGACCTTAAAGTACTAGATGTGTCTATGTTTCGCTGTGCGTGGTAAAC	1845
QY	2111	GGCGTGGCGGTGCGCTCGTACAGAAACAACTGCGACTATTGTCGCCCGGCAAGAAC	2170
Db	1846	GGCGTGGCGGTGCGCTCGTACAGAAACAACTGCTGACTACTTACTGTCGCCCGGCAAGAAC	1905
QY	2171	CTGTTGTCTGCAAACTGGGCTTGTAGATCAGGTATCTAGTGTCCGTCCGAAACATCTTCGTG	2230
Db	1906	CTGTTGTCTGCAAACTGGGCTGTGTAGTACAGTATCTAGTGTCCGTCCGAAACATCTTCGTG	1965
QY	2231	GGCGAGTAGAAGGGTGGGAGTGTACCGGAAATGGTACTTTCGAGGTTGACTATGGACAC	2290
Db	1966	GGTCCAGTAGAAGGGTGGGAGTGTACCGGAAATGGTACTTTCGAGGTTGACTATGGACAC	2025
QY	2291	ATAGAGAAGACCAACATATGATGCGCATCTACGATAGGATGGGCTTAACTACTTGGT	2350
Db	2026	ATAGAGAAGACCAACATATGATGCGCATCTACGATAGGATGGGCTTAACTACTTGGT	2085
QY	2351	TATGTCCCATACCCGGGTGGTGTGAGAAGTGGGAGGTAAACGGCGTGGGAGACGACTG	2410
Db	2086	TATGTCCCATACCCGGGTGGGAGAAATGGGAGGTAAACGGCGTGGGAGTGAACCTG	2145

QY	2411	TACTCGTAGCGGTTTGATGGCGCTTACCTCTGTCCGGGGAGGAAGACCCCGGTCAAT	2470
Db	2146	TACTCGTAGCGGTTTCGACGGCGCTTACCTCTGTCCGGGGAGGAAGACTCCCGTCAAT	2205
QY	2471	AGGACTCATGCTGGAAGAGCCTTATATTAGAAAGGTGACGTGATAGGTTGTGCTGATGGAC	2530
Db	2206	AGGACTCATGCTGGAAGAGCCTTATATTAGAAAGGTGACGTGATAGGTTGTGCTGATGGAC	2265
QY	2531	CTGACGGTACCANTCATCACTTCACTGTTCAACGGAGTGGGTGACGGGATCCTTCACC	2590
Db	2266	CTGACGGTACCANTCACTTCACTGTTCAACGGAGTGGGTGACGGGATCCTTCACC	2325
QY	2591	AACCTTCAATCTGGAAGGCATGTTCTTCCCGGTCACTAGCTGTCTCTAGTAACTGAGTTGT	2650
Db	2326	AACCTTCAATCTGGAAGGCATGTTCTTCCCGGTCACTAGCTGTCTCTAGTAACTGAGTTGT	2385
QY	2651	CGGTTCTCTGCTGGGCGGAGAACCGTGAAGTCTCCGGTACGCGGCTCCAGAAAGGTACTCC	2710
Db	2386	CGGTTCTCTGCTGGGCGGAGAACCGTGTCTCCGGTACGCGGCTCCAGAAAGGTACTCT	2445
QY	2711	CGGTTCTGAGTCTCTCTGCGGAGCAGATCCTCAGCTGGAGCGGCTCTTCTACTCTC	2770
Db	2446	CGGTTCTGAGTCTCTCTGCGGAGCAGATCCTCAGCTGGAGCGGCTCTTCTACTCTC	2505
QY	2771	GGCAACCTGTCCAAAGCGGCGCTTGGGCTGGACCCCGCTAGTACAGGACGATACGGCTTTT	2830
Db	2506	GGCAACCTGTCCAAAGCGGCGCTTGGGCTGGACCCCGCTAGTACAGGACGATACGGCTTTT	2565
QY	2831	GTGCTTACGCTGTGTTGATATCTTTACAGATTATCTCTGCTTACATATGTGGAAACAAATCAGA	2890
Db	2566	GTGCTTACGCTGTGTTGATATCTTTACAGATTATCTCTGCTTACATATGTGGAAACAAATCAGA	2625
QY	2891	GACAACTAGCTGAAATATTTACGAAATGTGGGCTATGAATAAGATCGAAGCAGGCTGG	2950
Db	2626	GATAAGCTAGCTGAAATATATACGAAATGTGGGCTATGAATAAGATCGAAGCAGGCTGG	2685
QY	2951	ATGTACGGCGACCGAGAGAGAACTTGGCAAGATCCACCCCTGCTCTGCGCTTCGAG	3010
Db	2686	ATGTACGGCGACCGAGAGAGAACTTGGCAAGATCCACCCCTGCTCTGCGCTTCGAG	2745
QY	3011	CGACTCCCCTGCTGAGAAACGATACGATATAAACTTGTCTGTGAGACACTCAAGACT	3070
Db	2746	CGACTCCCCTGCTGAGAAACGATACGATATAAACTTGTCTGTGAGACACTCAAGACT	2805
QY	3071	ATCTTGGCTCTGGGCTTACTACATCAGCTTAGATAAGCTTCCAGCAGCATCCGCAACGTT	3130
Db	2806	ATCTTGGCTCTGGGCTTACTACATCAGCTTAGATAAGCTTCCAGCAGCATCCGCAACGTT	2865
QY	3131	CGTCTGCCCAATGAAACCTTTTTCATGCACTCAACGGCTTCAAGCCAGCACCTCGACCTG	3190
Db	2866	CGTCTGCCCAACGAACTTTTTCATGCACTCAACGGCTTCAAGCCAGCACCTCGACCTG	2925
QY	3191	AGTGTGTCTCACTCTGACACCCAAAGATGGATGAGCTAGTAGGGCAGCTGGGTGAGAACACC	3250
Db	2926	AGTGTGTCTCACTCTGACACCCAAAGATGGATGAGCTAGTAGGGCAGCTGGGTGAGAACACC	2985
QY	3251	CACAACTTTGGGCGAGGAGGATACAGCAGGATGGACTTACCGACTTATATGAGGAC	3310
Db	2986	CACAACTTTGGGCGAGGAGGATACAGCAGGATGGACTTATGAGGACTTATATGAGGAC	3045
QY	3311	TCGGACATGATCGATCCCGCACCTTGGTGCCATACCCGAAAGTTGACAGTGCATCAAG	3370
Db	3046	TCGGACATGATCGATCCCGCACCTTGGTGCCATACCCGAAAGTTGACAGTGCATCAAG	3105
QY	3371	AAGGCCAAACAGGAGACAGCTCTCGGAGACTGTGAGGACCTCTGTGCTACGGGTATATG	3430
Db	3106	AAGGCCAAACAGGAGACAGCTCTCGGAGACTGTGAGGACCTCTGTGCTACGGGTATATG	3165
QY	3431	CTGGAACCCGCTTACTGGGAGCAGCATGAGCACTCTTGTGGAAAGCGTCAAAACAAAG	3490
Db	3166	CTGGAACCCGCTTACTGGGAGCAGCATGAGCACTCTTGTGGAAAGCGTCAAAACAAAG	3225
QY	3491	CAAGCCGACTTTCAGAAACATACCGCGCTGAGAAAGACTATGCCGCTCAGCTCTGGGAAGTGG	3550



311 GACATGGTGTGATGTCGTGCACACGACGAGAGGGGTGTCCTGGCTGCCGAAGGT 370  
Db  
61 GACATGGTGTGCTGTGTCGACACGACGAGAGAGGGGTGTCCTGGCTGCCGAAGGT 120  
Qy  
371 CTCGGCAACCGGCACATGCTTCTCTGGAGAAATATTCGGCAAGAAACATACCGCCTGATCTG 430  
Db  
121 TTCGGCAACCGGCACATGCTTCTCTGGAGAAATATTCGGCAAGAAACATACCGCCTGATCTG 180  
Qy  
431 TCGCAGTGTGTGTTGTGTCATCGAACAGCGCGCTTTTCAGTAAGAGCTTTACAGGAGTTGGTA 490  
Db  
181 TCGCAGTGTGTGTTGTGTCATCGAACAGCGCGCTTTTCAGTAAGAGCTTTACAGGAGTTGGTA 240  
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491 ACAGCTCGGGGATCTGAAACTTGGGAAAGAAACTTATAGGTAAAGGTACCGGTTCCTGGTTAT 550  
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241 ACGGCTCGGGGTTCTGAAACTTGGGAAAGAAACTTATAGGTAAAGGTACCGGTTCCTGGTTAT 300  
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551 CGTACGCTACTATACGGCAATGCTATTCTTTTGGGACATCTTAAACAGTGATATATACCTG 610  
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611 GCCTGCCCTGTCACATCATATCCAGATTAAGCTGGCCTTTGACGTGGGTCTCCAAACAG 670  
Db  
361 GCCTGCCCTGTCGACATCATATCCAGATTAAGCTGGCCTTTGACGTGGGTCTCCAAACAG 420  
Qy  
671 CACTCCCAAGGTGAAGCCTGCTGGTGGACCTGTCATCTGCGCAGCAACAGAGATCCGAG 730  
Db  
421 CACTCCCAAGGTGAAGCCTGCTGGTGGACCTGTCATCTGCGCAGCAACAGAGATCCGAG 480  
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731 GCGGAGAGGTGCGAGTCCGAGATGACTTTGATTTCTAGTCTCCGTGGCCATTGAGAGATAC 790  
Db  
481 GGTGAGAGGTGCGAGTCCGAGATGACTTTGATTTCTGTCTCCGTGGCCACTGAGAGATAC 540  
Qy  
791 TTGCACACACGAAAGAGAACGAAGTATCGATAGTGAAACGGCTGCTTCCAGTGACGCAC 850  
Db  
541 TTGCACACACGAAAGAGAACGAAGTATCGATAGTGAAACGGCTGCTTCCAGTGACCCAC 600  
Qy  
851 TGGTCCGTACAGCCCTATGGTACTGGTATATCGAGGATGAAGTATGGGCTATGTGTTTC 910  
Db  
601 TGGTCCGTACAGCCCTATGGTACTGGTATATCGAGGATGAAGTATGTAGGCTATGTGTTTC 660  
Qy  
911 GGAGGTGATGTGCTCAGGTCTTCCATGGAGGTGACGAGTGTCTCACTATACCTTAGCACT 970  
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661 GGAGGTGATGTGCTCAGGTCTTCCATGGAGGTGACGAGTGTCTCACTATACCTTAGTACC 720  
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## RESULT 6

US-10-668-767-9  
; Sequence 9, Application US/10668767  
; Publication No. US2004017114A1  
; GENERAL INFORMATION:  
; APPLICANT: Caspar, Timothy  
; APPLICANT: Cordova, Daniel  
; APPLICANT: Gutteridge, Steven  
; APPLICANT: Rauh, James  
; APPLICANT: Smith, Rejane  
; APPLICANT: Tao, Yong  
; APPLICANT: Wu, Lihong  
; TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors  
; FILE REFERENCE: B01533 US NA  
; CURRENT APPLICATION NUMBER: US/10/668,767  
; CURRENT FILING DATE: 2003-09-23  
; PRIOR APPLICATION NUMBER: 60/412,795  
; PRIOR FILING DATE: 2002-09-23  
; PRIOR APPLICATION NUMBER: 60/427,324  
; PRIOR FILING DATE: 2002-11-18  
; NUMBER OF SEQ ID NOS: 149  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 9  
; LENGTH: 16363  
; TYPE: DNA  
; ORGANISM: Drosophila melanogaster  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (15890)..(15890)  
; OTHER INFORMATION: n = a, c, g, or t  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(15327)  
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Matches 2983; Conservative 0; Mismatches 1192; Indels 42; Gaps 4;

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Qy 376 CAACCGGCACTGCTTCTCGAGAAATATTGCCGAAAGAAACATACCGCTGATCTGTGCA 435  
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; Sequence 22562, Application US/11097143
; Publication No. US2005020858A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; FILE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; PRIORITY FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
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; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22562
; LENGTH: 15606
; TYPE: DNA
; ORGANISM: DROSOPHILA
US-11-097-143-22562
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Db 466 CATACGACCAAGGAGAACGAAACAGTCTATTGTAAATGCCAGCTTCCATGTGACCCACTGG 525
QY 854 TCGGTACAGCCCTATGCTACTGTTATATCGAGGATGAAGTATGTGGGCTATGCTTCGGA 913
Db 526 TCGGTGACGCTTACCGCACCGGCACTCTCCAGGATGAAGTACGTGGGCTATGTCTTTGGC 585
QY 914 GGTGATGCTCAGGTTCTTCCATGAGAGTGACAGTGCTCTCACTATACCTTAGCACTTGG 973
Db 586 GGCATGCTGCTGCTTCTTCCATGGTGGCGACGAGTGCTGACCAACCGAGTACATGG 645
QY 974 ACAAAGGATGGGGGCAAAATATCGTAGTCTACAAAGAGGTTTCAGTGTCTCAAGCC 1033
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Db 2866 GCGGTGACACTACCCCAAGTTGGAGAGCTTGTGGACAGCTGGCGGAGCACTCAC 2925  
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Qy 3314 GACATGATCGATCCCGCACCTGGTGGCATTACCGGAGGTTGACGATGCCATCAAGAAG 3373  
Db 2986 GAAACACACAGGAGTCACACTTGGTGCCATATGCCAAAGTGGACGAGGCTATCAAGAAG 3045  
Qy 3374 GCCAACAGGACACAGCCTCGGAGACTGTGAGGACCTCTGTGGTCTACGGGTATATGCTG 3433  
Db 3046 GCCAACAGGACACAGCGTGGAGACAGTGGCAAGCTCTCTGGTTACGGATATGCTTG 3105  
Qy 3434 GACCCGCTACTGGGAGCAGCATGAAGCACTCTTGTGGAGCGGTCAAAACAGAAACAA 3493  
Db 3106 GATCTCCGACTGGCGAAGAAACGAGGCACTTCTGGCGAGGACAAACGCTCAAGTTC 3165  
Qy 3494 GCCGACTTCAGAAATACCGCGCTGAGAGNACTATGCCGTGACCTCTGGGAGTGGTAC 3553  
Db 3166 GCCGGATTCGCGACTTACAGGGTGGAGCGCAACTACCGCGTGACATCGGGCAAGTGGTAC 3225  
Qy 3554 TTCGAGTTTGAGATCTTAACGGCTGGACCTATGAGGGTGGGCTCGGCTCACTGATATG 3613  
Db 3226 TTCGAATTCGAGGTCTCACGTCGGACCAATGCGAGTGGGTGGGACGCGCGATTCG 3285  
Qy 3614 GCACAGGAATGATGCTGGCAAGACGAGAACTCTCTGGGCTTTTGATGTTACAATGAG 3673  
Db 3286 TATCGGAGCGATGCTGGGACGCGAGACACCAAGTTGGGCTTCGATGGACACAATGTG 3345  
Qy 3674 GAAAGGTGACAGCGGTAACTAGTCTTTCGGCAAGCAATGGGCTGTGGTGAGCTA 3733  
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Qy 3734 GTGGGGGTTCCTAGATCTCATTTGATAAGACGATAAGTTTCTCACTCAACGGTGAAGTTG 3793  
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Qy 3794 TTGATGATGCTCTTGGCGGAGAGACTACGTTTCTGATGT-----CCAGGTGACAAC 3847  
Db 3466 CTGATGACGCGCTGGGCGGCGAGACGACCTTTGCCGACGTAAACCGCGGGGGTGGC 3525  
Qy 3848 TTTGTACTGCTTGCACGCTTGGTGTGGGCCAAAGCCAGGTTAACTACGGTTCAGGAC 3907  
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Db 3586 GTGGACTCACTCAAGTTCTTCAACACTTGTGGCTGCAAGAGGATACGAGCCGTTCTGC 3645  
Qy 3968 GTCAATATGAAGAGAGAGCTGACTCACTGTGTACCAAAAGACCGCGCATCTTCGAGAT 4027  
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Db 3886 GCCAGACGCTGGGAGGAGATTAAGAAACCGGAGTACCGACTGATGCGCGAGGCGGAGATC 3945  
Qy 4268 GCT-----CAGATGTCCGCCCATATTTGACCAAGATCATGAGGAGCGGT 4309

Db 3946 GCTGCCCAAAATGAGGTCCAGACACAGGCGGCCCCACATGAGCACCATGTTTAAAGGTGGC 4005  
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Qy 4370 TC---CAAAGATGAAGCGCTTCTCAAGGCCACCAAGGATCCATGACAAAGAGGT 4426  
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Qy 4427 GTTACTATACAAAATTACA 4445  
Db 4126 ATAACTTCGAAACAGACA 4144

RESULT 8  
US-10-668-767-7  
; Sequence 7, Application US/10668767  
; Publication No. US20040171114A1  
; GENERAL INFORMATION:  
; APPLICANT: Caspar, Timothy  
; APPLICANT: Cordova, Daniel  
; APPLICANT: Guttridge, Steven  
; APPLICANT: Rauh, James  
; APPLICANT: Smith, Rejane  
; APPLICANT: Tao, Yong  
; APPLICANT: Wu, Lihong  
; TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors  
; FILE REFERENCE: BB1533 US NA  
; CURRENT APPLICATION NUMBER: US/10/668,767  
; CURRENT FILING DATE: 2003-09-23  
; PRIOR APPLICATION NUMBER: 60/412,795  
; PRIOR FILING DATE: 2002-09-23  
; PRIOR APPLICATION NUMBER: 60/427,324  
; PRIOR FILING DATE: 2002-11-18  
; NUMBER OF SEQ ID NOS: 149  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 7  
; LENGTH: 15413  
; TYPE: DNA  
; ORGANISM: Peregrinus falconis  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1264)  
; OTHER INFORMATION: n = a,c,g, or t  
; FEATURE: CDS  
; NAME/KEY: CDS  
; LOCATION: (17)..(15397)  
; OTHER INFORMATION:  
US-10-668-767-7

Query Match 41.6%; Score 2078.2; DB 8; Length 15413;  
Best Local Similarity 66.5%; Pred. No. 0;  
Matches 3172; Conservative 1; Mismatches 1475; Indels 120; Gaps 9;

Qy 266 GGGGAGCAAGCCAGCAGGATGATGTTTCAATCTTGGGTACGGAAGACATGGTGTGATG 325  
Db 29 GAGGTTGGATCTGAGCAGGATGATGTTTGGTCTTAGAACGGAAGACATGGTGTGCTG 88  
Qy 326 TCGTGCAACGAGCAGGAGAGGGTGTGCTGCTGCCAAGAGTCTCGGCAACCGGAC 385  
Db 89 TCATGTACAGCCACCGGTGAAAGAGTTTGGCTGCTGAGAGGATTTGGTAAACCGTCAT 148  
Qy 386 TGCTTCTCGAGAAATATTCGCGAACAAGATACCGCTGATCTGTGCGAGTGTGTTT 445  
Db 149 TGTTTCTGGAACATCATCGCTGACAGAAATATTCACACAGATTTGTCCATGTGTATT 208  
Qy 446 GTCATCCAAACAGGCGCTTTTCAGTAAGAGCTTTACAGAGTGTGGTAAACAGCTGCCGGATCT 505  
Db 209 GTTATTGAGCAAGCTTTATCGTTTCGAGCTTTTCAGGAATTTGGTACTGCTGCTGGATCA 268  
Qy 506 GAAACTGGGAAAGAAACTTTAGGTAAAGGTAACCGTTTCTGGTTTATCGTACGCTACTATAC 565

Db 269 GAA-----GAGGGTAAAGGAACTGGATCAGGACATAGGACCCCTATTGTAC 313  
Qy 566 GCGAATGCTATTCTTTTCGCGACATCTTAAACAGTGATATGTACTGGCGCTGCTGTCAACA 625  
Db 314 GCGAATGCTATTCTACTTCGCGATCAAAACAGTGATATGTACTGGCGCTGCTGTCAACC 373  
Qy 626 TCATCATCCAGGATAAGCTGGCCCTTTGACGTGGGTCTGCAACAGCACTCCCAAGGTGAA 685  
Db 374 AGCTCATCCAATGATAAATGTCAATTCGATGTGGTCTCCAAGAAATTCACAAGGTGAG 433  
Qy 686 GCCTCTGCTGGTGAACCTCGATCTCTGCGAGCAAAACAGAGATCGAGGGCGAGAGGTGCGA 745  
Db 434 GCCTGTGTGGTACTGTGCATCTCTGCTTCCAAGCAAAAGATCGAGGGGTGAGAGGTGCGA 493  
Qy 746 GTGCGAGATGACTTGATTTAGTCTCGGTGGCCATTTGAGAGATCTTCCACACAAACGAAA 805  
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Qy 806 GAGAACGAAGTATCGATAGTGAACGCGTCTGTTCCACGTGACGCACTGGTGGGTACAGCCC 865  
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Qy 866 TATGTACTGTGATATCGAGGATGAAGTATGTGGGCTATGTTCGAGGATGATGTGCTC 925  
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Qy 926 AGGTTCTTCCATGGAGGTGACGAGTGTCTCACTATACCTAGCACTTGGACAAAGATGGG 985  
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Db 734 GGCAGAGATATGTGGTTTATGAGGGAGGAGTGTGATGAGTCAAGCTGCTTCATTAAG 793  
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Db 794 AGACTAGAACTTGTGAGAACAAATGGGCGAGTGGTTTCATAAAATGGTACCACCCAATG 853  
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Qy 1166 TTAGTTAGCAGAGAGAAACCAACAGCTTCCCTGCTTCTGCTGCGCGCAGAGAG 1225  
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Qy 1226 GATGATCAGAAAGCAAGTGTAGAACCAAGGACTTGGAGGTCATAGGCGCGCCCATATC 1285  
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Qy 1346 AAGTCTTACGAAACCAAGAGAAAGCGTGGGTAAAGTAGAAGAGAAAGCAAGCGATTCTC 1405  
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Qy 1406 CACGAGGAAGGCAAGATGCAATGGCCCTCGACCTCTCCAGGTCAAGAGGAAGAATCT 1465  
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Qy 1526 GAACTCTTCAAGAGAACCGTCTGCTCACTCGATGTTCTTCGCTCAGTGAACCTGGCGAG 1585  
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Qy 1886 TTCCGGAACCTGAACCGGTTCAACTGGCTGTCTCGCGCTCGCTCGCGCCCTCGGCG 1945  
Db 1631 TTTGCGAATTCAAATTCGCTGAATTTGGCTGTTCAGCAGAGCTGGGCTCAAGCATCAAGT 1690  
Qy 1946 GAGGCGACCGGCATGCTCGACGTCTGCACCTGCATCTCATCGACTCGCCTGAAGCGCTC 2005  
Db 1691 GAAGGCGCGGAATGCTTGTGATTTGATTTGCAATTTGCTTCTCATTTGCTTGAAGCGTTG 1750  
Qy 2006 AATATGATGAGGGACGAACACATATAAAGTGTATAATCTCTTCTTTAGAAAACACGAGCGC 2065  
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Qy 2066 GACCTTAAGTACTAGATGTGCTATGTCTACTGTGCTGCGTAAAGGCTCGCGTGGCGC 2125  
Db 1811 GATCGGAAGTTTGGATGTTCTCTGTCTCACTGTGTGGGTAAATGGTGTGCTGTTGCT 1870  
Qy 2126 TCGTACAGAACACATCTCGGACTATTGCTGCGCCCGCAAGAACCTGTGCTGCAAACT 2185  
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Qy 2186 GCGCTTGTAGTACGCTATCTAGTGTGCTGCGTCCGAACATCTTCTGTTGGCGGAGTGAAGGG 2245  
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Qy 2246 TCGGCAGTGTACCGCAATATGTTACTTCAGGTGATATGAGACCATATGAGAAAGCAACA 2305  
Db 1991 TCTGAGTTTATCAAAAATGTTATTTTGAAGTTTACCAGTATGATCATTTGAGCAGCAACA 2050  
Qy 2306 CATATGATGCGCATCTACGCTAGGATGGCTAACTACTGTTATGTTATGCTCCATACCG 2365  
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Qy 2666 GGAGAACAGGTAGTCTCGGTACCGGCTCCAGAGGCTACTCCCGCTGTTGGAGTCT 2725  
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Qy	2786	CGGSCCTTGGCTGACACCCCGCTAGTACAGGACGATACGGCTTTTGTGTGCCTACGCCGTGTT	2845
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Qy	2906	AATATTCACGAAATGTGGCTATGAATAAGATCGAAGCAGCGCTGGATGTACGGCGACCAG	2965
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Qy	2966	AGAGAAGACTTGCACAAGATCCACCCCTGCTCGTGCCTTTCGAGCGACACTCCCGCCCGCT	3025
Db	2708	CGAGATGACATACGTAAAGTGCATCCCATGCTTAATCAGTTTCGACCAACTTCCACCAAGCT	2767
Qy	3026	GAGAAACGATACGATATACAACCTTGTGTGCAGACACTCAAGACATACTCTGGCTCTGGGC	3085
Db	2768	GAGAAGCGCTATGACTCACAACCTCGCAGTTCAAACCTCTCAAGACAATCTTGGCACTCGGC	2827
Qy	3086	TACTACATCAGCTTTAGATAAGCCTCCAGCAGCGCATCCGCAACGTTGCTGTGCCCAATGAA	3145
Db	2828	TACTACATAACGATGGATAGAGCTCTTCGCGTATAAAAACAAATTCGTCTTCCAAATGAG	2887
Qy	3146	CTTTTCATGAGTCCAAGGCTACAAGCAGCAGCACCTCGACCTGAGTGTGTCAACCTG	3205
Db	2888	CTTTTCATGCAATCAAAATGGCTACAGCCAGCAGCACCTTGATCTCTCAGCGGCATATCAATTA	2947
Qy	3206	ACCCCAAGATGGATGAGCTAGTAGGCCAGCTGTGCTGAGAAACCCACAACCTTTTGGGCC	3265
Db	2948	ACCCGAAATGGAGGAATTAGTTGATCACTAGCCGAGAAATACATAATCTATGGGCC	3007
Qy	3266	AGGAGAGGATACACAGCGGATGACATTAACGACTTAATGAGGACTCGGACATGCATCGA	3325
Db	3008	AAAGAACGATCCAACAAGGTGACGATGAGACTCAATGAGGACTCTGATATGTTGAGA	3067
Qy	3326	TCCCCGACCTGTGTGCCATACCCGAAAGGTTGACGATGCCATCAAGAAAGGCCAACAGGGAC	3385
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Qy	3386	ACAGCCTCGGAGACTGTGAGGACCCCTGCTGTCTACGGGTATATGCTGGACCCGCTTACT	3445
Db	3128	ACTGCAAGTGAACCGTTCAGAACTCTATTTGTGTATGGCTTCAATCTAGATATCCCCCACC	3187
Qy	3446	GGGAGAGCAGATGAAGCACTCTTGTGGAGCGTCAAAAACAGAAAGCCGACTTCAGA	3505
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Db	3248	ACGTACCGAGCAGAAAAAACAATATGCTGCTGACAAACGGGAAAAGTGATTTTGAATTTGAA	3307
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Qy	3626	ATGCTCGGACAAGACGAGAACTCTCTGGCTTTTGTATGTTACATGAGGAAAAAGTGTAC	3685
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Db 4622 ATCAATGAATATTTCTACGGTGTGGTATTTTCCCGTCAGGATCCAACTCATGTGTAT 4681  
Qy 4973 ATCGCTGGGTGACACCCAGTACCACT 5000  
Db 4682 GTCGGTGGGTGACAAACCCAGTACCCT 4709

RESULT 9

US-10-668-767-3  
; Sequence 3, Application US/10668767  
; Publication No. US20040171114A1  
; GENERAL INFORMATION:  
; APPLICANT: Caspar, Timothy  
; APPLICANT: Cordova, Daniel  
; APPLICANT: Gutteridge, Steven  
; APPLICANT: Rauh, James  
; APPLICANT: Smith, Rejane  
; APPLICANT: Tao, Yong  
; APPLICANT: Wu, Lihong  
; TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors  
; FILE REFERENCE: BBI533 US NA  
; CURRENT APPLICATION NUMBER: US/10/668,767  
; PENDING FILING DATE: 2003-09-23  
; PRIOR APPLICATION NUMBER: 60/412,795  
; PRIOR FILING DATE: 2002-09-23  
; PRIOR APPLICATION NUMBER: 60/427,324  
; PRIOR FILING DATE: 2002-11-18  
; NUMBER OF SEQ ID NOS: 149  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 15845  
; TYPE: DNA  
; ORGANISM: Myzus persicae  
; FEATURE:  
; NAME/KEY: Unsure  
; LOCATION: (36)..(37)  
; OTHER INFORMATION: n = A, C, G, or T  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (5807)  
; OTHER INFORMATION: n = a or t  
; US-10-668-767-3

Query Match 36.9%; Score 1846; DB 8; Length 15845;  
Best Local Similarity 63.3%; Pred. No. 0;  
Matches 2988; Conservative 0; Mismatches 1685; Indels 51; Gaps 8;  
Qy 278 GAGCAAGATGATGTTTCAATCTTGGTACGGAAGACATGGTGTGCATGTCTGTCGACAGG 337  
Db 301 GAACAGGACGATGTCTCGTTTCTCCGGACGGAAGATATGGTGTGTTTATCATGTATCCCG 360  
Qy 338 ACAGGAGAGAGGTGTGCTGCTCGGAGGTCTCGCAACCGGACCTGCTTCCTGGAG 397  
Db 361 ACCGGAGAGAGTGTGTTCTTGACGAGAGGATTTGGAAATCGGCAATGTACTTAGAA 420  
Qy 398 AATATTGCCCAAGAACATACCGCTGATCTGTGCGAGTGTGTGTTGTCTATCGAACAG 457  
Db 421 AATATTGCCGATAGAAATATCCACCGATTTATCACAGTGTGTTTGTCAITGAACAA 480  
Qy 458 GCGCTTTAGTAAGAGCTTTACAGGAGTTGGTAAACAGCTGCGGGATCTGAACCTGGAAA 517  
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Qy 518 GAAACTTAGTAAGGTACCGTTCGTGTTATCGTACCTACTATACGGCAATGCTATT 577  
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Db 589 TTATTGCGTCATCAAAAATAGTGATATATGTTAGCTTGTCTATCAACAAGTTCCTTCAAAT 648  
Qy 638 GATAAGCTGGCCCTTTTGTAGCTGGGCTCTGCAACAGCACTCCCAAGGTGAAGCTGCTGGTGG 697  
Db 649 GATAAAATTAATCTTTTGTAGCTTGGTTTACAAGAGCATTCACAAGGTGAAGCTTGTGGTGG 708  
Qy 698 ACCCTGCATCTCCAGCAAAACAGAGATCCGAGGGCGAGAAGGTGCGAGTCCGAGATGAC 757  
Db 709 ACTGTTTCATCTCGTCATCGAACCAACGATCAAGGGGTGAAGAAAGTTCCAGTCCGAGATGAT 768  
Qy 758 TTGATTCTAGTCTCCGTTGGCCATTGAGAGATACCTTGACACAAACGAAAGAGAAACGAAGTA 817  
Db 769 TTAATTTTGTAGTCTGTAGCAACTGAACGGTATTTGACACCCGCAAGAAAGAAACGAGTTA 828  
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Db 829 TCTGTAGTTAATGCTCATTTTCATGTAACCTCATTTGGTTCAGTACCAACCATATGGTACTCGT 888  
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Qy 998 GTAGTCTACAAAGAGGTTTCAGTGTCTCAAGCCCGTCTCTATGTCGCGCTCGAGCTG 1057  
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Qy 1058 GCTAGAACCAAGTGGGCGGAGGTTTCAATTAACCTGGTACCATCTCTATGAGGATTCGGCAC 1117  
Db 1069 GCTAGAACTAAATGGGCGGTTGCTTCAATTAATGGTACCATCCAATCGAATTAAGACAT 1128  
Qy 1118 ATCACTACTGAAAGATATCTTGGAGTTAAACACAGATGAGCTGATTTAGTTAGCAGA 1177  
Db 1129 CTGACAACTGGTGGTATTTAGGTGTCAATGAAACCAATGAATTCATTTAGTTTGCAGA 1188  
Qy 1178 GAGGAACCCACAAACAGCTTCTGTCGCTTCTGCGCTCCGCGGAGGAGGATGATCAGAG 1237  
Db 1189 GAAGAGCCACCATGTCATCTTACATTTTCTTACGCCCAAGAAAGACGACCAAAAA 1248  
Qy 1238 CAAGTGTGTAGAGACAAAGGATCTGAGGTCTAGCGCGCCCATCATCAAGTACGGTAC 1297  
Db 1249 ATAAATTTTAGAGGACAAAGATCTAGAGTAATTTGGTGCACCTATAAATTAAGTATGGTAC 1308  
Qy 1298 TCCACCGTCTATGTCAGCATTTCGAGACTCGCTTGTGGCTGTCTTAAAGTCTTACGAA 1357  
Db 1309 AGCAGTGTGTAGTGCACATTTCTGATACAGGTTTATGGTTAAACATATAAGTCTTATGAA 1368  
Qy 1358 ACGAAGAGAAAGCGGTGGGTAAGTAGAAGAGCAAGCGATTTCTCCAGGAGGAGGC 1417  
Db 1369 ACAGAGAGAGGTTGTCGGTAAAGTAGAAGAAACAAAGCAGTATTTACACGAGAGGT 1428  
Qy 1418 AAGTGGACGATGGCTCGACCTCTCCAGGTCAAGGAGGAGAAATCTATGATGCTCGA 1477  
Db 1429 AAGTGGACGATGGTTAGACTTTTAGTAGGAGTCAAGAGAGAGTCAAGAACTGCTAGA 1488  
Qy 1478 GTTATCAGAGAGTGTCTTCCGCTGTCTCAAGTTTATCAATGGCTCGGAACTCTTCAA 1537  
Db 1489 GTAAATACCAATGCTCTTTCATTTATTCACAGTTTTATTTCTGGATTCGAGAACTTACAA 1548  
Qy 1538 GAGAACCGTCTGCTACATCGATGTTCTTCCGCTCAGTGAACCTCGGGCGAGATGGTGTGTGT 1597  
Db 1549 AGTAACAGCGCTTCGTCATTTATTTTGTTCATTCGTTATCTTAATGAATGTCATGTGT 1608  
Qy 1598 CTTGAAGATCTCACCAACTACTTCGACAGCCCGATGAGGATATGGAAACAGAGAAAG 1657  
Db 1609 CTAGAGATTTAAATAAATTTACTTTGCTCAACCTGAAGAGGATATGGAGCAGCAAGAAAA 1668  
Qy 1658 CAAAACAAATTCGCGCCCTCCGCAACCGTACGAGCTGTTCCAGAGAGAGGCACTATG 1717  
Db 1669 CAAAACCGATTTAGAGCATTAAGAAATAGACAAAGATTTTATTTCAAGAGAGAGGAATATTA 1728



Qy	1718	AACGTGATCCCGAAGCTATAGACAAGATCAACGTGCTCAGTCCGAGGGGTTCTCGCT	1777
Db	1729	AAATTAATCTTAGAAGCCATTGATAAAGTTAAACATTTATCATCATCTCAGGGATTTCATGGTC	1788
Qy	1778	GGATTCTCGGGGAGACGAATCTGGACAGAGCTGGGAAATGATATCTGGATATTTGTAT	1837
Db	1789	AGTT---TAGCCGGTGATGAGTCTGGACAAGTTGGGATGTGATTTCTGGTTATTTATAC	1845
Qy	1838	CAGTTGCTGGCGGCAATAATAAAGGCAACACACGAACCTGCGCGCAGTTTCGCGAACTCG	1897
Db	1846	CAGTTGTTAGCTGCAATTATTAAGGAAATCATACCAACTGTGCTCAATTGCTAACTACT	1905
Qy	1898	AACCGGTTCAACTGGCTGTTCTCGCGCTCGGCTCGCAGAGGCTCGGGCGAGGGCACCGGC	1957
Db	1906	AACCGATTAAATTTGGTTATTTCAGCGGTTTAGGATCTCAAGCATCCAGTGAAGGAACGGT	1965
Qy	1958	ATGCTCGACGTGCTGCACTGCATCCTCATCGACTCGCTGAAGCGCTCAATATGATGAGG	2017
Db	1966	ATGTTAGATGCTTTCATTTGTTCTCATCGATTCTCAGAAAGCTTTAAATATATGATGAAA	2025
Qy	2018	GACGAACACATAAAGTGATTAATCTCTATTAGAAAAGCAGCGACGCCCTTAAAGTA	2077
Db	2026	GACGAACATAAAGTTATAATATCACTTTTGGAAAAACATGCTGCTGATCCAAAAGTG	2085
Qy	2078	CTAGATGTCTATGTTCACTCTCGCGTCGGTAAACGGCGTCGGGTGCGCTGTCACAGAAC	2137
Db	2086	TTGGATGTTTATGTTCTCTGCTGTGTTGGTAACGGTGTAGCTGTGAAGAAGTTCCAAAAT	2145
Qy	2138	AACATCTCGCACTATTGCTGCGCGGCAAGAACCTGTTGTCGAACTGCGCTGTGTAGAT	2197
Db	2146	AAATATATGTGATTTCTTATTAAGAAAGAAAAATTTACTTCTTCAAACTTACTTGTGTAC	2205
Qy	2198	CACGTATCTAGTGTCCGTCGAACATCTTCTGCGCGCAGTAGAAGGTCGCGAGTGTAC	2257
Db	2206	CACGTAGCGGCTACGTCCTCCCAATATTTTGTGTGTCATGTAAGTGGATCTGCTGTTTAT	2265
Qy	2258	CGCAAAATGTTACTTCGAGGTGACTATGGACACATAGAGAAGACACACATATGATGCCA	2317
Db	2266	AGAAAAATGTTATATGAAGTGGCAATAGATCATGTAGAACAACTACTCATTTAAATCCG	2325
Qy	2318	CATCTAGCATAGAGTGGCTTAACACTACTGTTATGTCCTCATACCCGGGTGGTGTGAG	2377
Db	2326	CACATTCGCATTGAATGGGCAAAATACAGCTGGTTATGTTTCCATATCTCTGGTGGTGAGAA	2385
Qy	2378	AAGTGGGAGGTAAACGGCGTGGGAGACGACCTGACTCTGTCGTCGCGGTTTGTAGGCGCTAC	2437
Db	2386	AAATGGGGCGAACCAGGTTGGGGATAATTTATACITTTTGGATTGTAGGATCATAT	2445
Qy	2438	CTCTGGTCCGGGAGGAAGACCCCGGTCAATAGGACTCATGTGTAAGAGCCTTATATT	2497
Db	2446	TTATGGACAGGAGACGTAACTCAGGAGT---GATGCCCGGAACACAAATTTCTAACATTT	2502
Qy	2498	AGGAAGGTGACGTGATAGGTTGTGCAATGGACCTGACGGTACCCTCATCAACTTCATG	2557
Db	2503	AAAAAAAGTGTATGATTTGGCTGTGCAATTAGATTAACTATTCCAAATTAACTTTTACA	2562
Qy	2558	TTCAACGGAGTGGGGTGACGGGATCTTTCAACCACTTCAATCTGGAAGGCATGTTCTTC	2617
Db	2563	TTGAACGGTCAACTTGTCCAAGTGGCTTTAGAGACTTCAATTTAGATGGGATGTTTTC	2622
Qy	2618	CCGGTCATCAGCTGCTTAGTAAGCTGAGTTGTGCGTTCTGCTGGCGGAGAACACGGT	2677
Db	2623	CCAGTAAATTAGTTGTTCTCAAAAAGTCAGTTGTGCTTTTATTTATTTGGGTGGAGATCAGGT	2682
Qy	2678	AGACTCCGGTACGGGCTCGAAGAGGCTACTCCCGCTGGTGGAGTCTCTCCTCGCCGAC	2737
Db	2683	CGATTGAAGTTTACTCTCTCCAGACGAATTTCTCCCTTATTTGAACCTTATTAACCTCAA	2742
Qy	2738	CAGATCTCTCAGCTGGAGCCGTGCTTCTACTTTCCGGCAACCTGTCCAAAGCGGCGCTTGCT	2797
Db	2743	CAAAATTTGACAAATTGATCCCTGTTTATTTTGGGAACCTTAATAAATGCGTCTCACG	2802

Qy	2798	GGACCCCGCTAGTACAGGACGATACGGCTTTTGTGCTACGCTGTTGTATCTTTACAG	2857
Db	2803	GGTCCATGTTATGTTGAGACGATGATGAGCATTTTGTTCCAATCCAGTTGATCTTCGATG	2862
Qy	2858	ATTACTCTGCTTACATATGTGGAAACAAATCAGAGACAAGCTAGCTGAAATATTTACGAA	2917
Db	2863	GTCACTTGGCTAGTTTACATAGAAAATATTTAAAGACAAATTAGCAGAGAAATTTACGAA	2922
Qy	2918	ATGTGGCTATGAATTAAGATCGAAGCAGGCTGATGACGGCCACGACGAGAGAGACTTG	2977
Db	2923	ATGTGGCAATGAATTAATTTGAAGCTGGTTGGCAATATGGCGATTAAGAAATGATACT	2982
Qy	2978	CACAAGATCCACCCCTGCTCGCTCGAGCGACTCCCGCCCGCTGAGAAACGATAC	3037
Db	2983	AGGAAGTATCATCCATGTTTAAATACAGTTTGACAAGTTGCTCAGCCGAGAACGTTAT	3042
Qy	3038	GATATACAACTTCTGCTGTCAGACACATCAAGACTATCCTGGCTCTGGCTACTACATCAGC	3097
Db	3043	GAITCTCAATTAGCTGTGCAACCGCTTAAACCGTTATTGCGTTAGGTTATCACAATCT	3102
Qy	3098	TTAGATAAGCTCCAGCACGATCCGCAAGCTTCGCTGCTGCCAATGNAACCTTTTCATCGAG	3157
Db	3103	ATTGATAATCCACGCTCCGCAATTAAACACAGTCCGGCTGCCCAACGAACCATTTATGCAA	3162
Qy	3158	TCCAACGGCTTACAAGCAGCACCACTCGACTCGTCTGCTCACCTGTACACCCCAAGATG	3217
Db	3163	TCCAATGGATATAAACAGCACCACTAGATTATCTGCTATCATTTTGTTCAGNAANAATG	3222
Qy	3218	GATGAGCTAGTAGCCAGCTGGCTGAGAACACCCACAACCTTTTGGCCAGGGAGAGATA	3277
Db	3223	GAAGAACTAATTGATCAGTTAGTCGGGNAATACATAAATCTATGGGCAAAAGAAATA	3282
Qy	3278	CAGCAGGATGGAATTAACGACTTAATGAGGACTCGGACATGCATCGATCCCGCACTG	3337
Db	3283	CAGCAAGGATGGACATATGGATTAAATGAAGAAATTAACAATGTTGGCAGTCTCTCATTTA	3342
Qy	3338	GTCCCATACCCGAAGTTGACGATGCCATCAAGAAGGCCAAACAGGACACACGCTCCGAG	3397
Db	3343	GTACCGTACAGAAAGTAGACGAGCTATTAAANAAGCTAATAGAGATACAGCAAGCGAA	3402
Qy	3398	ACTGTGAGGACCTGCTGCTACGGGTATATGCTGGACCCGCTACTTGGGGAGCAGCAT	3457
Db	3403	ACAGTCGCGACATATTGTTGTTATGTTTACAAATTTAGATCCCGCAACTGGAGAAACAAAC	3462
Qy	3458	GAAG---CACTCTGTTGGAGCGTCAAAACAGAACGACCCGACTTCAGAACATACCGC	3514
Db	3463	GAAGCGACACTCTCTAACAGATGCAACTCTAATAGATATTGACGTTTTCAGAACATTCGT	3522
Qy	3515	GCTGAGAAGAACTATGCCGTGAGTCTGGAAGTGGTACTTCGAGTTTGAGATCCTAACG	3574
Db	3523	CGGAAAAAACGTTATGCCGTTTCTAGTGGAAAAATGGTACTTCGNAATTTGAGTACTGACA	3582
Qy	3575	GCTGGACCTATGAGGGTCGGCTGGGCTCACGCTGATATGGCACCCAGGAATGATGCTCGGA	3634
Db	3583	AGTGGACCTATCGGGTTGGATGGCCAGGTTCCATGTTTCCCGGGTTATCAAAATCGGC	3642
Qy	3635	CAAGACGAGAACTCTCGGGCTTTTGATGTTTACAATGAGAAAAAGTTGACAGCGGTAAAC	3694
Db	3643	AGTGTGAAAAATTTCTTGGGCAATTTGATGTTTAAACGAAGAAAAAATTTACATGGGACA	3702
Qy	3695	ACTGAGTCTTTTCGGCAAGCAATGGGCTGTTGGTGACGCTAGTGGGGGTGTTCTTAGATCTC	3754
Db	3703	GCCGAATCATTTGGTAGACAGTGGCAAGTTGGAGATGTCGTGGAGTGTGTTTATGATTTA	3762
Qy	3755	ATTGATAAGACGATAAGTTTCTCACTCAACGGTGAGTTGTTGATGGAATGCTTCTTGGCGGA	3814
Db	3763	ATGGAACCATACATAAGCTTTTCGATGAACGGAGAAATTAATAATGGATACGTTAGGAGGG	3822
Qy	3815	GAGACTACGTTTGTGATGTCAGGGTGACAACTTTGTACTGCTTCGACGCTTGGTGTGTC	3874
Db	3823	GAACAACATTTCTGAAGTCCAAGGAGAAAGGATTTGTACTCTGCTTTTACGCTGGGACTA	3882
Qy	3875	GGCAAAAAGCCAGGTTTAAACATACGGTCAAGACGTGAACACGCTGAAATACTTCAACAAC	3934



Db 3883 GCACAAAAGCAAAATTGACATTTGGTCAAGACGTTAACTCATTTGAAATACCTTCACGACT 3942  
QY 3935 TGTGCTGTCAGGAGGGATGAACCACTTCTGTGTCATATGAAGAGAGAGCTGACTCAC 3994  
Db 3943 TGTGACTTCAAGAAGGATGAACCACTTCTGTGTAATGAAGAGGCTGTGCTTAT 4002  
QY 3995 TGGTACACCAAGACACGACCGGATCTTCGAGATACGGATGAGATGATCGACACACCAAGAATA 4054  
Db 4003 TGGTATCTAGGATCAACCAATTTTNGAATACTGACGA---TTTTCGTCTGTTAT 4059  
QY 4055 GATGTACACGAGATACAGCTGGTTCAGATACACCTCCATGCTCAAGATTTCCACAAAC 4114  
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QY 4115 AGTTTGTAGACGATGGAGAACTAACTGGGAGTTCTTACGTCCTCTACTGCTGCTCATC 4174  
Db 4120 ACATTTGAACCACTGGAAGCAATTTGGGAATTTTACGGCTATCATTTACCTGTCATA 4179  
QY 4175 TGCCATAACGAGTTCATTGACAGGACGAGAAAGCCAGCGTTGGGTAGAAATCAAGGAC 4234  
Db 4180 TGTCTACCAAGTTTATTGGCGATCAAGAAACAAAGGGGATGCGAAGAAATAGAATT 4239  
QY 4235 CGCCAAACGGATCCTAATGAAGAGGAGTGAAGCTCAGATGCCGCCATATTACACAG 4294  
Db 4240 AGGCAACACAGGTTATTGTCGCAATCTGAGCATGCT---ACTCTGCTCATATTGAACGA 4296  
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Db 4417 ATCAACACCAACCCACCCAGACCAACCAAGAGGGTCATTATCGAGGATGATGACITTA 4476  
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Db 4477 A-----CAATCGAAATGATGGAAATTTGAAATCGTTTCATCTAGTGAATTTTC 4527  
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QY 4595 CGCGGGAAGCAGTATGCTGCTAAATCCCGTAAATCCAAACACCAACACCGCCCTTCAGT 4654  
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QY 4835 ATGACGACGAGCACTCTCGCGAGTCGGCTACGGAACCTGTGCGCAATGAGATCTTCGAT 4894  
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QY 4895 GCAGAGTTTGAAGCTCAATAGATATTTTATGAGTCAAGATCTACCCAGGTCAA 4954  
Db 4873 TTAGAATGTTTAAATTAATAATAGATATTACTATGTTGTAAGAAATATTCGGGTCAA 4932  
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US-10-668-767-5  
; Sequence 5, Application US/10668767  
; Publication No. US20040171114A1  
; GENERAL INFORMATION:  
; APPLICANT: Caspar, Timothy  
; APPLICANT: Cordova, Daniel  
; APPLICANT: Gutteridge, Steven  
; APPLICANT: Raun, James  
; APPLICANT: Smith, Rejane  
; APPLICANT: Tao, Yong  
; APPLICANT: Wu, Lihong  
; TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors  
; FILE REFERENCE: B1533 US NA  
; CURRENT APPLICATION NUMBER: US/10/668,767  
; PRIOR FILING DATE: 2003-09-23  
; PRIOR APPLICATION NUMBER: 60/412,795  
; PRIOR FILING DATE: 2002-09-23  
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; NUMBER OF SEQ ID NOS: 149  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 5  
; LENGTH: 15315  
; TYPE: DNA  
; ORGANISM: Periplaneta americana  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(15312)  
; OTHER INFORMATION:  
US-10-668-767-5  
Query Match 36.7%; Score 1835.2; DB 8; Length 15315;  
Best Local Similarity 63.2%; Pred. No. 0;  
Matches 2992; Conservative 0; Mismatches 1693; Indels 51; Gaps 9;  
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QY 326 TCGTCACAGCGACAGGAGAGAGGTTGCTGGCTGCCGAGGTTCTCGGCAACCGGCAC 385  
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QY 446 GTCATCGAAGCGGCTTTTCAAGAGCTTTTACAGGAGTTGGTAACAGCTCGGGATCT 505  
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QY 506 GAACTCGGAAGAAAACCTTAGTTAAAGTACCGGTTCTGTTTATCGTACGCTACTATAC 565  
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QY 746 GTCGAGATGACTTGAATCTAGTCTCCGTGGCATTGAGAGATATTGACACAACGAAA 805

Db 481 GTTGGAGATGATCTAAATTTTGTGTGTGGCAACTGAAACGGTATTTTGACACACCGCCAAA 540  
Qy 806 GAGAACGAAATGATCGATAGTGAACCGCTCGTTCACGTGACGCACTGGTCGGTACAGCCC 865  
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Qy 866 TATGGTACTGGTATATCGAGGATGAAGTATGTGGGCTATGTTCGGAGGTGATGTGCTC 925  
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Qy 926 AGGTTCTTCCATGGAGGTGACAGTGTCTACTATACCTAGCACTTGGACAAAGGATGGG 985  
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Qy 1106 AGGATTCGGCACATCACTACTCTGGAAGATATCTTGGAGTTTAACGACCAGAAATGACTGTAT 1165  
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Qy 2006 AATATGATGAGGACGAAACACATAAAAGTGATATCTCTCTATTAGAAAACGACGACGC 2065  
Db 1738 AATATGATGAAGATGAACATATAAAAGTAATAATATCTCTTTTGGAAAAACATGGTCGT 1797  
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Qy 2246 TCGGCAGTGTACCGCAAAATGGTACTTTCGAGGTGCACTATGACCAACATAGAGAAGACCACA 2305  
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Db 2455 TTATTACTCTCAACAAAATTTTGACAAATCGATCCGTCGTTCTATTTTGGAAATCTTTAGTAAA 2514  
Qy 2786 CGGCGCTTGGCTGGACCCCGCTAGTACAGGACGATACGGCTTTTGTGCTTACGCCCTGTT 2845  
Db 2515 TGGGTACTCAGGACCGTGGTATGTTGAAGATGATACAGATTTGTTCCAAATCCAGTT 2574  
Qy 2846 GATACCTTTACAGATTAATCTGCTCTACATATGTGGAACAAATACAGAGCAAGCTAGCTGAA 2905  
Db 2575 GATACATCAATGGTCACCTTTACCTAGTTTACATAGAAAAATATAAAGATATAATTAGCAGAG 2634  
Qy 2906 AATATTCAGAAATGTGGGCTATGAATAAGATCGAACGAGCTGGATGTACGGCGACGAG 2965  
Db 2635 AATATTCAGAAATGTGGCAATGAATAAAATTTGAAGCTGGTTGGCAATATGGTGATAAA 2694

QY 2966 AGAAGAGACTTGCACAAGATCCACCCCTGCTCGTCCCTCGACGCACTCCCGCCGCT 3025  
 Db 2695 AGAATGATACCTAGGAAATATCATCATGTTTAAATACAGTTTGGCAAGTTCAGCC 2754  
 QY 3026 GAGAAACGATACGATATACAACTTGTGTGAGACACTCAAGACTATCTGTGCTCTGGC 3085  
 Db 2755 GAGAAAGCGTATGATTTCTCAATTAGCTGTGCAACGCTTAAACCGTTATTTGCGTGGGA 2814  
 QY 3086 TACTACATCAGCTTAGAATAGCTCCAGCAGCCTCCGCAACGTTTCGCTGCCCCAATGAA 3145  
 Db 2815 TATACATATCCATCGATATCAACGCTCCGCAATTAACCGTAGGTTGCCCCAAGNA 2874  
 QY 3146 CTTTTATGAGCTCAACCGCTTACAGCCAGCAGCAGCCTCGACCTGAGTGTCTACCCCTG 3205  
 Db 2875 CCATTTATGCAATCCAAATGTTTACAAACCCAGCAGCAGCTAGATTTTATCTGCAATAAATTTG 2934  
 QY 3206 ACACCCAGATGAGTAGTAGGCTAGGCTAGGCTGGCTGAGAACACCCACACCTTTGGGCC 3265  
 Db 2935 TCAGGGAATGGAAGAAATTAATGACCAAGTTAGCTGGAATACACATTAATTTATGGGCA 2994  
 QY 3266 AGGAGAGGATACAGCAGGATGGACTTACGGACTTAATGAGGACTCGGACATGCATCGA 3325  
 Db 2995 AAGAAAGAAATACAAAGGATGGAGCTATGTTTAAATGAAGAAATTAACAAATGTACGC 3054  
 QY 3326 TCCCGCACCTGCTGCATACCCGAGGTTGACGATGCCATCAAGAGGCCCAACAGGGAC 3385  
 Db 3055 AGTCTCTATTTAGTACCGTACAGCAAGTAGATGACGCTATTAAAGCTAATAGAGAT 3114  
 QY 3386 ACAGCTCGGAGACTGTGAGGACCTGTGCTGAGGCTATGCTGGGATATGCTGGACCCGCTACT 3445  
 Db 3115 ACAGCAAGTGAACAGCTCGCACTTTATAGTATATGTTTACAACTTAGACCCACCGACT 3174  
 QY 3446 GGGAGCAGCATGAG--CACTCTGTTGGAAGCGTCAAAACAGAGCAAGCAACCGACTTC 3502  
 Db 3175 GAGAAACAAACGAAAGCGCACTCTCTAACAGACGAAACACTTAATAGATCTTTGAGCTTC 3234  
 QY 3503 AGAACATACCGGCTGAGAAAGCACTATGCGCTCAGCTCTGGGAAGTGTACTTTCGAGTTT 3562  
 Db 3235 AGAACATATCGTCTGAAAGAAACATATGCTGTTGCAAGTGAATGGTATTTCGAGTTT 3294  
 QY 3563 GAGATCTTAACGGCTGGAACCTATGAGGCTCGGCTCGCTCAACGCTGATATGGCACAGGA 3622  
 Db 3295 GAGATATTGACAAACCGGCCCATCGAGTTGGATGGGCGAGGTTTACATGTTCTCCGGGT 3354  
 QY 3623 ATGATGCTCGGACAGACAGAACTCTGGGCTTTTGAATGGTTCACATGAGAAAGAGT 3682  
 Db 3355 TATCAATCGGTAGTGACGAAATTTCTGGGCAATTTGATGGTTTATACGAAAGAAATTT 3414  
 QY 3683 TACAGCGGTAACTCAGTCTTTTGGCAAGCAATGGGCTGTTGGTACGCTAGTGGGGGTG 3742  
 Db 3415 TATATGGGCACAGCCGAATCATTTGGAGGCACTGCAAGTTGGAGATGCTGTGGAGTG 3474  
 QY 3743 TTTCTAGATCTCATTTGATAGAGATAGATTTCTCACTCAACGGTGAATTTGTATGGAT 3802  
 Db 3475 TTTTATAGACTAATGATCATACAAATAGTTTTCGTTGAATGGAGAAATTAATTAATGGAT 3534  
 QY 3803 GCTCTTGGCGGAGAGACTAGTTGCTGATGCTGAGTCCAGGTTGACAACTTTGCTGCTGCTG 3862  
 Db 3535 ACATTTGGGAGGAAACTACGTTTCTGAAAGTTCAAGGAGAGGATTTGCTGCTGCTGCT 3594  
 QY 3863 ACCTTTGGTGTGGGCAAAAGCCAGGTTTAAACATACGCTGAGGAGTGAACGCTGAA 3922  
 Db 3595 ACTCTGGGACTAGGACAAAGAAAGCAAAATTAATCTTTTGGTCAAGACGTAACCTCATTTGAAA 3654  
 QY 3923 TACTTCACAACATGCTGCTGAGGAGGATATGAACCAATTTCTGTCTCAATATGAAGAGA 3982  
 Db 3655 TACTTCACGACTTGTGCTCTCAAGAGGATATGAACCAATTTTTCGTTAAACATGAAGAGA 3714  
 QY 3983 GAGTGACTACCTGTTACCAACAGACCGGCTGCTGAGAAATACGATGAGATGATGATC 4042  
 Db 3715 CCAGTAACATATTTGGTATACTAAGGATCAACCAATATTTGAAATACTGATGA--CTTT 3771  
 QY 4043 GACACCAGATAGATGTGACCAAGATACCAAGCTGTTTCAGATACACCTCCACTCAAG 4102

Db 3772 TCCTGTGTAAATGTGATGTACAAAGATTCACAGCTGTTTCAGATACACCACTGTTCTAAA 3831  
 QY 4103 ATTTCCCAACACAGCTTTGAGACGATGAGAAAGCTAACTCGGAGTCTTCTACGCTCTCA 4162  
 Db 3832 ATAGTCTATATATCATTTTGAACCATGGAAGAGCTAATTCGGATTTTACGGCTACT 3891  
 QY 4163 CTGCTGTCTATCTGCCATTAACAGATTCTTACGAGGCGAGAAAGCCAGCGTTGGGTA 4222  
 Db 3892 TTGCTGTCTATGTCTACCAAAATTTTATTGATGAACAAAGAAACAAAGAGAGATGGCAA 3951  
 QY 4223 GAAATCAAGGACCGCCCAACGATCCTAATGAAGGCGAGTTGAAGCTCAGATGTCGCC 4282  
 Db 3952 GAAATCAAGATTTAGCGAGCACAGGTTATTGCAAACTTGAGCATGCT---ACTCCTGCT 4008  
 QY 4283 CATATTGACAGATCATGAGGAGCGGTTTCAACCATGAACGATATTTAAAGGTTTGCACCTAC 4342  
 Db 4009 CATATTGACAAATTAATGAATCAGGATTTTCAATGATGATATTAAGAGCTTTCATCGA 4068  
 QY 4343 GAAGCAATCAAGGAGGTTGCCAGCTCCAGATGAAGAGCGCTGCTTCAAGGCCACA 4402  
 Db 4069 GGTATTTCGGATGATCTCTGTAGAAAACGATGAAATGATGCCAAACACTGCACCTTTTACCA 4128  
 QY 4403 CGTAAGGATCCATGACAGAGGTTTACTATACAAATTAACAAATTTGCAACCGAGC 4462  
 Db 4129 CCAAGAGGAAAAAATCAACCCACCCAGCCAGCCAGCAACGATGATGATGATGATGATGAT 4188  
 QY 4463 CAAGTCAAGCGATGACCGGTCGACCACTGAAAGCTGAAATGGCCAGGATGATGATGATGAT 4522  
 Db 4189 CAGCATGACTTAA-----CGATCGAAATGACGGAAGTTGAAATGCTGATCTAGT 4239  
 QY 4523 GCGCAAGGTTTTCAGCCCTGATGAAGAGGACGAAGAGGGGACGATGCTGCTTCAAGTTC 4582  
 Db 4240 GAAATGAAATTTTAAATATATATATATCAGCAAAACGCTAATGGCCAGGACATAAACAAAGAT 4299  
 QY 4583 TTCAGAACAGCGCGCGGAAAGAGTGTGCTGCTAAATCCGCTAAATCCGAAACCAACCA 4642  
 Db 4300 GACAGAAAAAAGAGAGGACGTTCTCCATTTTCGATTTTTCGAGAAAAAAGAGGGCT 4359  
 QY 4643 GACCCCTTCAGTGATACCGAAGTATCACAGAACGCTGCTGCTGAGGAGGCTAACCTCAG 4702  
 Db 4360 TCGGATAATCTTAAAGAGCAAAACTCCGATCCAGCTAGAAATGTGTTAGATCAGT 4419  
 QY 4703 ATCAAGTGTACAGGCGCAATCAAGATATAACCGCATGAACGCGCTCCTAGCAGGACC 4762  
 Db 4420 AATGCTGCTCAGACACCTAATACATTAATGAAGAAATACTCC---CCAAATAGAGT 4475  
 QY 4763 AACCTGTATGGAGCCAAAGTTGGTTTGAACCTGGAACGCTCAGATGCGGAGCGCCACCA 4822  
 Db 4476 TTCACAAATGGACTTAAATTTGGTTCCACAGCTATTCTGATAGACAGGAGGTTCCAAA 4535  
 QY 4823 GACAGAGCAGATGACAGCCAGCACTCTCGCGCAGTCCGCTACGGAACCTGTCGCAAT 4882  
 Db 4536 AGCA-----ATGTCATTTTACCTTCATCAGCAGGATTTGAATTCGTGGGAAT 4584  
 QY 4883 GAGATCTTCGATGACAGGTTTGAAGCTCATCAATGATGATCTTTTATGGAGTCAGGATC 4942  
 Db 4585 GAAATTTTGAATTTGAATTTTAAATTAATAACGAGTATTACTATGTTGTTAAGATA 4644  
 QY 4943 TACCAGGTCAGAACCCCAACCATGATGATGCTGCTGGTGGTACCCAGCAGTACCA 4998  
 Db 4645 TTTCCCGGCAAGACCTTACACAGTTCAGTGGGATGGTTTACTACTCAATTTCA 4700

RESULT 11

US-11-097-143-22561/c  
 ; Sequence 22561, Application US/11097143  
 ; Publication No. US2005020858A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Venter, J. Craig  
 ; APPLICANT: et al.  
 ; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID  
 ; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE

; TITLE OF INVENTION: DROSOPHILA GENES.  
; FILE REFERENCE: CL000728  
; CURRENT APPLICATION NUMBER: US/11/097,143  
; CURRENT FILING DATE: 2005-04-04  
; PRIOR APPLICATION NUMBER: 60/157,832  
; PRIOR FILING DATE: 1999-10-05  
; PRIOR APPLICATION NUMBER: 60/160,191  
; PRIOR FILING DATE: 1999-10-19  
; PRIOR APPLICATION NUMBER: 60/161,932  
; PRIOR FILING DATE: 1999-10-28  
; PRIOR APPLICATION NUMBER: 60/164,769  
; PRIOR FILING DATE: 1999-11-12  
; PRIOR APPLICATION NUMBER: 60/173,383  
; PRIOR FILING DATE: 1999-12-28  
; PRIOR APPLICATION NUMBER: 60/175,693  
; PRIOR FILING DATE: 2000-01-12  
; PRIOR APPLICATION NUMBER: 60/184,831  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: 60/191,637  
; PRIOR FILING DATE: 2000-03-23  
; NUMBER OF SEQ ID NOS: 43008  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 22561  
; LENGTH: 24236  
; TYPE: DNA  
; ORGANISM: DROSOPHILA  
US-11-097-143-22561

Query Match 29.1%; Score 1455.8; DB 13; Length 24236;  
Best Local Similarity 67.0%; Pred. No. 0;  
Matches 2256; Conservative 0; Mismatches 872; Indels 237; Gaps 4;  
  
QY 546 GTTATCGTACGCTACTATACGGCAATGCTATCTTTCCGACATCTTAACAGTATATGT 605  
DB 22012 GTACTTGATCGCTTCCACTTGGCCAGCAAGATAAATCTAAACAATCTTACACTTTGCGAGT 21953  
  
QY 606 ACCTGGCTGCTGTCAACATCATCATCCAGGATAAGCTGGCTTTGACGTGGGTCTGC 665  
DB 21952 ACTTGGCATGTCTGTCCACCTCTCTCGTCAACGACAAGCTGTCTTCCAGCTGGGCTTGC 21893  
  
QY 666 AACGACCTCCCAAGGTGAAGCTCTGTGTGACCTCTGCATCTCTGCCAGCAAAACAGAGAT 725  
DB 21892 AGGACACAGCCAGGAGAGGCTTGTGTGGACGTTTCATCCGCGAGCAAGCAGCGCT 21833  
  
QY 726 CCGAGGCGAAGAGTGTGCGAGATGACTTGAATCTAGTCTCCGTGGCCATTTAGA 785  
DB 21832 CTGAGGCGAAGAGTGTGCGGCTCGGAGATGATCTGATCTGTGTCTCCGTGCCACCGAAC 21773  
  
QY 786 GATACCTGCACACCAAGAACGACGAGATATCGATAGTGAACGCGTCTCCACGCTGA 845  
DB 21772 GTTATTTGCATACGACCAAGGAGAACGACGATCTATTTGTAATGCCAGCTTCCATGTGA 21713  
  
QY 846 CGCACTGGTCCGTACAGCCCTATGTTACTTGTGTATATCGAGGATGAAGTATGTGGGCTATG 905  
DB 21712 CCCACTGGTCCGTGAGCCCTACGCAAGGCAATCTCCAGGATGAAGTACGTGGGCTATG 21653  
  
QY 906 TGTTCGAGGTGATGTCTAGTTCCTTCATGAGGTGACAGGTCTTCACTATACCTA 965  
DB 21652 TCTTTGGCGGCGATGTGTGCTTTCTTCCATGTTGGCGAGAGTGCCTGACCATACCGA 21593  
  
QY 966 GCACCTTGCAAAAGATGGGGGCAAA- 993  
DB 21592 GTACATGGGTCGTGAGGCGGACAAAGTAAGTTTATCATCTCGAAATGACTTAAAGTCAAC 21533  
  
QY 994 -----TATCGTAGTCTACAAAGGAGGTTTCAGTG 1021  
DB 21532 TATACAAAGTACCCCTTCAATCCCTGACAGTATTTGTTATTACGAGGCGGCGTGTGTC 21473  
  
QY 1022 ATGCTCAAGCCCGTTCTATATGGCCCTGGAGCTGGCTAGAAACAAAGTGGGCGGAGGT 1081  
DB 21472 ATGGCACAGGCGAGGTCCGTGTGGGCGCTTGGAACTCGCTCGAACCAAGTGAAGTGTGGC 21413  
  
QY 1082 TTCATTACTGTTACCTCTATGAGGATTCGGCACATCATCTACTTGGGAAGATATCTTGGGA 1141

DB 21412 TTTTATCAACTGGTACCAACCGATGCGCATACGCGACATACCACTGACGCTACTTGGGC 21353  
QY 1142 GTTAAACGACAGAAATGAGCTGTATTTAGTTAGCAGAGAGAAACCCACAAAGCTTCTGT 1201  
DB 21352 GTCAACGACACAGCAACGAACTGATTTAGTTTAAAGAGGAGGCTTCGATTTGCCACGACG 21293  
QY 1202 GCCTTTCCTGCTGCGCAGGAGAAAGGATGATCAGAAAGCAAGTGTTTAGAAAGCAAGGACTTG 1261  
DB 21292 ACTTTTCTGCTGCGCAGGAAAGGACGACGAGAAAGAGTGTGTTGAGGACAGGACTTG 21233  
QY 1262 GAGGTATAGCGCGCCCATCATCAAGTACGCTGACTTCCACCGTCAATTTGTGACGATTCG 1321  
DB 21232 GAGGTGATCGCTCGCGCATCATCAAGTACGCGACACTACCGTCACTCGTTTCAGCACTGC 21173  
QY 1322 GAGACTGGCTGTGGCTGTCTTATAGTCTTACGAAACGAAAGAGGCTGGGTAA 1381  
DB 21172 GAGACTAGCTTGTGGCTCAGCTACAAGAGTTATGAGACGAAAGAGGCGTAGGAAAG 21113  
QY 1382 GTAGAAAGAGCAAGCGATTCTCCAGAGAAAGGCAAGATGACGATGGCTCGACCTC 1441  
DB 21112 GTGAGGAGAAAGCAAGCGATCTTGCCAGAGAGGCAAGATGACGATTTGCTCGACTTC 21053  
QY 1442 TCCAGGTCAACAGGAGGAAGTCTATGACTGTCTGAGTTATCAGGAAGTGTTCCTGCTG 1501  
DB 21052 TCGCGCTCCAGGAGGAGGAGTCCAAGACAGCTCGTGTCTATCCGAAAGTCAGCAGCTC 20993  
QY 1502 TTCACTAAGTTTA----- 1514  
DB 20992 TTCACCCAGTTTATACGTAGTGACTTGAAGTCTTTTACGAGTGAATTTCTTATCGTA 20933  
QY 1515 -----TCAATGGCTCGAAACTCTTCAAGAGAAACCGTCTGCTCACTCGAGTGTCT 1562  
DB 20932 TTCACACTCAATTTTCAGAGCTTGGAAACACTGAGTCAATCGCGACACTCCCAATTTCT 20873  
QY 1563 TCGCGTCAGTGAACCTTGGGCGAGATGGTGTCTTTGAAGATCTCACCAACTACTTTCG 1622  
DB 20872 TCCAAAGAGTCAACCTCAACGAGATGCTCATGTGCTTGAGGACTTGAATTAACACTTTT 20813  
QY 1623 CACAGCCGATGAGGATATG----- 1642  
DB 20812 CGAAACCGAAGACGATATGGGTAAGTCAATCAAAATATGACCTAAGATGTTCAATAA 20753  
QY 1643 -----GAACACGAAGAAAGCAAAACAAATTCGCGCGCTCCGCA 1683  
DB 20752 AATCTATACTAATTTTCAGAGCACAGGAGAAACAGAACCGATTCGTCGCTCGCA 20693  
QY 1684 CCGTCAGGACCTGTTTCAAGAGGAAGGCATATCGAACCTGATCTCTCGAAGCTATAGACAA 1743  
DB 20692 CCGACAGGATCTGTTCCAGGAGGAGGCGTCTCAATCTGATCTCTGGAGGCCATTTGACAA 20633  
QY 1744 GATCAACGTCGTCACGTCGCCAGGTTTCTGGCTGGATTTCTTGGCGGAGACGAATCTGG 1803  
DB 20632 GATCAACATAATCACTTCGAGGCTTCTTAGCCAGCTTCTTGGCCGCGACGAGACCG 20573  
QY 1804 ACAGAGCTGGGAATGATATCTGGATATTTGTATCATGTTCTGTCGCGCAATAATAAAGG 1863  
DB 20572 CCAGAGCTGGATCTCATCTCCACTATTTGTACCAACTCTTGGCCGCAATCATCAGGG 20513  
QY 1864 CAACACACGAACTGCGCGCATTTTCGGAACCTCGAAACCGGTTTCACTGGCTGTCTCGCG 1923  
DB 20512 CAACCAACGAACTGCGCCCACTTTCGCGAACAGTAAACCGACTCACTAAGTGGCTATTTCTCCG 20453  
QY 1924 CTTGGCTCGAGGCTCGGCGAGGCAACCGGATGCTCGAGCTGTGCACTGCATCCT 1983  
DB 20452 CTTGGTTCGAGGCTTCCAGCGAGGTTCCGCGATGTTGGACGACTTCTACTGCGTGT 20393  
QY 1984 CATGACTCGCTCAAGCGCTCAATATGATGAGGAGCGAAACACATAAAGTGAATAATCTC 2043  
DB 20392 GATCGATTCGCCAGAGGCACTAAACATGATGCGGAGTAGACACATCAAGTGTGATCATCTC 20333  
QY 2044 TCTATTAGAAAGCAACGAGCGGACCCCTAAAGTACTAGATGTGTATGTTTCACTCTGCT 2103

Db 20332 CCTGCTGGAGAACACAGCGCAGGAGCCCGAAAGCTCTAGACGTTCTGTGTCTCTGTGCGT 20273  
Qy 2104 CGGTAAACGGCTCGGGTGGCTGCTGTCACAGAAACAACTCTCGGACTATTTCCTGCCGG 2163  
Db 20272 GGGTAATGAGTGGCGGTGGATCTCTCCAGAAACAACTTTCGACTTTTTCGTAACGGG 20213  
Qy 2164 CAAGAACCTGTTGCTGCAAACTGCGCTGTGTAGATCACGTPATCTAGTGTCCGTCGAAACAT 2223  
Db 20212 CAAGAATCTGTTGTACAGACGCTCTCTGTGGACCATGTGGCCAGCATCCGACCGAAACAT 20153  
Qy 2224 CTTCTGGGCCGAGTAGAAGGTCGGCAGTGTACCGCAATAGTACTTCGAGTGAATAT 2283  
Db 20152 CTTCTGGGTGCGGTGGACGCTTCTTCCATGTACCAAGAGTGGTACTTTCGAGTGAACCAT 20093  
Qy 2284 GGACACATAGAGAGACACACATATGATGACCATCTACGCATAGGATGGCTAAACAC 2343  
Db 20092 GGATCACATCGAAGACACACCATGATGCCACCTTGGCTGGCTGAATATAC 20033  
Qy 2344 TACTGGTTATGTCCCATACCCGGGTGGTGTGAGAAAGTGGGAGGTAAACGGCTGGAGA 2403  
Db 20032 TTCCGGGTATGTACCGTATCCCGGAGCGCAAGAGTGGGTGGCAATGGAGTAGGCGA 19973  
Qy 2404 CGACTGTACTGTACGGGTGTGATGGCGCTTACCTCTGGTCGGCGGAGGAGAACCC 2463  
Db 19972 TGACCTGTACTCTTTGGATTTGATGGTGCCTTTCTTGGACGGGAGGTTCGCAAAACAT 19913  
Qy 2464 GGTCAATAGACTCATGCTGAAGAGCCTTATATTAGGAAGGTGAGTATAGGTTGTC 2523  
Db 19912 AGTGTGGACGGCTGCCGAGAGGCCCTTATTCGTAAGGCGATGTTATTGGCGTTGC 19853  
Qy 2524 ATTGGACCTGAGGTACCCTCATCAACTTTCATGTTCAACGGAGTGGGTGACGGGATC 2583  
Db 19852 CATTGACCTTTCTGTGCCCATCATCAGCTTACTTTTACGGAGTAAGAGTGGCGGTAG 19793  
Qy 2584 CTTACCAAACTTAACTCTGGAAGGCATGTTCTTCCGGTTCATCAGCTGTCTAGTAAGCT 2643  
Db 19792 CTTTAGGAGCTTAACTCTGGAAGGCATGTTCTTCCGGTGTGATGCTCATCAAACT 19733  
Qy 2644 GAGTTGTCGGTTCCTGCTGGCGGAGAACACGGGTAGACTCCGGTAGCGGCTCCAGAGG 2703  
Db 19732 AAGCTGTGCGCTTCCTTTTCGAGGTGATCATGGTGTGTTTAAAGTTTGGCCCGCCATGG 19673  
Qy 2704 CTACTCCCGCTGGTGGAGTCTCTCTCGCGAGCAGATCCTCAGCGCTGGAGCGGTCTT 2763  
Db 19672 ATTCCTGCGCTCGTGCAGTGTCTATGCGGAGCAGATCTCTCAGTCTGATCTTGTCTT 19613  
Qy 2764 CTACTTCGGCAACCTGTCCAAGCGGCTTGGCTGGACCCCGCTAGTACAGACGATAC 2823  
Db 19612 CTACTTTGGTAACTTTGGCAAGAACTGTTTGGCGGACCATGGCTTATTGAGGACGACAC 19553  
Qy 2824 GGCTTTTGTGCTACGCTGTGATATCTTACAGATTACTTGCCTACATATGTGGAACA 2883  
Db 19552 TGCTTTTGTTCGAAGCCGCTTGATACCAAGGCTGTGACATTGCCAAAGTTCTGTGGACCA 19493  
Qy 2884 AATCAGAGCACTAGCTGAAATATTCAGGAAATGTGGCTTATCAATAAGATCAAGC 2943  
Db 19492 AATCAAGGAGACTGCGGAGAAATATCCAGGATGTGGCTCTTAAACAAATCGAGC 19433  
Qy 2944 AGGCTGGATGTACGGGACACAGAGAGAATTTGCAAGATCCACCCCTGCTCGTGC 3003  
Db 19432 GGGCTGTCTGGGCGAGCACCAGATGACTACCAACCGCATCTCTTGCCTCACCCA 19373  
Qy 3004 CTTTCGAGGACTCCCGCGCTGAGAAAAGATACGATATACAACTTGTGTGAGACACT 3063  
Db 19372 TTTTCGAGAGCTTCCCGCGCGGAAAAGCGATACGCAATCAACTAGCTGTGCAACGCT 19313  
Qy 3064 CAR-----GA 3068  
Db 19312 GAAGTAAGTTGGCTTACTCTTAAGGAAATTAACATATATGACCTCTTACTCTATAGGA 19253  
Qy 3069 CTATCTGGCTCTGGGCTACTACATCAGCTTAGATAAGCCTCCAGCAGCATCCGCAAG 3128  
Db 19252 CGATTATCTCGCTGGGATCTACATTAACCATGACCAAGCCACCGACGCAATTCGCCCG 19193

Qy 3129 TTCTGTCGCCCAATGAACCTTTTCATGCTAGTCCAAAGGCTAACAGCCAGACACACTCGACC 3188  
Db 19192 TGGCGCTGCCCAACGAGATCTTCATGCAAGGCAATGGCTACAAGCGGCTCCACTTGACC 19133  
Qy 3189 TGAGTGTCTCACCCTGACACCCAGATGGATGAGTGTAGTAGGCGAGCTGGCTGAGAAC 3248  
Db 19132 TAAGCGCGTGTGACACTCAACCCCAAGTTGGAGGAGCTTGTGACAGCTGGCCGAGAAC 19073  
Qy 3249 CCCCAACCTTTGGGCCAGGAGGAGATACAGCAGGATGGACTTACCGACTTAATGAGG 3308  
Db 19072 CTCACATCTGTGGCAGCGGAGCGCATCCAGAGGCTTGGACTTATGGTCTGAACGAG 19013  
Qy 3309 ACTCGGACATGCATCGATCCCGCACCTTGGTGCCATACCCGAAGGTTGACGATGCCATCA 3368  
Db 19012 ATAGTGAACCCACAGGAGTCCACACTTTGGTGCCATATGCCAAAGTGGACGAGGTATCA 18953  
Qy 3369 AGAAGGCCAACAGGAGACACAGCTCGGAGACTGTGAGGAGCCCTGTGCTACGGGTATA 3428  
Db 18952 AGAAGGCCAACAGGAGACACAGCTCGGAGACAGCTCGGAGACAGTGTGCTTACGGATATG 18893  
Qy 3429 TGCTGACCCCGCTACTCGGGAGCAGCATGAAGCACTCTTGTGGAAGCTCATAAACACA 3488  
Db 18892 TTTTGGATCTCTCGACTGCGGAGAACGAGGAGCACTTCTGGCCGAGGACAAACGCTCA 18833  
Qy 3489 AGCAAGCCGACTCTTCAAGAACATACCCGCTCGAGAGAACATATGCCGTCTGAGTAAGT 3548  
Db 18832 AGTTCGCGGATTCGGACTTACAGGTTGAGCGCAACTACGCCGTGACATCGGCAAGT 18773  
Qy 3549 GGTACTTCGAGTTGAGATCTTAACGGCTGAGCACTATGAGGCTCGGCTGGGCTCAGCTG 3608  
Db 18772 GGTACTTCGAAATTCGAGTCTCTCAGCTCGGACCAATGCGAGTGGGTTGGGACCGGCG 18713  
Qy 3609 ATATGCCACCGAGATGATGCTCGCACAAGACGAGCACTCTCTGGGCTTTTGTGTTACA 3668  
Db 18712 ATTGCTATCCGGAGCGATGCTGGCAGGAGGACCAACGATTTGGGCTTCGATGAGACA 18653  
Qy 3669 ATGAG 3673  
Db 18652 ATGTG 18648

RESULT 12  
US-10-305-720-1154  
; Sequence 1154, Application US/10305720  
; Publication No. US20040010136A1  
; GENERAL INFORMATION:  
; APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.  
; TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expression  
; FILE REFERENCE: PA-0002-1 CON  
; CURRENT APPLICATION NUMBER: US/10/305,720  
; CURRENT FILING DATE: 2002-11-26  
; PRIOR APPLICATION NUMBER: 09/016,434  
; PRIOR FILING DATE: 1998-01-30  
; NUMBER OF SEQ ID NOS: 1490  
; SOFTWARE: PERL Program  
; SEQ ID NO 1154  
; LENGTH: 4078  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: GenBank ID No. US20040010136A1 g1526977  
US-10-305-720-1154

Query Match 16.8%; Score 840.8; DB 7; Length 4078;  
Best Local Similarity 55.0%; Pred. No. 2.3e-260;  
Matches 2105; Conservative 0; Mismatches 1622; Indels 101; Gaps 19;  
Qy 343 AGAGAGGTTGCTGGCTGGCTGGCGAAGGTTCCGCAACCGGCACTGCTTCTCTCGAGAAAT 402  
Db 217 ACAGAAGCTATGCTTGGCAGCAGAGGATTTGGCAACAGACTTTGTTTCTTGGAGTCCAC 276



Db 2398 AGATCTGAGTGGCCCCAAGCATCTCGTTCCGAATTAATGACAAACCTGTTCAAGGAATGTT 2457  
 Qy 2587 CACCAACTTCAATCTGGAGGATGTTCTTCCGGTCAATCAGCTGCTAGTAAGCTGAG 2646  
 Db 2458 TGAGAAATTTCAACATCGATGGGCTCTTCTTCCAGTCGTAGTTCTCTGCGAGGAATAA 2517  
 Qy 2647 TTGTGGGTTTCTGCTGGGCGGAGAACACAGGTAGACTCCGGTACGCGGCTCCAGAGGCTA 2706  
 Db 2518 AGTACGCTTCTGCTTGGAGGCGACATGGAGAAATTCAAAATTTCTTCCCTCCACCTGGGTA 2577  
 Qy 2707 CTCCTGGCTGGTGGAGTCTCTCTGCGGAGAGATCCCTCAGCTGGAGCCGTGC----- 2761  
 Db 2578 TGCTCTCTTTATGAAGCTGTTCTTGCCAAAAGAAAGTTGAAAGTGGAAACACAGCCGGA 2637  
 Qy 2762 -TTCTACTTCGGCAACTCTGCAAGCGGCTTGGCTGGACCCCGCTAGTAGTACAGACGA 2820  
 Db 2638 GTACAAAGCAAGAAAGNACTTACACGCGACCTCTGGGCCCCACAGTTTCCCTGACGGA 2697  
 Qy 2821 TACGGCTTTTGTGCGCTACGCTGTTGATATCTTTACAGATTACTCTGCTTACATATGTGA 2880  
 Db 2698 AGCTGCTTTCACACCCATCCCTGTGGATACAGCCAGATCGTGTGGCTTCCCTCATCTAGA 2757  
 Qy 2881 ACAATACAGAGCAAGCTAGCTGAAATATTCAGAAATGTGGGCTATGAATAAGATCGA 2940  
 Db 2758 AAGAATAAGAGAAAATGCGCAGAGAAATATCCATGAACCTCTGGTTATGAATAAAATTGA 2817  
 Qy 2941 AGCAGCTGGATGTACGGCGCACAGAGAGAACTTGCACAGATCCACCCCTGCTGCT 3000  
 Db 2818 GCTTGGCTGGCAGTAGTGGTCCGGTTAGAGATGACAAAGAGACAAACCCATGCTGCT 2877  
 Qy 3001 GCGCTTCGAGCGACTCCCGCGCTGAGAAAGGATACAGATATACAACTTGTGTGCGAGAC 3060  
 Db 2878 GGAGTTCTCAAGCTGCTGAACAGGAGCGCAATTACAACTTACAAATGCTGCTTCGAGAC 2937  
 Qy 3061 ACTCAAGACTATCTGGCTCTGGGCTACTACAT---CAGCTTAGATAAGCCCTCCAGCAG 3117  
 Db 2938 CCGTGAAGACTTTGTTGGCATTAGGATGTCATGTGGGTATATCAGATGAACATGCTGAAGA 2997  
 Qy 3118 CATCCGCAAGTTCGCTGCCCAATGAACCTTTTCATGCACTCCAGGTCGCAAGGCTGCAAGCCAGC 3177  
 Db 2998 CAAGGTGAATAAATGAAGCTACCCAGAAATTAACCAAGCTGCAAGGTTGATACAAAGCTGC 3057  
 Qy 3178 ACCACTCGACCTGAGTGTGTCACCTGACCCAGATGAGTGTAGTAGGCGAGCT 3237  
 Db 3058 CCTATGACCTGAGCTTTATCAACTCACTCCATCGCAAGAGCAATGCTGCAAGTT 3117  
 Qy 3238 GCGTGAAGACACCCAACTTTGGCCAGGAGAGGATACAGCAGGATGCACTTACCG 3297  
 Db 3118 GGCAGAAATGCACATAATGTGTGGCGCGGGATCGAATCCGCGCAGGCTGGACTTATGG 3177  
 Qy 3298 ACTTAATGAGGACTCGGACATGATCGATCCCGGACCTGGTGCCATACCCGAGGTTGA 3357  
 Db 3178 CATCCAACAGGAGCTAAGAAACAGAAATAATCCTGCGCTTGTTCCTACACTCCTCTGGA 3237  
 Qy 3358 CGATGCCATCAAGAGGCCAAACAGGACACAGCTCGGAGACTGTGAGGACCTGCTGCT 3417  
 Db 3238 TGACCGAACAAGAAATCAACAGGACAGCCCTCCGAGGCTGTGCGCAGCTGCTGGG 3297  
 Qy 3418 CTACGGGTATATGCTGGACCCGCTACTGGGGAGCAGCATGAGCACTCTTGTGGAAGC 3477  
 Db 3298 GTACGCTCAACTTGGAGACCC-----AGATCAAGATCATGACGACGAGCCGAACT 3351  
 Qy 3478 GTCAAAACAGAACAGCCGATTTCAAGACATACCGGCTGAGAGAACTATGCGCTCAG 3537  
 Db 3352 GTGACGCGCACCGGGGAAAGTTCCGAATCTTCCGTGCGGAGAGAACCTATGCACTGAA 3411  
 Qy 3538 CTCTGGAGAGTGTAATTGAGTTTTCAGATCTTAACGGCTGACCTATGAGGCTCGGCTG 3597  
 Db 3412 GCGCGGACGGTGGTATTTTGAATTTGAGACGGTCACTGCTGGAGACATGAGGCTTGGTTG 3471  
 Qy 3598 GCGTCAAGCTGATATGGCACCCAGGAATGATGCTCGGACAAAGACAGAACTCTCTGGGCTTT 3657  
 Db 3472 GAGTCTCTGTTGTCAACCGGATCAGGAGCTTGGCTCAGATGAACGCTTTCGCTT 3531

Qy 3658 TGATGTTTCAATGAGGAAAAAGTGTACAGCGGTAACTGAGTCTTTTCGCAAGCAATG 3717  
 Db 3532 TGATGCTTCAAGGCCAGCGGTGTCATCAGG---CAATGAACACTATGGCGCTCTTG 3588  
 Qy 3718 GCGTGTGGTACAGTAGTGGGGTGTCTCTAGATCTCATTTGATAGACGATAAGTTTCTC 3777  
 Db 3589 GCAAGCAGCGCATGTGCTGGGTGTATGGTTGACATGAACGAAACACCATGATGTTTCA 3648  
 Qy 3778 ACTCAACGCTGAGTTGTTGATGATGCTCTTGGCGGAGAGACTAGTTTGTCTGATGTCCA 3837  
 Db 3649 ACTGAATGGTGAATCCCTTCTTGATGATTCAGGCTCAGAACTGGCTTTTCAAGACTTTGA 3708  
 Qy 3838 GGGTGACAA---CTTTGTACCTGCTTGCACGCTTGGTGTGCGCCAAAAAGCCAGGTTAA 3894  
 Db 3709 TGTGGCGATGGAATTCATACCTGCTGTAGCCCTTGGAGTGGCTCAAGTGGGTAGGATGA 3768  
 Qy 3895 ATACGCTCAGACGTAACACGCTGAAATACTTTCAACAATGTGTGTCAGAGGAGGATA 3954  
 Db 3769 CTTTGAAGAGTGTGAGCACCCTTGAATAATTTCAACCATCTGTGGCTTACAGAGGGCTA 3828  
 Qy 3955 TGAACCATCTGCTCAATATGAAGAGAGAGCTGACTCACTGCTACACCAA-AGACCAGC 4013  
 Db 3829 TGAACCATTTGCGGTTAATAACACAGGATATATACCATGTGGCTGAGCAAGAGGCTTC 3888  
 Qy 4014 CGATCTTCGAGAAATACGGATGAGATGATCGACACACAGAAATAGATGTGACAGGATACCA 4073  
 Db 3889 TCAGTTTCTTCAAGTTCCATCAACCATGAACA----TATAGAGGTGACCAAGATAGACG 3944  
 Qy 4074 CTGGTTCAAGATACACTCCATGCTCAAGATTTCCCAACAACAGTTTG 4121  
 Db 3945 GCACCATAGACAGTTTCCCATGTTTAAAGGTCACTCAGAAAGTCTTTTG 3992

RESULT 13

US-10-276-774-552  
 ; Sequence 552, Application US/10276774  
 ; Publication No. US20040053245A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hyseq, Inc.  
 ; APPLICANT: Tang, Y, Tom et al  
 ; TITLE OF INVENTION: No. US20040053245A1el Nucleic Acids and Polypeptides  
 ; FILE REFERENCE: 21272-030  
 ; CURRENT APPLICATION NUMBER: US/10/276,774  
 ; CURRENT FILING DATE: 2002-11-18  
 ; PRIOR APPLICATION NUMBER: 09/560,875  
 ; PRIOR FILING DATE: 2000-04-27  
 ; PRIOR APPLICATION NUMBER: 09/496,914  
 ; PRIOR FILING DATE: 2000-02-03  
 ; NUMBER OF SEQ ID NOS: 2700  
 ; SOFTWARE: Custom  
 ; SEQ ID NO 552  
 ; LENGTH: 14302  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-10-276-774-552

Query Match 16.8%; Score 840.8; DB 8; Length 14302;  
 Best Local Similarity 55.0%; Pred. No. 5e-260;  
 Matches 2105; Conservative 0; Mismatches 1622; Indels 101; Gaps 19;  
 Qy 343 ACAGAGGGTGTGCTGGCTGCGAAGGTCTCGGCAACCGGCACTGCTCTCGGAGAATAT 402  
 Db 217 ACAGAGCTATCTTGGCAGCAGAGGATTTGGCAACAGACTTTGTTCTTGGAGTCCAC 276  
 Qy 403 TGCCGA---CAAGAACATACCCCTGATCTGTCGAGTGTGTGTTGTCATCGAACAGC 459  
 Db 277 TTCCAATCCAGAAATGTGCCCGCAGACCTCTCCATCTGCACTTTGTGTCGAGCAGTC 336  
 Qy 460 GCTTTCAAGAGCTTTTACAGGATTTGTTAAAGTGTGGGATCTGGAACCTG----- 512  
 Db 337 CCTCTCTGTCCGGGGCTGACAGGATGCTGCTAAACACCGTGGAGAAATCAGAGGGCA 396



QY 513 -----GGAAGAAACTTAGGTAAAGGTACCGGTTCTGGTTATCGTAC 555  
Db |||||  
397 AGTTGATGTGAAATAATGAAATTCATGATGAAGACTGCTCAAGGTGGTGTCTATCGAAC 456  
QY GCTACTATACGGCAATGCTATCTTTTTCGACATCTTTAAACAGTATATGTAACCTGGGCTG 615  
Db |||||  
457 ACTCCTCTACGGACATGCCATATTGCTGGCCATTCCTATAGTGGCATGTATCTGTCTG 516  
QY |||||  
616 CTTGTCAACATC---ATCATCCAGGATPAAGCTGGCCTTTGACGTGGGTCTGCAACAGCA 672  
Db |||||  
517 CTTGTCCACCTCCCGGCTTCAACTGATAAGCTGGCTTTTGTATGTTGGCTTGAAGAGGA 576  
QY |||||  
673 CTCCCAAGGTGAAGCTCTGGTGAACCTGCATCTCTGCCAGCAAAACAGAGATCCGAGGG 732  
Db |||||  
577 CACCACAGGGAGGGCTTGTGGTGACCATACACCTGCCTCTAAGCAGCGATCAGAAGG 636  
QY |||||  
733 CGAGAAGGTGCGAGTCCGAGATGACTTGATTTCTAGTCTCCGTGGCCATTGAGAGATACTT 792  
Db |||||  
637 AGAAAAAGTACGAGTTGGAGATGACCTCATCTTAGTTAGCGTGTCTCTGAAAGGTACTT 696  
QY |||||  
793 GCACACAAAGAAAGAAACGAAGTATCGATAGTGAACCGCTGTTCCACGTGACGCACTG 852  
Db |||||  
697 GCACCTGTCTTATGCAACGCGCAGCTTACACGTGATGCGCTTTTCCAGCAGACTCTCTG 756  
QY |||||  
853 GTCGGTACAGCCCTATGTTACTGTGTATATCAGGATGAAGTATGTGGGCTATGTGTCGG 912  
Db |||||  
757 GAGCGTGGCCCAATCAGCTCAGG-----AAGTGAGCGCAGCCCAAGGGTATCTCAITGG 810  
QY |||||  
913 AGGTGATGTGCTCAGGTTCTTCCATGGA---GGTGACGAGTGTCTCACTATACCTTAGCAC 969  
Db |||||  
811 TGGTGTATGTCCTCAGGTTGCTGATGGACACATGGACGAGTGTCTCACTGTCCCTTCAGG 870  
QY |||||  
970 TTGGACAAAGGATGGGGGCAAAATATCGTAGTCTTACAAAGGAGGTTTCAGTGTATCTCA 1029  
Db |||||  
871 AGACATGGTGAAGACGCGGAGAACTGTTCAATTATGAAGGTGGCGTGTGTCTGTCA 930  
QY |||||  
1030 AGCCCGTTCTCTATGGCCGCTGGAGCTGGCTGAGTGAACCAAGTGGGCGGAGGTTTCATTAA 1089  
Db |||||  
931 TGCACGTTCCCTTTGGAGACTAGACGCTAAGAGTTTGCCTGGAGTGGGAAGCCACATAAG 990  
QY |||||  
1090 CTGTGTACCATCCTATGAGGATTCGGACATCACTACTGGAAGATATCTTGAGGTAAACA 1149  
Db |||||  
991 ATGGGGAACAGCCATTCGACACTACGCCATGTCAACACAGAAATACTTGAGTCTCATGGA 1050  
QY |||||  
1150 CCAGAAATCAGCTGTATTTAGTTAGCAGAGAGAAACCCACACAGCTTCCCTGTGCTCTG 1209  
Db |||||  
1051 AGACAAACCTTCTACTCATGGACAAAGAAAGCTGATGTAAATCAACAGCATTTAC 1110  
QY |||||  
1210 CTTGCCGAGGAAGAGATGATCAGAAGCAAGTGTTAGAACAACAGGACTTGGAGGTAT 1269  
Db |||||  
1111 CTTCCGGTCTTCAAGGAAATAATTGGATGTAGGGGTGAGA---AAAGAAGTAGATGGCAT 1167  
QY |||||  
1270 AGGCGCGCCCATCATCAAGTACGGTGACTCCACCGTCACTGTGACGATTCGGAGACTGG 1329  
Db |||||  
1168 GGGAAACATCTGAATAAAATAACGGTGACTCAGTATGCTATATACAAATGTAGACACAGG 1227  
QY |||||  
1330 CTTGTGGCTGTCTTATAAGTCTTACGAAACGAAGAAGAAAGCGTGGGTAAAGTAGAAGA 1389  
Db |||||  
1228 CCTATGGCTTACTTACCAGTCTGTGGAAGTGAATCCGTGAGATGGGATCTATACAAG 1287  
QY |||||  
1390 GAAGCAAGGATTTCTCCAGAGGAAGCAAGATGACAGATGGCTTCGACCTCTCCAGGTC 1449  
Db |||||  
1288 TAAG---GCTATTATGCTATCATGAAGGCCACATGGATGATGCAATAAGTTTGTTCAGATC 1344  
QY |||||  
1450 ACAGAGGAGNATCTATGACTGCTCGAGTTATCAGGAAGTCTTCTCGCTGTTCACTAA 1509  
Db |||||  
1345 CCAGCATGAAGAAATCACGACAGCCGAGTTATCCGGAGCACAGTCTTCTCTTTTCAATAG 1404  
QY |||||  
1510 GTTTATCAATGGCCTGGAAATCTTTCAAGAGAAACCGTGTCTCACTCGATGTTCTTCGCGTC 1569  
Db |||||  
1405 ATTTATAGGGCCCTTGATGCTCTCAGCAAGAAAGGAAGGCTTCCACAGTCGATTTGCC 1464  
QY |||||  
1570 AGTGAACCTGGGCGAGATGGTGTATGTCTTGAAGATCTCAACCACTACTTCGCGACAGCC 1629

Db |||||  
1465 TATAGAGTCG-----TAAGCCTAAGTCTGAGGATCTCATTTGGCTACTTCCACCCCCC 1518  
QY |||||  
1630 CGATGAGGATATGGAACACGAAGAAAGCAAAACAATTCGCGCCCTCCGCAACGCTCA 1689  
Db |||||  
1519 AGATGAGCATTTAGAGCATGAAGACAAACAGACAGACTACGAGCCCTGAAGAAATCGGCA 1578  
QY |||||  
1690 GGACCTGTTCCAGAGAGGAGGCATCTGAACCTGATCCTCGAAGCTATAGACAAGATCAA 1749  
Db |||||  
1579 AAATCTCTTCCAGAGAGGGAATGATCAACCTCGTCTGTGATGATGTCATAGACCGTTGCA 1638  
QY |||||  
1750 CGTGCTCACCTCCAGCGGGTTCCTGGCTGAATTCCTGCGGGGAGACGAATCTGGACAGAG 1809  
Db |||||  
1639 CGTCTACAGCAGTGCAGCACATTTGCTGTATGTTGCTGGGCGA---GAAGCAGGAGATC 1695  
QY |||||  
1810 CTGGGAAATGATATCTGGATATTTGTATCATAGTTGCTGGCGGCAATAATAAAGCAACCA 1869  
Db |||||  
1696 TTGGAAATCCATTTCTGAATTTCTGTATGATTTGCTGGCGCTCTAATTAGAGGAAATCG 1755  
QY |||||  
1870 CACGAATGCGCGAGTTTCGGAACTCGAACCGGTTCAACTGGCTGTTCTCGCCCTCGG 1929  
Db |||||  
1756 TAAAACTGTGCTCAATTTTCTGGCTC-----CTCGACTGGTTGATCAGGAG 1803  
QY |||||  
1930 CTGCGAGCCCTCGGGCGAGGGCACCGGCATGCTCGAGTGTGCACTGCACTCTCATCGA 1989  
Db |||||  
1804 ATTGGAAGACTGGAAGCTTCTTCAGGCATTTCTGGAAGTTTACACGTGTTTAGTAGA 1863  
QY |||||  
1990 CTGCGCTGAAGCGCTCAATATGATGAGGGAGCAACACATAAAAGTATTAATCTCTCTATT 2049  
Db |||||  
1864 AAGTCCAGAAAGCTCTAAATATTTAAAGAAAGGACATATTAATCTATTATCTCACTTTT 1923  
QY |||||  
2050 AGAAAGCAAGGAGCGGACCTAAAGTACTAGATGTCTATGTTCACTCTGCGTCGGTAA 2109  
Db |||||  
1924 AGACAAACATGGAAGAAATCACAAAGGTTCTGGAGTCTTGTGCTCACTCTGTGTTGCCA 1983  
QY |||||  
2110 CGGCGTCCGGTCCGCTCGTCAGACAAACATCTGCGACTATTGTGTCGCCGCAAGAA 2169  
Db |||||  
1984 CGGGTTGAGTCCGTTCTAACAGCATCTCATCTGTGACAACTCTCTACCAGGAAGAGA 2043  
QY |||||  
2170 CTTGTTCTGCTCAAACTCGCTTTGATATCATAGTATCTAGTGTCCGTGCGAATCTTCGT 2229  
Db |||||  
2044 CTTGTTATTGACACACGCTCTTGTGAACCATGTGAGCAGCATGAGACCAATATTTTCT 2103  
QY |||||  
2230 GGGCCGAGTAGAGGTTGCGCAGTGTACCGCAATGTTACTTTCGAGGTGACTATGGACCA 2289  
Db |||||  
2104 GGGCGTCAGTGAAGGTTCTGCTCAGTATAAGAAATGGTACTATGAATGTATGTTGGACCA 2163  
QY |||||  
2290 CATAGAG---AAGACCACACATATGATGCCACATCTACGCATAGGATGGGTAAACACTAC 2346  
Db |||||  
2164 CACAGACCCCTTTGTGACAGCTGAAGCAACTCACCTGCGAGTGGCTGGGCTTCCACTGA 2223  
QY |||||  
2347 TGGTTATGTCCCAATACCCGGTGGTGTGAGAAAGTGGGAGGTAAACGCGTGGGAGACGA 2406  
Db |||||  
2224 AGGATATTTCTCCCTACCTCGAGGGCGGAAGATGGGGTGGAAATGGTGTGGAGATGA 2283  
QY |||||  
2407 CTTGTACTCGTACGGGTTTGAATGCGGCTTACCTCTGTCGCGCGGAGGAGACCCCGGT 2466  
Db |||||  
2284 TCTCTTCTCTATGGATTGATGGCCCTTCATCTCTGTCAGGTTG-----TATTGTCG 2337  
QY |||||  
2467 CAATAGGACTCATCTGAAGAGCCCTTATATTAGAAAGGTCACGTGATGAGTTTGTGCAAT 2526  
Db |||||  
2338 TACTGTAACTCACAACCAACATCTGTTAAGAACTGATGATGTCATCAGTTGCTGTTT 2397  
QY |||||  
2527 GGACCTGACGGTACCCCATCATCACTTCACTGTTCAACGAGTGGGGTGAACGGATCTTT 2586  
Db |||||  
2398 AGATCTGAGTGCCCAAGCATCTCGTTCCGAAATTAATGGAACAACCTGTTCAAGGAATGTT 2457  
QY |||||  
2587 CACCAACTTCAATCTGGAAGCATGTTCTTCCCGGTCATCAGCTCTCTAGTAAGCTGAG 2646  
Db |||||  
2458 TGAGAAATTTCAACATCGATGGCCCTCTTCTTCCAGTCTGTTAGTTTCTCTGAGGAATAA 2517  
QY |||||  
2647 TTGTCGGTTCTGCTGGGCGGAGAACCGGTAGACTCCGGTACGCGGCTCCAGAGGCTA 2706

2518 AGTACGCTTTCTGCTGGAGGCGACATGAGAAATTCAAATTTCTTCTCCACCTGGTA 2577  
2707 CTCCTCCGCTGGTGGAGTCTCTCTCCGCGCAGCAGATCTCTCAGCTGGAGCCGTGC----- 2761  
2578 TGTCTCTTGTATGAGCTGTCTCTGCAAAAGAAAGTTGAAAGTGAACACACAGCGAGA 2637  
2762 -TTCTACTTTCGCAACCTGTCCAAGCGGCGCTTGGCTGGACCCCGCTAGTACAGAGCA 2820  
2638 GTACAAGCAAGAAAGAACTTACACACGCGACCTGTGGGCCCAACACAGTTTCCCTGACGCA 2697  
2821 TAGGGCTTTTGTGCTTACCGCTTGTGATCTTTACAGATTAATCTGCTTACATATGTGA 2880  
2698 AGCTGCTTTTACACCCATCTCTGTGATACCGACAGATCGTGTGCTTCTCATCTAGA 2757  
2881 ACAATACAGAGCAAGCTAGCTGAAATATTCACGAAATGTGGCTTATGAATAAGATCA 2940  
2758 AAGAATAAGAGAAAACTGGCAGAGATATCATGAACTCTGGTTATGAAATAAAATTGA 2817  
2941 AGCAGGCTGGATGTAGCGGCGACAGAGAGAAGCTTTGCAACAAGATCCACCCCTGCTCGT 3000  
2818 GCTTGGCTGCGAGTATGGTCCGTTAGAGATGACAAAGAGACAAACCCATGCTGCTGT 2877  
3001 GCGCTTCGAGCAGCTCCCGCCGCTGAGAAACGATAGATATACAATCTGTGTGAGAC 3060  
2878 GGAGTTCTCCAAGCTGCTGAAACAGAGCGCAATTACAACCTTACAAATGTGCTTGAGAC 2937  
3061 ACTCAAGACTATCTCGCTCTGGCTACTACAT---CAGCTTAGATAAGCCTCCAGCAG 3117  
2938 CTTGAAGACTTTGTTGGCATTAGGATGTCTATGGGTATATCAGATGAACATGCTGAAGA 2997  
3118 CATCCGCAACGTTGCTGCGCAATGAACCTTTTCATGCAGTCCAAAGGCTTACAAGCCAGC 3177  
2998 CAAAGTGAATAAATAAGAGCTACCCAGAAATTACAGCTGACAAAGTGATACAGCCTGC 3057  
3178 ACACCTGACCTGAGTGTGTACCTGTACACCCAAAGATGGATAGCTAGTAGGCCAGCT 3237  
3058 CCTATGGACCTGAGCTTTATCAAACTCAACCCCATCGCAAGAACAAATGGTGACAAGTT 3117  
3238 GCGTGAGACACCAACCTTTGGCCGAGGAGAGATACAGCAGGGATGACTTACCG 3297  
3118 GGCAGAAATGACATAAATGTGTGGCGCGGATCGAATCCGGCAGGGCTGACTTATGG 3177  
3298 ACTTAATGAGGACTCGGACATGCTATCCCGCACCTGTGCGCATACCCGAAAGTTCA 3357  
3178 CATCCAGAGAGCTTAAAGAACAGAGAAATCTCGCTTGTTCCTACACTCTCTGA 3237  
3358 CGATGCCATCAAGAGGCCCAAGGACACAGCTCGGAGACTGTGAGACCCCTGTGT 3417  
3238 TGACCGAAACCAAGAAATCCAAACAGGACAGCCTCGCGAGGCTGTGCGCACGCTGCTGG 3297  
3418 CTACGGGTATGCTGGACCCGCTACTGGGAGCAGCATGAGCACTCTTGTGGAAGC 3477  
3298 GTACGGCTCAACTTGGAGACCC-----AGATCAAGATCATGCGCCAGAGCCGAAGT 3351  
3478 GTCAAAACAGAACAGCCGACTTCAGAACATACCGCGCTGAGAGAAATATGCGGCTCAG 3537  
3352 GTGACGGGCAACCGGGAAGGTTCCGAATCTTCCGTGCGGAGAACCTATGCACTGAA 3411  
3538 CTCTGGGAAGTGTACTCTGAGTTTGAGATCTTAACGGCTGGAACCTATGAGGCTGGCTG 3597  
3412 GCGCGGACGGTGATATTTTGAATTTGAGACGGTCACTGTGGAGACATGAGGGTGTGTTG 3471  
3598 GCGTACGGTGTATGTCACCCAGGAATGATGCTCGGACAGAGCAATCTCTGGGCTTT 3657  
3472 GAGTCGCTCTGCTGTCAACCCGATCAGGAGCTTGGCTCAGATGAACGTCCTTTGCCCTT 3531  
3658 TGATGTTCAATGAGGAAAAAGTGTACAGCGGTAAACACTGAGTCTTTTGGCAAGCAATG 3717  
3532 TGATGCTTCAAGGCCACCGGCTGGCATCAGG---CAATGAACATATGGGCGCTCTTG 3588  
3718 GCGTGTGTGAGTGTAGTGGGGGTGTTCTCTAGATCTCATTTGATPAAGACGATAGTTTCTC 3777  
3589 GCAAGCAGGCGATGTCGTGGGGTGTATGTTGATGATGAACGACACACCATGATGTTTCA 3648

3778 ACTCAACGGTGTGATGTTGTTGATGATGCTCTTGGCGGAGAGACTACGTTTGTGTATGTCCA 3837  
3649 ACTGAATGGTGAATCCCTTCTTGATGATTAGGCTCAGAACTGGCTTTCAAGGACTTTTGA 3708  
3838 GGGTGACAA---CTTTGTACCTGCTTGACCGTGTGTCGCGCAAAAGCCAGGTTAAC 3894  
3709 TGTGGCATGGATTCATACCTGTGTAGCCCTGGAGTGGCTCAAGTGGGTAGGATGAA 3768  
3895 ATACGGTCAGGACGTGAACACGCTCAAAATACCTTCAACAATGTGCTCTGACAGAGGATA 3954  
3769 CTTTGGAAAGGATGTCAGCACCTTGAATATTTTCCATCTGTGCTTACAGAGGGCTA 3828  
3955 TGAACCAATCTGTGTCAATATATGAAGAGAGACGTGACTCACTGTGTACACAA-AGACCAGC 4013  
3829 TGAACCAATTTGCGGTTAATACAAACAGGATATTACCATGTGCTGAGCAAGAGGCTTC 3888  
4014 CGATCTTCAGAAATACGGATGAGATGTCGACACAGATAGATGTGACCAAGATACCAG 4073  
3889 TCAGTTTCTTCAAGTTCCATCAACCATGAACA-----TATAGAGGTGACCAAGATAGACG 3944  
4074 CTGGTTTCAGATACCTCCATGCTCAAGATTTTCCCAACAACGTTTG 4121  
3945 GCACCATAGACAGTTCCCATGTTTAAAGTCACTCAGAAGTCTTTTG 3992

RESULT 14  
US-10-887-553A-490  
; Sequence 490, Application US/10887553A  
; Publication No. US20050085436A1  
; GENERAL INFORMATION:  
; APPLICANT: Garza, Dan  
; APPLICANT: Li, Hao  
; TITLE OF INVENTION: Method to treat conditions associated  
; TITLE OF INVENTION: with insulin signalling dysregulation  
; FILE REFERENCE: 4-33262  
; CURRENT APPLICATION NUMBER: US/10/887,553A  
; PRIOR FILING DATE: 2004-07-08  
; PRIOR APPLICATION NUMBER: 60/485,883  
; PRIOR FILING DATE: 2003-08-07  
; NUMBER OF SEQ ID NOS: 1208  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 490  
; LENGTH: 15731  
; TYPE: DNA  
; ORGANISM: human  
US-10-887-553A-490

Query Match 16.8%; Score 840.8; DB 10; Length 15731;  
Best Local Similarity 55.0%; Pred. No. 5.3e-260;  
Matches 2105; Conservative 0; Mismatches 1622; Indels 101; Gaps 19;

343 AGAGAGGTGTGCTGGCTGCGAAGGTCTCGGCAACCGGCACTGCTTCTCGAGATAT 402  
217 ACAGAAGCTATGCTTGGCAGCAGAAAGGATTTGGCAACAGACTTTGTTCTTGGAGTCCAC 276  
403 TGCCGA---CAGAACATACCGCTGATCTGCGAGTGTGTTGTTCATCGAACAGGC 459  
277 TTCCAATTCCAAGAATGTGCCCCCAGACCTCTCCATCTGCACCTTTGCTGAGCAGTCT 336  
460 GCTTTTCAGTAAGAGCTTTTACAGAGTTGGTAAACAGTCTGCGGATCTGAAACTG----- 512  
337 CTTCTCTGTCGCGGCTGTCAGGATGCTGGCTAACACCGTGGAGAAATCAGAAGGCA 396  
513 -----GGAAAGAAAACTTAGTAAAGTACCGGTTCTGGTTATCGTAC 555  
397 AGTTGATGTGAAAAATGGAATTTGATGATGAAGACTGCTCAAGGTGGTGGTCAAC 456  
556 GCTACTATACGCAATGCTATTCTTTTGGGACATCTTAACAGTGTATGTACTCTGCGCTG 615  
457 ACTCTCTACGACATGCCATATGCTGCGCCATTCCTATAGTGGCATGATCTGTGCTG 516  
616 CTTGTCAACATC---ATCATCCAGGATAAGCTGGCTTTTGAGCTGGGTCTGCAACAGCA 672

[illegible]

Db	1579	AAATCTCTTCCAGAGAGGGAATGATCAACCTCTGCTTGCTTGTAGTGCATAGACCGTTTGCA	1633
Qy	1750	CGTCGTCACTCCACGAGGGTTCCTGGCTGGATTCCTCTGGGGGAGACGAATCTTGGACAGAG	1809
Db	1639	CGTCTACAGCAGTGCAGCACATTTTCTGTGATGTTGCTGGCGA--GAAGCAGGAGATC	1695
Qy	1810	CTGGGAATGATATCTGGATATTTTGTATCACTGTTGCTGGCGGCATTAATAAAGGCAACCA	1869
Db	1696	TTGGAAATCCATTTCTGAATTTCTGTATGATGTTGCTGGGGCTCTAATTAGAGGAATCG	1755
Qy	1870	CAGCACTGCGCGCAGTTTCGGCAACTCGAACC GGTTCAACTGGCTGTTCTCGCGCTCGG	1929
Db	1756	TAAAACTTGTCTCAATTTTCTGGCTC-----CCTCGACTGGTTGATACGACG	1803
Qy	1930	CTCGCAGGCTCGGGCGAGGGCACCGGCATGCTCGACGTCTGCACTGTCATCTCATCGA	1989
Db	1804	ATTGGAAGACTGGAAGCTTCTTCAGGCATTTCTGGAAGTTTACACTGTGTTTACTAGA	1863
Qy	1990	CTCGCTTGAAGCGCTCAATATGATGAGGGACGAACACATAAAAGTGATTAATCTCTCTATT	2049
Db	1864	AAGTCCAGAAGCTCTAAATATTAATAAGGAAGACATAATTAATCTATTATCTCACTTTT	1923
Qy	2050	AGAAAACGACGGACGGACCCCTAAAGTACTAGATGTCTATGTTTCACTCTGGCTCGGTAA	2109
Db	1924	AGACAAACATGGAAGAAATCACAAAGTTCTGGAATGTTTGTGTCTCACTCTGTGTTTGCCA	1983
Qy	2110	CGGGCTCGGGTGGCTCGTCCAGAACAACTCTCGCACTATTTCCTGCTCGCCGGCAAGAA	2169
Db	1984	CGGGTTGCAGTCGGTTCAAACAGCATCTCATCTGTGACATCTCTACCAGGAAGAGA	2043
Qy	2170	CCTGTTGCTGCAAACTGCGCTTGTAGATCAGTATCTAGTGTCCGTCCGAACATCTTCGT	2229
Db	2044	CTTGTTATTGCAGACACGTCCTTGTAACCATGTCCAGCATGAGACCCAATATTTTCT	2103
Qy	2230	GGGCCGAGTAGAAGGTGCGCAGTGTACCGCAATGGTACTTCGAGGTGACTATGACCA	2289
Db	2104	GGGCGTCAGTGAAGGTTCTGCTCAGTATAAGAAATGGTACTATGAATGATGGTGACCA	2163
Qy	2290	CATAGAG--AAGACACACATATGATGCCACATCTACGCATAGGATGGCTAACTACTAC	2346
Db	2164	CACAGACCTTTGTGACACTGAGCACTCACTTCGAGTGGCTTGGCTTCCACTGA	2223
Qy	2347	TGGTTATGTCCTCATACC CGGGTGGTGAGAAAGTGGGAGGTAAACGGCGTGGGACGA	2406
Db	2224	AGGATATTCTCCCTACCTCGAGGGGCGAAGAGTGGGGTGGAAATGGTGTGGAGATGA	2283
Qy	2407	CTGTACTCGTAGGGTTGATGGCGCTTACTCTCGTCCGGCGGAGGAGACCCCGT	2466
Db	2284	TCTCTTCTCCTATGGAATTTGATGGCTTCTATCTCTGCTCAGGTTG-----TATTGCTCG	2337
Qy	2467	CAATAGACTCATGCTCAACAGCCTTATATTTAGGAAGGTGACGTGATAGGTTGTGCATT	2526
Db	2338	TACTGTAACTCACCMAACCAACATCTGTTAAGAACTGATGATGTCATCAGTTGCTGTTT	2397
Qy	2527	GGACCTGACGGTACCATCATCACTTCATGTTCAAACGGAGTGGGGTGAACGGATCTT	2586
Db	2198	AGATCTGAGTGCCCAAGCATCTCGTTCCGAATTAATGGACAACTGTTCAAGGAATGTT	2457
Qy	2587	CACCAATTCAATCTGGAAGGCATGTTCTTCCCGGTCACTAGCTGTCTTAGTAAGCTGAG	2646
Db	2458	TGAAATTTTCAACATCGATGGCTCTTCTTTCCAGTCGTAGTTTCTCTGCAAGGAATAA	2517
Qy	2647	TTGTCGGTTTCTCTGCGCGGAGACACGCTAGACTCCGCTACGCGGCTCCAGAAAGCTA	2706
Db	2518	AGTAGCGTTTCTGCTTGGAGGGCGCATGAGAAATTCAAATTTCTCTCCACTGGGTA	2577
Qy	2707	CTCCCCGCTGTGTGAGTCTCTCTCGCGCAGCAGATCCTCAGCCTCGAGCCGTGC-----	2761
Db	2578	TGCTCTCTTGTATGAGCTGTTCTGCCAAAGAAAGATGGAAGTGAACACAGCCGAGA	2637
Qy	2762	-TTCTATTCTCGGCAACTCTGTCAAAGCGGCTTTGGCTGGAACCCCGCTAGTACAGACGA	2820
Db	2638	GTACAGCAAGAAAGAACTTACACACGCACTGCTGGGCCCACTAGTTTCCCTGACGCA	2697

QY	2821	TACGGCTTTTGTGCGCTACGGCTGCTGATACTTTTACAGATTACTCTGCGCTACATATCTGGA	2880
Db	2698	AGCTGCTTACACACCATCCCTGTGTGATACACGCCAGATCGTGTTCCTCATCTAGA	2757
QY	2881	ACAAATCAGAGACAAGCTAGCTGAAATATTTACGAAATGTGGGCTATGAATAAGATCGA	2940
Db	2758	AAGAAATAGAGAAAACTGSCAGAGAATATCCATGAACCTCGGTTATGAATAAAATTTGA	2817
QY	2941	AGCAGGCTGGATGTACGGCGACAGAGAGAAGACTTGCACAAGATCCACCCCTGCCCTCGT	3000
Db	2818	GCTTGGCTGGCAGTATGTCCGTTTAGAGATGACAAACAAGAGACAACCCATGCTCGTGGT	2877
QY	3001	GCCCTTCGACGCACTCCCGCCGCTGAGAAAACGATACGATATACAACTTGCTGTGCAGAC	3060
Db	2878	GGAGTTCTCCAAGCTGCCTGAAACAGGAGCGCAATTACAACTTACAAATGTGCTGTGAGAC	2937
QY	3061	ACTCAAGACTATCCTGGCTCTGGGCTACTACAT---CAGCTTAGATAAAGCCTCCAGCACG	3117
Db	2938	CCTGAAGACTTTGTTGGCATTTAGGATGTCTATGTGGGTATATCAGATGAACATCTGAAGA	2997
QY	3118	CATCCGCAACGTTGCTGTGCCCAATGAACCTTTTCATGCAGTCCAAACGGCTACAAGCCAGC	3177
Db	2998	CAAGGTCAAAAAATGAAGCTACCCCAAGAAATTACCAGCTGACAAGTGGATACAAAGCCTGC	3057
QY	3178	ACACTCGACCTGAGTGTCTGACCCCTGACACCCAGATGGATGAGCTAGTAGGCCAGCT	3237
Db	3058	CCCTATGGACCTGAGCTTTATCAAACCTCACCCCATCGCAAGAGCAATGGTGACAAAGTT	3117
QY	3238	GGCTGAGAACACCCACAACCTTTTGGGCCAGGAGAGGATACACAGGATGGAATTTACGG	3297
Db	3118	GGCAGAAAATGCACATATGTTGTGGCGCGGATCGAATCCGGACGGCTGGAATTTATGG	3177
QY	3298	ACTTAATGAGGACTTCGACATGTCATCCCGCACCTCGTGCCCATACCCGAAGGTTGA	3357
Db	3178	CATCCAACAGGACGTAAAGAACAGAGAAATCCTCGCTTGTTCCTTACACTCCTCTGGA	3237
QY	3358	CGATGCCATCAAGAGGCCAACAGGACACAGCCTCGGAGACTGTGTAGGACCCCTGCTGCT	3417
Db	3238	TGACCGAAACCAAGAAATTCACAAAGGACAGCCTCCCGAGGCTGTGCGCACGCTGTCTGG	3297
QY	3418	CTACGGGTATGCTGGACCGGCTACTTGGGGAGCAGCATGAAGCACTCTTGTGTGAAGC	3477
Db	3298	GTAACGGCTACACACTTGAAGCAC-----AGATCAAGATCATGCAAGCCAGACCCGAAGT	3351
QY	3478	GTCAAAACAGAACGACCGACTTCGAAACATACCGGCTGAGAAGAACTATGCGGTCAG	3537
Db	3352	GTGCAGCGGCACCGGGAAAGGTTCCGAACTTCCGTCCGCGCAGAGAACCTATGCAGTGAA	3411
QY	3538	CTCTGGGAAGTGTGTACTCGAGTTTGAGATCCTAACGGCTGGACCTATGAGGGTCGGCTG	3597
Db	3412	GGCCGACGGTGTATTTTGAATTTGAGACGGTCACTGCTGGAGACATGAGGGTTGGTTG	3471
QY	3598	GGCTACGCTGATATGCGCACAGGAATGATGCTCGGACAAAGACGAGAACTCTCTGGGCTTT	3657
Db	3472	GAGTCGCTCTGGTTGTCAACCGGATCAGGAGCTTGGCTCAGATGAACGTCGCTTTGCGCTT	3531
QY	3658	TGATGGTTACAAATGAGGAAAAGTGATACGGGTAAACACTGAGTCTTTTTCGCAAGCAATG	3717
Db	3532	TGATGGCTTCAAGGCCCCAGCGGTGGCATCAGGG---CAATGAACACTATGCGGCGCTCTTG	3588
QY	3718	GGCTGTTGGTGACGTAGTGGGGGTGTTCCCTAGATCTCATTTGATAAGACGATAAGTTTCTC	3777
Db	3589	GCAAGCAGGCGATGCTGCTGGGGTGTATGGTTGACATGAACGAACACACCATGATGTTTAC	3648
QY	3778	ACTCAACGGTGAAGTTGTGTGATGGAATGCTCTTGGCGGAGAGACTACGTTTGTGATGTCCA	3837
Db	3649	ACTGAATGGTGAATTCCTTCTTGATGATTCAGGCTCAGAACTGGCTTTTCAAGGACTTTGA	3708
QY	3838	GGGTGACAAA---CTTTGTACTGCTTGCACGCTTGGTGTGGGCCAAAAAGCCAGGTTTAAAC	3894
Db	3709	TGTTGGGCGATGGATTCATACCTGTGTGTAGCTTGGAGTGGCTCAAGTGGGTAGGATGAA	3768

## RESULT 15

RESULTS 13  
US-10-276-774-500

US-10-276-774-500 : Sequence 500 Application IIS/10276774

Sequence 500, Application US/10  
Publication No. US20040053245A1

; Publication No. US20  
: GENERAL INFORMATION:

; GENERAL INFORMATION:  
: APPLICANT: Hysac Inc

APPLICANT: Hyseq, Inc.

APPLICANT: Tang, Y, Tom et al

; TITLE OF INVENTION: No. US  
 THIS REFERENCE 01070 030

; FILE REFERENCE: 21272-030

; CURRENT APPLICATION NUMBER: US/10

; CURRENT FILING DATE: 2002-11-18

; PRIOR APPLICATION NUMBER: 09/560,875

;  
PRIOR FILING DATE: 2000-04-27

; PRIOR APPLICATION NUMBER: 09/496

;  
PRIOR FILING DATE: 2000-02

; NUMBER OF SEQ ID

; NUMBER OF DEPENDENT: 1  
; SOFTWARE: CUN; SOFWAVE. 50  
; SEO ID NO 50; SEQ ID NO: 35  
; LENGTH: 15

LENGTH: 13393  
TYPE: DNA

TYPE: DNA  
ORGANISM: Homo

Query Match	Score	DB 8	Length
Best Local Similarity	16.6%	831.4	15359
Matches 2083	54.8%	Pred. No. 5.9e-257	
Conservative	0	Mismatches 1611	Indels 105; Gaps 18;

265	QY	GGGGGAGCAAGCGAGCAAGATGATGTTTCAATCTTGGGTACGGAAGACATGGTGTGCAT	324
133	Db	GGGTGACGCAAGGCGAAGACGAGGTCAGTTCTCGCGACGACGATGAGTGGTGCT	192
325	QY	GTCTGTGCACACGGACAGAGAGAGGG-----TGTGCCTGGCTGCCGAAGGTC	372
193	Db	GCAGTGCACGCGTACCGTGTCTCAAGGACAGCTCAAGCTCTGCCTGGCGCGAGGGGCT	252
373	QY	CGGCNAACGGCACTGCTTCTTGGAGAAATATTCGCGACA--AGACATACGCCCTGATCT	429
253	Db	CGGCAACCGCGCTGTCTTCTTGGAGCCCACTAGCAACGCGCAGAATGTGCCCCCCGATCT	312
430	QY	GTCCGAGTGTGTTGTTCATCGACAGCGCTTTTCAGTAAGAGCTTTACAGAGATTGGT	489
313	Db	GGCCATCTGTTGCTTCTGCTCGTGGACAGTCCCTGTCTGTGCGAGCCCTGCAGAGATGCT	372
490	QY	AACAGCTCGGGGATCTGAAACTTGGGAAAGMAAACTTAGTTAAAGGTACCGGTTCTGGTTA	549
373	Db	-----GGCTAACGCGTGGAGCTGGCGTGGAGTCAATCCAGGGCGGGGACA	420
550	QY	TCGTACGCTACTATACGGCAATGCTATTCTTTTGGGCATCTTAAACAGTATATGTACCT	609
421	Db	CAGGACGCTCTGTATGGCATGCCATCCTGCTCGGCATGCACACAGCCGATGTATCT	480
610	QY	GGCCTCGCTGTCAACATCATCTCCAG---GATAAGCTGGCTTTTGACGTGGGTTCGA	666
481	Db	GAGCTGCCTCAACACTCCCGCTCCATGACTGACAAAGCTGGCTTCGATGTGGACTGCA	540
667	QY	ACAGCACTCCCAAGGTGAAGCCTGCTGTGTGGACCTTGATCTCTGCAGCAAAACAGAGATC	726

Db 541 GGAGGACCAACAGGAGAGGCTTCTGTGTGACCATGACCCAGCCTCCAGCAGAGGTC 600  
Qy 727 CGAGGGCAGAGAGGTCGAGTCGAGATGATCTTGTATCTAGTCTCCGTCGAGATGAGAG 786  
Db 601 TGAAGGAGAAAGGTCGCGTGTGGGATGACATCATCTTGTGAGTGTCTCTCCGAGCG 660  
Qy 787 ATACTTGACACACAGAAAGAGACGAGTATCGATAGTGAACCGTCTGTTCCAGCTGAC 846  
Db 661 CTACCTGACCTGTGACCGCCAGTGGGAGCTCCAGGTTGACGCTTCTTCATGACGAC 720  
Qy 847 GCACCTGGTCGTTACAGCCCTATGTTGTTGTTATATCGAGGATGAAGTATGTTGGCTATGT 906  
Db 721 ACTGTGGAACATGAACCCCATCTGCTCCGCTGG- - - - - AAGAGGCTTCTGT 768  
Qy 907 GTTCGAGGTGATGTGCTCAGGTTCTTCCATGGAGGTGACGAGTGTCTCACTATACCTAG 966  
Db 769 GACGGGAGGTACGCTCTCCGCTCTTTCATGGACATATGATGATGTCTGACCATTTTC 828  
Qy 967 CACTTGGACAAAGGATGGGGGCAAAATATCGTAGTCTTACAAAGAGGTTTCACTGATGTC 1026  
Db 829 CCCTGCTGACAGTGTATGACGAGCAGACTTGTCTACTATGAGGGGGAGCTGTGTGAC 888  
Qy 1027 TCAAGCCGTTCTCTATGCGCCTGGAGCTGGCTAGAACCAAGTGGGCGGAGGTTTCAT 1086  
Db 889 TCATGCCCGCTCCCTCTGGAGCTGGAGCCTACTGAGAACTAGCTGGAGTGGAGCCACT 948  
Qy 1087 TAACGTGTACCATCTATGAGGATTCGGCAGCATCACTAGGAAGATATCTTGGAGTTAA 1146  
Db 949 GCGCTGGGGCAGCCACTCCGAGTCCGCGATGTCACTACCGGGAGTACCTAGCGCTCAC 1008  
Qy 1147 CGACCAGAAATGAGCTGTATTTAGTTAGCAGAGAGGACCCACACAGCTTCTCTGCTT 1206  
Db 1009 CGAGACACAGGCTCTGTGTGTGTGACCGCAGCAAGGCTCACCAAGGCTACTCTCT 1068  
Qy 1207 CTGCTGCGCAGGAGAGGATGATCAAGCAAGTGTAGAACAGAGGACTTGGAGGT 1266  
Db 1069 CTGCTTCGCGATCTCAAAG- - - GAGAGCTGATGTGCCCCCAAGCGGATGTGGAGGG 1125  
Qy 1267 CATAGGCGCGCCATCATCAAGTACGCTGACTCCACCGTCACTGTGACGATTCGGAGAC 1326  
Db 1126 CATGGCCCCCTGAGATCAAGTACGGGAGTCACTGTGCTGTGTCGAGCATGTGGCTC 1185  
Qy 1327 TGGCTTGTGCTGCTTATTAAGTCTTACGAACGAGAGAGGCGTGGGTAAAGTAGA 1386  
Db 1186 AGGACTGTGCTCACTATGCGCTCCAGACCCCAAGGCCCTGCGGCTCGGC- - - GTGCT 1242  
Qy 1387 AGAGAAGCAAGGATTTCTCCAGGAGAGGCAAGATGACGATGCGCTCGACCTCTCCAG 1446  
Db 1243 CAAGAAGAGGCCATGCTGACACGAGGGGCCACATGGACGACGACATGTGCTGACCCG 1302  
Qy 1447 GTCCAGGAGGAAGATCTATGACTGCTCGAGTTATCAGGAAGTGTCTTCTGCTGTTCCAC 1506  
Db 1303 CTGCCAGGAGGAGTCCAGGCCCGCGCATGATCCACAGCAATGSCCTATACAA 1362  
Qy 1507 TAAAGTTATCAATGCGCTGGAATCTTTCAAGAGAACCGTGTCTCACTCGATGTTCTTGG- 1565  
Db 1363 CCAGTTCTCAAGAGCTTGGACAGCTTCAGCGGGAAGCCACGCGGCTCGGGGCCACCCGC 1422  
Qy 1566 - - - - - CGTCAGTGAACCTGGGCGAGATGGTGTGTTCTTGAAGATCTCACCAACTACTT 1620  
Db 1423 TGGCAGCGGCTGCCCATCGAGGGCGTTATCTGAGCCTGCGAGGCTCATCATCTT 1482  
Qy 1621 CGCAGGCCGATGAGGATATGGAACACGAGAAAGCAAAATTTCCGGCCCTCCG 1680  
Db 1483 CGAGCTCTCCCTCCGAGGACTTGCACACGAGGAGAGCAGAGCAAGCTGCGAGCCTGCG 1542  
Qy 1681 CAACCGTCAGGACTTGTTCAGAGGAGAGGATATCTGAACCTGATCTCTGAGGCTATAGA 1740  
Db 1543 CAACCGCAGAGCCTCTTCCAGGAGGAGGATGTCTCCATGTTCTGAAATTTGATAGA 1602  
Qy 1741 CAAGATCAACCTGCTGACGTCACGTCACGCTTCTGCTGATTTCTTGGCGGAGGAGATC 1800

Db 1603 CCGCCTAAATGTCTACACCACCTGCTGCCACTTTTGTGTGAGTTT- - - CGAGGGGAGGAGGC 1659  
Qy 1801 TGACACAGCTGGGAATGATATCTGGATATTTGTATCACTTGTGCGGCAATAATAA 1860  
Db 1660 AGCGAGTCTTGAAAGAGATTTGTAATCTTCTATGAACTCTAGCTTCTCTAATCCG 1719  
Qy 1861 AGCAACCAACCAAGCTGCGCGAGTTTCGCGAACTTCGAAACCGGTTCAACTGGCTGTTCTC 1920  
Db 1720 TGGCATCTGAGCAACTGTGCTCTT- - - - - CTCACAACTTGGACTGGCTGGTCTG 1773  
Qy 1921 GCGCTCTGGCTCGCAGGCTTCGGGCGAGGCAACCGCATCTCGACCTGCTGCACTGAT 1980  
Db 1774 CAAGCTGATCTGGAGGCTCGT- - - - - CTGGCATCTGGAGGCTCTGTACTGTGT 1827  
Qy 1981 CCTCATGCTCGCTGGAAGGCTCAATATGATGAGGAGCAACACATAAAGTGATAAT 2040  
Db 1828 CCTCATGAGAGTCCAGAGGTTCTGAACATCATCCAGGAGATCATCATCAAGTCCATCAT 1887  
Qy 2041 CTCTCTATTAGAAAGCAGCGACCGACCTTAAAGTACTAGATGTGTATGTTTCACTCTG 2100  
Db 1888 CTCTCTCTGACAGCATGGAGGAAACCAAGGCTCTGGACGTGTATGCTCTCTCTG 1947  
Qy 2101 CGTCGTAACCGGCTCGCGTCTGTCACAGAAACATCTGCGACTATTTGCTGCTC 2160  
Db 1948 TGTGTGTAATGTGTGCTGTACGCTCAACCAAGATCTTATTACTGAGAACTTGTCTGCC 2007  
Qy 2161 CGGCAAGAACTGTTGCTGCAAACTGCGCTTGTAGATCACTATCTAGTGTGCTGCCGAA 2220  
Db 2008 TGGCGGTGAGCTTCTGCTGACAGCAAACTCATCACTATGTTCACAGCATTCGCCCAA 2067  
Qy 2221 CATCTTCTGCGGCGAGTAGAAGGTCGCGAGTGTACCGCAAAATGGTACTTTCGAGGTGAC 2280  
Db 2068 CATCTTGTGGCGAGCGAGGACCAACGAGTACAGCAATGTTGAGTGTAT 2127  
Qy 2281 TATGGACCA- - - CATAGAGAGACCAACACATATGATGACCATCTACGATAGATGGGC 2337  
Db 2128 GGTGACGAGTGTACTTCTGACAGCTCAGGCGACCACTTGGCGGTGGCTGGGC 2187  
Qy 2338 TAACACTACTGTTATGCTCCATACCGGCTGTTGTTGAGAGTGGGAGGATACGCGT 2397  
Db 2188 CCTCACGAGGCTTACACCCCTTACCTGGGCGGCGAGGCTGGGCGGCAACGGGT 2247  
Qy 2398 GCGAGACGACTGTACTGCTACGCGTTTGTGCGCTTCTGCTGCTCGGCGGAGGAA 2457  
Db 2248 CGGGATGACTCTTATCTTCTACGCTTGTATGAGTGCATCTCTGGACAGACACGTCG 2307  
Qy 2458 GACCCCGGTCAATGAGTCTCATGCTGAAGACCTTATATTAGGAAAGTGAAGTGTAGG 2517  
Db 2308 ACGCCCACT- - - - - GACTTCCCGAGGCGAGCACCTCTGCGCCCTGGAAGACGTGATCAG 2361  
Qy 2518 TTGTGCAATTGACCTGAGGTAACCATCATCACTTCTTCAACGAGTGGCGGTGAC 2577  
Db 2362 CTGTGCTGGACCTCAGCGTGGCTCTCTCTTCCGATCAACGCGTGGCTGTGCA 2421  
Qy 2578 GGGATCTTCAACCACTTCAATCTGGAAGCATGTTCTTCCCGTCACTCACTGCTCTAG 2637  
Db 2422 GGGTGTCTTTGAGTCTTCAACCTGAGCGGCTCTTCTTCCCTGTTGTGAGTCTCGGC 2481  
Qy 2638 TAAGCTGAGTGTGCTGCTGCGCGAGAACCGGTAGACTCGGTCAGCGGTCTC 2697  
Db 2482 TGGTGTCAAGTGGTCTCTCTTGTGGCGCATGTTGAATTTCAAGTCTCTGCGCC 2541  
Qy 2698 AGAAGGTACTTCCCGTGGTGGAGTCTCTCTGCGCAGCAGATCTCAGCCTGGAGC 2757  
Db 2542 ACCTGGTATGCTCCATGCGCATGAGGCTGTCTCTCTCGAGAGGAGTCTCATCTGAAAC 2601  
Qy 2758 GTGCTTCTACTTGGCAACCTGTCCAAGCGG- - - - - CTTTGGCTGGACCCCGCTAGT 2811  
Db 2602 CATCAAGAGTATCGACGGAGGGGCCCGGGGCTCTCACTGTGGGCCCTCAGTCTG 2661  
Qy 2812 ACAGGACGATACGCGCTTTTGTGCTACGCTGTTGATATCTTTACAGATTTACTTGCCTAC 2871  
Db 2662 CCTCTCACACGACCTTCTGCGCTTCCCTGTGGACACTGTCCAGATTTGCTGCGGCC 2721



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Result No.	Score	Query Match	Length	DB	ID	Description
c 3	1	821.4	16.4	15563	8	US-11-266-748A-57467, A
	2	63	1.3	1406	8	Sequence 57467, A
	3	54.8	1.1	583	8	Sequence 31954, A
c 5	4	54.8	1.1	583	8	US-11-266-748A-377158
	5	43.4	0.9	349	8	Sequence 377158, A
	6	43.4	0.9	349	8	Sequence 460537, A
c 7	7	42	0.8	8428	8	US-11-266-748A-373619
	8	39.6	0.8	838	9	Sequence 373619, A
	9	39.2	0.8	1189	9	Sequence 456998, A
c 10	10	39.2	0.8	4017	9	US-11-266-748A-456998
	11	39.2	0.8	2394	9	Sequence 1, Appli
	12	39	0.8	895	9	Sequence 14642, A
c 14	13	39	0.8	1739	9	US-11-056-355B-14642
	14	39	0.8	1847	9	Sequence 1911, Ap
	15	38.8	0.8	604	7	Sequence 4053, Ap
c 17	16	38.8	0.8	1841	9	Sequence 4140, Ap
	17	37.6	0.8	2240	9	Sequence 12749, A
	18	37.6	0.8	850	9	Sequence 12750, A
c 19	19	37.6	0.8	2167	6	Sequence 3341, Ap
	20	37.6	0.8	2252	6	Sequence 8216, A
	21	37.6	0.8	2300	6	Sequence 814, App
c 22	22	37.2	0.7	1420	9	Sequence 65, Appl
	23	37.2	0.7	1613	9	Sequence 22166, A
	24	37.2	0.7	1420	9	Sequence 20887, A
c 25	25	37.2	0.7	1420	9	Sequence 14899, A
	26	37.2	0.7	1420	9	Sequence 14900, A
	27	37.2	0.7	1420	9	Sequence 14900, A

Query Match	16.4%	Score	821.4	DB	8	Length	15563
Best Local Similarity	54.6%	Pred. No.	2.8e-243				
Matches 2082	Conservative	0	Mismatches	1631	Indels	102	Gaps
18							
Qy	346	GAGGTGTGCTGGCTGCGAAGGTTTCGGCAACGGCACTGCTTCGTGAGAAATATGC	405				
Db	172	GAAGTTCTGCTGGCAGCCGAGGACATTGGGAATCGCCTGTGCTTCGTGAGCAACCACTTC	231				
Qy	406	CGA---CAAGAAACATACCGCCTGATCTGTGCGAGTGTGTTTTGTCTATCGAACAGGGCGCT	462				

Db 232 AGAAGCCAAAGTACATCTCTCCAGATCTCTCGGTCTGCAATTTTGTCTGGAAAGTCCCT 291  
Qy 463 TTCAAGTAAGAGCTTTTACAGGAGTTGGTAACAGCTGCGGATCTGAAACTGGGAAGAAAA 522  
Db 292 ATCTGTACAGCCCTGCAGGAAATGCTTGGCCAAACACAGG-----TGAAATGGCGG 342  
Qy 523 CTTAGTTAAAGTACCGGTTCTGGTTATCGTACGCTACTATACGGCAATGCTATCTTTT 582  
Db 343 CGAAGGGCAGCACAAAGGAGTGGCCACAGGACCCCTGTATATACGGCCATGCAATTCTCCT 402  
Qy 593 GCGACATCTTAACAGTGATATGTAACCTGCGCTGCTGCTGCTCAACATCATCCCCAG---GA 639  
Db 403 GAGGCATCTTTACGCGGAATGTATCAACATGCTTGACTACATCAAGATCCCAGACAGA 462  
Qy 640 TAAGCTGGCCTTTGACGTGGGTCTGCAACAGCAGCACTCCCAAGGTGAAGCTCTGCTGGAC 699  
Db 463 CAACCTTGCTTTGATGTAGTCTACGGGAACATGCCACAGGAAAGCTGTGGTGGAC 522  
Qy 700 CCGTCACTCTGCGACAAACAGAGATCCGAGGGCGAGAAAGGTGCGAGTACGATGACTT 759  
Db 523 TATACATCTGCTTCCAAACAGAGTCCGAAGGAGAAAGTTGCAATTTGGCGATGACCT 582  
Qy 760 GATTTAGTCTCCGTGGCATTGAGAGATCTTGCACACCAACGAAGAGACGAATATC 819  
Db 593 CATCTCGTCAAGGTGCTCTCTGAAAGATACCTTCACTCTCAGTATCAAAATGGTAACAT 642  
Qy 820 GATAGTGAACCGCTCGTTCCACGTGACGCACTGGTGGGTACAGCCCTATGCTACTGGTAT 879  
Db 643 ACAGTGGATGCCTCTTTATGCAACACTCTGGAATGTACATCC-----TACGTGCTC 696  
Qy 880 ATCGAGGATGAAGTATGTGGGCTATGTGTTGGAGGTGATGTGCTCAGGTTCTTCCATGG 939  
Db 697 AGGAAGTAGCATCGAAGAGGATACCTACTTGGTGGCATGTAGTACGCTCTTTTCCATGG 756  
Qy 940 AGGTACAGAGTGTCTCACTATACCTAGCACCTTGGACAAAGATGGGGGCAAAATATCGT 999  
Db 757 TCATATGAATGTTTGAAGATACCACTACAGACCAGAAATGATCCCAAGCAGGAGAT 816  
Qy 1000 AGTCTACAAAGGAGGTTCAAGTATGTCTCAAGCCGTTCTCTATGGCGCTGGAGCTGGC 1059  
Db 817 ATCTTACGAGCTGGGGAGCTGGGACTCGAGCAGGCTCTCTTGGAGATGGAACCCCT 876  
Qy 1060 TAGAACCAAGTGGCGGAGGTTTCAATTAAGTGTACCATCTATGAGGATTCGGCAGAT 1119  
Db 877 TCGGATAAGCTGGAGTGGCAGTAAACATCAGATGGGCGCAGGCTTTCCGACTCCGGCATCT 936  
Qy 1120 CACTACTGGAAGATATCTTGGAGTTAAACAGCAGATGAGCTGTATTTAGTTAGCAGAGA 1179  
Db 937 CACCACAGGCCACTACCTGGCCTTGACAGAGACCAAGGCCCTTATCTGCAAGACCGGGC 996  
Qy 1180 GGAACCCCAACAGCTTCTGTGCTTCTGCTCGCCGAGGAGAGGATGATCAGAAGCA 1239  
Db 997 AAAGTCAGACACCAAGTCCAAGCTTCTCTTTCGGGCACTCAAGGAACTCAAGGAGA 1056  
Qy 1240 AGT-----GTTAGAAGCAAGGACTTGGAGTCAATAGCGCGCCCATCATCAAGTACGG 1293  
Db 1057 ATTAGACTCCAGTCAACAGCGAGACATAGAAGGCATGGGAGTTCCAGAAATCAAGTATGG 1116  
Qy 1294 TGACTCCACCGTCAATGTGACAGATTCGGAGACTGGCTGTGGCTGTCTTATAGTCTTA 1353  
Db 1117 AGATTTCTGTCTCTTGTGACAGATATAGCCAGTGGTCTGTGGGTGACCTTCAAAAGCACA 1176  
Qy 1354 CGAAACGAAGAAAGGCGTGGGTAAAGTGAAGAGAGCAAGCGATTTCTCCAGGAGA 1413  
Db 1177 AGACGCCAAACTTCCCGCTGGGACCTCTAAAGAAAG---GTCACTACTCCATCAGGA 1233  
Qy 1414 AGGCAAGATGGAAGTATGGCCTCGACCTCTCCAGGTCAAGGAGGAGAAATCTATGACTGC 1473  
Db 1234 AGGCCACATGGATGATGATTAACACTGACAGAGATGCCAGCGTGAAGGAGTCCAGGCTGC 1293  
Qy 1474 TCGAGTTATCAGGAAGTGTCTTCGCTGTTCATTAAGTTTATCAATGCTTCAAGTCTT 1533

Db 1294 TCGGATCATCGGAAACACTACAGCTTATTTTTCAGCCAGTTTGTTCAGTGGAAACAA----- 1347  
Qy 1534 TCAAGAGAACCGTCTGTCACCTCGATGTTCTTTCGGCTCAGTGAACCTTGGCGGAGATGGTGAT 1593  
Db 1348 -----TCGCACAGCTGCCCCCATCACCTCGCTATAGAAGAAGTCTCTGCA 1392  
Qy 1594 GTGTCTTTGAAGATCTCACCAACTACTTTCGCACAGCCCCGATGAGGATATGGAACACGAGA 1653  
Db 1393 GACCTTACAGGACTTTGATCGCTTACTTTCAGAGCCCCAGAGGAGGAGATGCCACATGAAGA 1452  
Qy 1654 AAAGCAAAACAAATTCGCGCCCTTCGCAACCGTTCAGGACTGTTCGCAAGGAGGAGAT 1713  
Db 1453 CAAGCAGAACAGCTCGCTCACTCAAAAAACAGACAAAACTTTTCAAGGAAGAGGAAT 1512  
Qy 1714 ACTGAACCTGATCTCTGAAAGCTATAGACAAGATCAACGTCTGTCACGTCGCCAGGGTTCTCT 1773  
Db 1513 GTTGGCCCTTGTCTTAAATTTGCAATTTGACCGCTTAAATGTCTACAAATAGCTAGCACACTT 1572  
Qy 1774 GGCTGGATTCCTGGCGGAGACGAATCTGACAGAGCTGGGAAATGATATCTGATATTTT 1833  
Db 1573 TGCAGGA-----TTGCAAGGGAAGAGATGGCATGGCTTGGAAAGAAATTTCTGAACCTCT 1629  
Qy 1834 GTATCAGTTGCTGGCGCAATAATAAAGGCAACCAACAGAACTGCGCGCAGTTTCGGAA 1893  
Db 1630 CTACAAATTTGCTGCTCTCTCATTTCGCGGAAACAGAAACAAATTCGCTCAATTT----- 1683  
Qy 1894 CTGAAACGGTTCACTGGGCTGTCTCGGCTCGGCTCGCAGGCTCGGCGGAGGGCAC 1953  
Db 1684 CTCAATTAACCTTGATTTGGCTCATCAGTAAATTTGACAGACTAGAACTTCTCT-----C 1737  
Qy 1954 CGCATGCTCGACGTGTGCATCTCATCTCATCTCGCTCGCTGAAGCGCTCAATATGAT 2013  
Db 1738 AGGTATCTTGAAGTTTTCATCTGATCTTAACTGAAGCCAGAAAGCTTAAATCTGAT 1797  
Qy 2014 GAGGAGCAACACATAAAAGTGATTAATCTCTATTAGAAAAGACGAGACGCGACCTTAA 2073  
Db 1798 AGCGGAGGGCCACATCAAGTCGATCATCTCCCTTTGGATAAGCAGCGCGGGAATCACA 1857  
Qy 2074 AGTACTAGATGTGTATGTTTCACTCTGGTGGTAAACGGCTCGGGTGGCTCGTCA 2133  
Db 1858 GGTCTCGATATCTGCTCTCTCTCTGCAATGGGGTTGCAAGTGAAGGAGGAGCAACA 1917  
Qy 2134 GAACCAATCTGCGACTATTGCTGCGCGCAAGAACTGTGCTGCAAACTGGGCTTGT 2193  
Db 1918 GAATCTGATCTGACAACTTGTGCTGCGCGGAGAACTTCTCTGCGAGACACGACTGAT 1977  
Qy 2194 AGATCAGGTATCTAGTGTCCGTCCGAAACATCTTCTGGGCGCAGTAGAAGGGTGGCAGT 2253  
Db 1978 TAAAGATGAACAGTATCCGGCCAAACATCTTCTGGGAGTCCGGAGGGCTCAGCCCA 2037  
Qy 2254 GTACCGCAAAATGGTACTTTCGAGGTGACTATGGACCACTAGAGAAGACC---ACACATAT 2310  
Db 2038 GTACAAGAAGTGTACTTTCGAGCTGATTAACAGCAGGTGGACCCCTTCTTAAACAGCAGA 2097  
Qy 2311 GATGCCACATCTACGATAGGATGGGTAAACACTTACTGTTTATGTCTCCATACCCGGGTGG 2370  
Db 2098 GCCACACATCTCGGGTGGCTGGGCTCTTCTTCAGGCTATGCCCATACCCAGGAGG 2157  
Qy 2371 TGGTGAAGATGGGGAGGTAAACGGCTGGGAGACGACTGTACTGTTACGGGTTGATGG 2430  
Db 2158 TGGAGAAGATGGGGAGGCAATGTTGTTGGTGAACGACCTGTACTCTATGGCTTTGATGG 2217  
Qy 2431 CGCTACTCTTGGTCCGGCGGAGAGACCCCGTCAATAGGACTCATGCTGAAGAGCC 2490  
Db 2218 ACTTCACCTTTGGTCAGGCCGATACCCAGAGCTGT-----GGCTTCCATCAACAGCA 2271  
Qy 2491 TTATATTAGGAAAGTGAAGTGTGATAGTTGTGCAATTTGGACCTGACGGTACCCATCATCAA 2550  
Db 2272 CCTCTGATATCGGATGACGTGGTAAAGTGTCTGCTGACCTCGGGGTGCCAGCATCTC 2331  
Qy 2551 CTTTATGTTCAACGGAGTGGGGTGAACGGGATCTTCAACCACTTCAATCTTGAAGAGGAT 2610  
Db 2332 ATTCCGATCAATGGGACCGCTGACGGGATGTTTGAAGAACTTTCAACACAGACAGGGCT 2391

Qy	2611	GTCTCTCCCGGTCAATCAGCTGCTCTAGTAAGCTGAGTTGTCGGTTCCTGCTGGCGCGAGA	2670
Db	2392	CTTCTTCCCTGTGATGAGCTTTTCAGCAGGTGTCAAAGTAGCTTCTCTGATGGTGGACG	2451
Qy	2671	ACACGGTAGACTCCGGTACCGGCTCCAGAAAGCTACTCCCGCGTGGTGGAGTCTCTCTCT	2730
Db	2452	TCATGGAGAGTTAAAGTTCCTGCTCCTCTGGCTATGCCCCTTGCTGCTATGAAGCCTTACT	2511
Qy	2731	GC CGCAGCAGATCCTCAGCCTGGAGCGGTGCTTCTACTCTCGGCCAACTCTGTC	2784
Db	2512	TCCAAAGAGAAGATGAGATTGGAGCCTGTCAAAGAAATATAAAGTGATGCTGATGGCAT	2571
Qy	2785	GC CGCCTTGGCTGGACCCCGCTAGTACAGGACGATACGGCTTTTGTGCTTACGCCCTGT	2844
Db	2572	TAGAGATCTCTTGGGTACCAACCCAGTTCTCTCCCAAGCTCTTTATCCCATGCCCCGT	2631
Qy	2845	TGATACTTTACAGATTACTCTGCGCTACATATGTGGAACTAATCAGAGACAAGCTAGCTGA	2904
Db	2632	AGACACAGTCAGTTATTTTGGCCACCTCACCTAGAAAGATCCGAGACAGACTAGCTGA	2691
Qy	2905	AAATATTCAAGAAATGTGGGCTATGAATAAGATCGAAGACAGGCTGGATGTACGGCGACCA	2964
Db	2692	AAACATCCATGAGCTTTGGGGAATGAATAAAATAGAACTTGGCTGGACTTTTCGGCAAGAT	2751
Qy	2965	GAGNAGAGCTTGCACAAGATCCACCCTGCTGCTCGCTTCCGCGCATCTCCGCCCCG	3024
Db	2752	ACGAGATGACAATAAAGACAACACCCTTGCTTGTGGAGTTTCAAAGCTTCCCAAGAAC	2811
Qy	3025	TGAGAAACGATACGATATACAACCTGTGTGACAGACACTCAAGACTATCTGGCTCTGGG	3084
Db	2812	TGAGAGAACTATAACCTGCAATGTCAACTGAACCTTAAACCCCTTTGGCCCTGGG	2871
Qy	3085	CTACTACATCAGCTTAGATAAGC---CTCCAGCAGCGCATCCGACAGTTCGTCTGCCCAA	3141
Db	2872	GTGCCACATTCGCTCATGTTAACCCAGCTGCTGAGGAGGATCTCAAGAAAGTCAAACTGCC	2931
Qy	3142	TGAACCTTTCAATGCAAGTCCAAACGGCTACAAGCCAGCACACCTGCAAGCTGAGTGTGTCAC	3201
Db	2932	CAAAAACATATGATGTCCAAACGGCTATAAGCCAGCCCTTTGGATTTGTCTGATGTGAA	2991
Qy	3202	CCTGACACCCAGATGATGAGCTAGTGTAGCCAGCTGGCTGAGAACACCCACACACCTTTG	3261
Db	2992	GCTGTTACCTCTCAAGAAATTTTGTGGAATAAGCTTGCAGAAATGCACACATGTTTG	3051
Qy	3262	GGCCAGGGAGAGGATACAGCAGGAGTGGACTTACGGACTTAATCAGGACTCGGACATGCA	3321
Db	3052	GGCAAAAGACAGAAATAAACAAGATGGAACCTATGGCATCCACAGAGTTTGAAGACAA	3111
Qy	3322	TCGATCCCGGCCTCTGGTGCATACCCGAGGTTTGACGATGCCATCAAGAGGCCAACAG	3381
Db	3112	AAGAAATCCCGCTCTGGTGCCATATGCATTACTGGATGAGCGTACCAAGAAGTCAAAACAG	3171
Qy	3382	GGACACAGCCTCGAGACTGTGAGAACCTCTCTGGTCTACGGGTATATGTCTGAGACCCGCC	3441
Db	3172	GGACAGCCTCGCGGGAAGCTGTGCGCACTTTTGTGTGGTTACGGGTATAACATTTGAGCCATC	3231
Qy	3442	TACTGGGGAGCAGCATGNAGCACTCTTGTGGAAGCTCAAAAAGAGCAAGCCGACTT	3501
Db	3232	-----AGACCAAGAACTAGCTGACTCGGCTGTGGAGAGGTACGATAGACAAGAT	3282
Qy	3502	CAGAACATACCGCTGAGAGAACTATGCCGTCAAGCTCTCGGGAAGTGGTACTTTTCGAGTT	3561
Db	3283	CCGATTTTTCGGGTAGAGCGATCTTATGCAAGTGAATCTGGAAGTGTATTTTGTGTT	3342
Qy	3562	TCAGATCCTAACCGGTGGACCTATGAGGGTCCGCTGGGCTCACGCTGATATGGACCACGG	3621
Db	3343	TGAAGTGTGACTGGAGGAGACATGCGAGTCCGCTGGCGAGGCCAGGCTGCTGCACCTGA	3402
Qy	3622	AATGATGCTCGGACAAGACAGAACTCTCTGGGCTTTTGTATGGTTTACAATGAGGAAAAAGT	3681
Db	3403	TGTGAGCTGGGGCCGATGACCAAGCCTTTGTGTTTGAAGGCAACAGGGCCAGCGCTTG	3462

Qy	3682	GTACAGCGGTAA	CAC	TGAGTCTTTCCG	CAGCAATCGG	CTGTTGGT	GACAGT	TACTG	GGGGT	3747		
Db	3463	GCATCAAGGAAG	---	TGGGTATTTT	GGGGCGTAC	CTGGCAGC	CAAGGGGAT	GTGTCG	ATG	3519		
Qy	3742	GTTCCTAGATCT	CATTGATAAG	CAGTAAGT	TTCTC	ACTCAAC	CGGTGAG	TTGTTG	ATGGA	3801		
Db	3520	TATGATTAAC	TCTGGATGATC	TTCAATGAT	CTTCA	CAC	TGAATGGG	AGCTG	CTGATCAC	3579		
Qy	3802	TGCTCTTTGG	CGGAGAGACT	ACGTTT	TGTTGAT	GTCCAG	GGTGACAA	---	CTTTGTAC	CTGC	3858	
Db	3580	CAACAAAGG	CTCTCAACT	TGCCTTCG	CTGACTAC	GAGATTG	GAAATGG	CTTCGTG	CGCCAT	3639		
Qy	3859	TTGCACGCT	TGGTGT	TCGGCCAA	AAAGCCAG	GTAA	CATACGG	TCAAG	ACGTGAAC	ACGCT	3918	
Db	3640	CTGCTGTCT	GGGTC	TATCTC	GAGATCGG	CCCGCAT	GAAATCTCGG	ACAGATGCC	AGTACCTT	3699		
Qy	3919	GAATACTT	CACAA	CATGTG	CTG	CAGGAGG	GATATGA	ACCATTC	TGTCTCA	ATGAA	3978	
Db	3700	CAAGTTTTAT	ACCATGTG	CGGTCT	CCAAG	AGGGCTTT	GAGCCTTT	TGCTGTCA	ACATGAA	3759		
Qy	3979	GAGAGCGT	GACTC	ACTGGT	TACACCA	AGACCC	AGCCGATCTT	CGAGAA	TACGGATG	AGAT	4038	
Db	3760	CAGAGATG	TGTCTAT	GTGGTTC	AGCAAG	CGCCTCC	CGACGT	TTGTCAA	---	CGTGCC	AAA	3816
Qy	4039	GATCGAC	ACCAG	AATAGAT	GTGAC	CGGATAC	CAAGCTGG	TTTCAG	ATACAC	CTCCAT	GCCT	4098
Db	3817	GGATCTCC	ACATAG	AGGT	CATGAG	ATTGAT	GGCACC	ATGG	ACAG	CCCTCC	GTCTCT	3876
Qy	4099	CAAGATTTCC	CAACA	ACGTTT	TGAG	ACGATG	GAGA	4133				
Db	3877	CAAGGTGAC	GCAT	AAGA	CATTGG	CA	CACAGA	ATA	3911			

## RESULT 2

```

US-11-266-748A-31954
; Sequence 31954, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE OF INVENTION: 55815-0102 (319189)
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 31954
; LENGTH: 1406
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-31954

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Query Match 1.3%; Score 63; DB 8; Length 1406;  
Best Local Similarity 70.6%; Pred. NO. 3.4e-08;  
Matches 84; Conservative 0; Mismatches 35; Indels

Qy 675 CCCAAGGTGAAGCTGCTGGTGGACCTGATCTGCCAGCAACACAGATCCGAGGCG 734  
Db 789 CCATAGGAGAGCGCTTGCTGGTGGACCATGACCCAGCCCTCCAAGCAGAGGCTCTGAAGAG 848  
Qy 735 AGAAGGTGCGAGTCGGAGATGACTTGATTCTAGTCTCGTGGCCATTGAGAGATCTTG 793  
Db 849 AAAAGTCCGCTTGGGGATGACATCATCTTGTGAGTGCTCTCCGAGCGCTACCTG 907

## RESULT 3

US-11-266-748A-377158/c  
; Sequence 377158, Application US/11266748A  
; Publication No. US20060134663A1  
; GENERAL INFORMATION:  
; APPLICANT: Harkin, Paul  
; APPLICANT: Johnston, Patrick  
; APPLICANT: Mulligan, Karl  
; TITLE OF INVENTION: Transcriptome Microarray Technology and

; TITLE OF INVENTION: Methods of Using the Same  
; FILE REFERENCE: 55815-0102 (319189)  
; CURRENT APPLICATION NUMBER: US/11/266,748A  
; CURRENT FILING DATE: 2005-11-03  
; PRIOR APPLICATION NUMBER: EP 04105479.2  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105482.6  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105483.4  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105507.0  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105485.9  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105484.2  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: US 60/662,276  
; PRIOR FILING DATE: 2005-07-18  
; NUMBER OF SEQ ID NOS: 483996  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 377158  
; LENGTH: 583  
; TYPE: DNA  
; ORGANISM: Homo Sapiens

US-11-266-748A-377158

Query Match 1.1%; Score 54.8; DB 8; Length 583;  
Best Local Similarity 65.6%; Pred. No. 6.8e-06;  
Matches 80; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

Qy 3162 ACGGCTACAAGCCAGCACCCTGAGCTGCTGTCACCCCTGACACCCCAAGATGGATG 3221  
Db 455 AAGGCTACAACCTCAGCCCCCGACCTTAGTGTACCTGTCCCGGAGCTGCAGG 396  
Qy 3222 AGCTAGTAGGCGAGCTGCTGAGAACACCCCAACCTTTGGCCGAGGAGGATACAGC 3281  
Db 395 CCATGGCAGAACAACTGGCAGAAAATTACCACACACGTCGGGCGGAAGAAGCAGG 336  
Qy 3282 AG 3283  
Db 335 AG 334

## RESULT 4

US-11-266-748A-460537  
; Sequence 460537, Application US/11266748A  
; Publication No. US20060134663A1  
; GENERAL INFORMATION:  
; APPLICANT: Harkin, Paul  
; APPLICANT: Johnston, Patrick  
; APPLICANT: Mulligan, Karl  
; TITLE OF INVENTION: Transcriptome Microarray Technology and

; TITLE OF INVENTION: Methods of Using the Same  
; FILE REFERENCE: 55815-0102 (319189)  
; CURRENT APPLICATION NUMBER: US/11/266,748A  
; CURRENT FILING DATE: 2005-11-03  
; PRIOR APPLICATION NUMBER: EP 04105479.2  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105482.6  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105483.4  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105507.0  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105485.9  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105484.2  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: US 60/662,276  
; PRIOR FILING DATE: 2005-03-14  
; PRIOR APPLICATION NUMBER: US 60/700,293  
; PRIOR FILING DATE: 2005-07-18  
; NUMBER OF SEQ ID NOS: 483996  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 460537  
; LENGTH: 583  
; TYPE: DNA  
; ORGANISM: Homo Sapiens

US-11-266-748A-460537

Query Match 1.1%; Score 54.8; DB 8; Length 583;  
Best Local Similarity 65.6%; Pred. No. 6.8e-06;  
Matches 80; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

Qy 3162 ACGGCTACAAGCCAGCACCCTGAGCTGCTGTCACCCCTGACACCCCAAGATGGATG 3221  
Db 129 AAGGCTACAACCTCAGCCCCCGACCTTAGTGTACCTGTCCCGGAGCTGCAGG 188  
Qy 3222 AGCTAGTAGGCGAGCTGCTGAGAACACCCCAACCTTTGGCCGAGGAGGATACAGC 3281  
Db 189 CCATGGCAGAACAACTGGCAGAAAATTACCACACACGTCGGGCGGAAGAAGCAGG 248  
Qy 3282 AG 3283  
Db 249 AG 250

## RESULT 5

US-11-266-748A-373619  
; Sequence 373619, Application US/11266748A  
; Publication No. US20060134663A1  
; GENERAL INFORMATION:  
; APPLICANT: Harkin, Paul  
; APPLICANT: Johnston, Patrick  
; APPLICANT: Mulligan, Karl  
; TITLE OF INVENTION: Transcriptome Microarray Technology and  
; TITLE OF INVENTION: Methods of Using the Same  
; FILE REFERENCE: 55815-0102 (319189)  
; CURRENT APPLICATION NUMBER: US/11/266,748A  
; CURRENT FILING DATE: 2005-11-03  
; PRIOR APPLICATION NUMBER: EP 04105479.2  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105482.6  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105483.4  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105507.0  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105485.9  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105484.2  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: US 60/662,276  
; PRIOR FILING DATE: 2005-03-14  
; PRIOR APPLICATION NUMBER: US 60/700,293

Query Match 0.9%; Score 43.4; DB 8; Length 349;  
Best Local Similarity 57.9%; Pred. No. 0.017; 56; Indels 0; Gaps 0;  
Matches 77; Conservative 0; Mismatches 56; Indels 0; Gaps 0;  
QY 3151 CATGAGTCCAAAGCGGTACAGCCAGCACCTCGACCTGAGTGTGCTGACCTGACACC 3210  
DB 148 CAACAGGGCAACACTAGACTCTGCTCCCTCGACCTCTCAACAGTTGTGCTCTCCAG 207  
QY 3211 CAAGATGATGAGCTAGTAGGCGACCTGGCTGAGAACCCACACCTTTGGGCCAGGGA 3270  
DB 208 AGAGCTCCAGGGAATGTTGGAGTCTGCTGAGAACTATCACAATATCTGGGCCAAGAA 267  
QY 3271 GAGGATACAGCAG 3283  
DB 268 GAAGAAGCTGGAG 280

RESULT 6  
US-11-266-748A-456998/c  
; Sequence 456998, Application US/11266748A  
; Publication No. US20060134663A1  
; GENERAL INFORMATION:  
; APPLICANT: Harkin, Paul  
; APPLICANT: Johnston, Patrick  
; APPLICANT: Mulligan, Karl  
; TITLE OF INVENTION: Transcriptome Microarray Technology and  
; FILE REFERENCE: 55815-0102 (319189)  
; CURRENT APPLICATION NUMBER: US/11/266,748A  
; CURRENT FILING DATE: 2005-11-03  
; PRIOR APPLICATION NUMBER: EP 04105479.2  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105482.6  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105483.4  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105507.0  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105485.9  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105484.2  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: US 60/662,276  
; PRIOR FILING DATE: 2005-03-14  
; PRIOR APPLICATION NUMBER: US 60/700,293  
; PRIOR FILING DATE: 2005-07-18  
; NUMBER OF SEQ ID NOS: 483996  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 456998  
; LENGTH: 349  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
US-11-266-748A-456998

Query Match 0.9%; Score 43.4; DB 8; Length 349;  
Best Local Similarity 57.9%; Pred. No. 0.017;  
Matches 77; Conservative 0; Mismatches 56; Indels 0; Gaps 0;  
QY 3151 CATGAGTCCAAAGCGGTACAGCCAGCACCTCGACCTGAGTGTGCTGACCTGACACC 3210  
DB 202 CAACAGGGCAACAGACTAGCTCTGCTCCCTCGACCTCTCAACAGTTGTGCTCTCCAG 143  
QY 3211 CAAGATGATGAGCTAGTAGGCGACCTGGCTGAGAACCCACACCTTTGGGCCAGGGA 3270

Db 142 AGAGCTCAGGGAATGTTGGAGTCTGCTGAGAACTATCACAATATCTGGGCCAAGAA 83  
QY 3271 GAGGATACAGCAG 3283  
DB 82 GAAGAAGCTGGAG 70  
RESULT 7  
US-11-330-363-1/c  
; Sequence 1, Application US/11330363  
; Publication No. US20060121577A1  
; GENERAL INFORMATION:  
; APPLICANT: Melji Seika Kaisha, Ltd.  
; TITLE OF INVENTION: Midcamycin biosynthetic genes  
; FILE REFERENCE: 138451 US  
; CURRENT APPLICATION NUMBER: US/11/330,363  
; CURRENT FILING DATE: 2006-01-12  
; PRIOR APPLICATION NUMBER: US/10/229,148  
; PRIOR FILING DATE: 2002-08-28  
; PRIOR APPLICATION NUMBER: 210516/2002  
; PRIOR FILING DATE: 2002-07-19  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 84428  
; TYPE: DNA  
; ORGANISM: Streptomyces mycarofaciens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: Complement ((1)..(675))  
; OTHER INFORMATION: ORF42 (fragment)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: Complement ((1168)..(2202))  
; OTHER INFORMATION: ORF41  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: Complement ((2220)..(3215))  
; OTHER INFORMATION: ORF40  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: Complement ((3237)..(4691))  
; OTHER INFORMATION: ORF39  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: Complement ((4695)..(5948))  
; OTHER INFORMATION: ORF38  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: Complement ((6048)..(6629))  
; OTHER INFORMATION: ORF37  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: Complement ((6653)..(7945))  
; OTHER INFORMATION: ORF36  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (8149)..(9015)  
; OTHER INFORMATION: ORF35  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (9012)..(9335)  
; OTHER INFORMATION: ORF34  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (9328)..(10458)  
; OTHER INFORMATION: ORF33  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (10521)..(11603)  
; OTHER INFORMATION: ORF32  
; FEATURE:  
; NAME/KEY: CDS



APPLICANT: Brover, Vyacheslav  
APPLICANT: Alexandrov, Nickolai  
TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding  
FILE REFERENCE: 2750-1590PUS2  
CURRENT APPLICATION NUMBER: US/11/056,355B  
PRIOR FILING DATE: 2005-02-14  
PRIOR FILING DATE: 2004-02-13  
NUMBER OF SEQ ID NOS: 119966  
SEQ ID NO 14642  
LENGTH: 838  
TYPE: DNA  
ORGANISM: Zea mays subsp. mays  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)..(838)  
OTHER INFORMATION: Ortholog of Ceres Seq. ID no. 12468112  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)..(838)  
OTHER INFORMATION: Ortholog of Ceres Seq. ID NO 15225703  
OTHER INFORMATION: as cited in SEQ ID NO 59527  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)..(838)  
OTHER INFORMATION: Ortholog of Ceres Seq ID NO 12615972  
OTHER INFORMATION: as cited in SEQ ID NO 62455  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)..(838)  
OTHER INFORMATION: Ortholog of Ceres Seq ID NO 13596229  
OTHER INFORMATION: as cited in SEQ ID NO 68800  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)..(838)  
OTHER INFORMATION: Ortholog of Ceres Seq ID NO 15179393  
OTHER INFORMATION: as cited in SEQ ID NO 0  
US-11-056-355B-14642

Query Match 0.8%; Score 39.6; DB 9; Length 838;  
Best Local Similarity 49.5%; Pred. No. 0.46;  
Matches 102; Conservative 0; Mismatches 104; Indels 0; Gaps 0;  
QY 2580 GATCCTTACCAACTCAATCTGGAAGGCATGTTCTTCCCGGTATCAGCTGCTCTAGTA 2639  
DB 179 GGTCCATCTACCAACAGATTGCGGCCATGCTGAACCTGATCATCTCGCGGCATCA 238  
QY 2640 AGCTGAGTTGCGGTTCTCTGCTGGCGGAGAACAGGTAGACTCCGGTACGCGGCTCCAG 2699  
DB 239 ACCTGGCGTCCGGTACTCCCGCAGTTTGACAACTTCGCGCACATCGCGGGTTCCGA 298  
QY 2700 AAGGCTACTCCCGTGGTGGAGTCTCTCTCCCGCAGAGATCTCAGCTTGGAGCCGT 2759  
DB 299 CAGGCTTCTCTCGGCTTCGTGCTGCTGATCAGCCCAAGTTCGGGTGGCTGGAGCAGC 358  
QY 2760 GCTTCTACTTCGGCACTCTCCAG 2785  
DB 359 CCTTCGGTCCCAAGCAAGTCCAG 384

RESULT 9  
US-11-218-305-1911  
Sequence 1911, Application US/11218305  
Publication No. US2006014195A1  
GENERAL INFORMATION:  
APPLICANT: MONSANTO TECHNOLOGY, LLC  
APPLICANT: McLaird, Paul L.  
APPLICANT: Tao, Nengbing  
APPLICANT: Wu, Kunsheng  
TITLE OF INVENTION: Polymorphic Markers and Methods of Genotyping  
FILE REFERENCE: 38-21 (53660)B

CURRENT APPLICATION NUMBER: US/11/218,305  
CURRENT FILING DATE: 2005-09-01  
PRIOR APPLICATION NUMBER: US 60/606,880  
PRIOR FILING DATE: 2004-09-01  
NUMBER OF SEQ ID NOS: 25043  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 1911  
LENGTH: 4017  
TYPE: DNA  
ORGANISM: Zea mays  
US-11-218-305-1911  
Query Match 0.8%; Score 39.6; DB 9; Length 4017;  
Best Local Similarity 49.5%; Pred. No. 1.3;  
Matches 102; Conservative 0; Mismatches 104; Indels 0; Gaps 0;  
QY 2580 GATCCTTACCAACTTCAATCTGGAAGGCATGTTCTTCCCGGTATCAGCTGCTCTAGTA 2639  
DB 3340 GGTCCATCTACCAACAGATTGCGGCCATGCTGAACCTGATCATCTCGCGGCATCA 3399  
QY 2640 AGCTGAGTTGCTGCTCTGCTGGCGGAGAACAGGTAGACTCCGGTACGCGGCTCCAG 2699  
DB 3400 ACCTGGCGTCCGGTACTCCCGCAGCTTGACAACTTCGCGCACATCGCGGGTTCCGA 3459  
QY 2700 AAGGCTACTCCCGTGGTGGAGTCTCTCTCCCGCAGAGATCTCAGCTTGGAGCCGT 2759  
DB 3460 CAGGCTTCTCTCGGCTTCGTGCTGATCCAGCCCAAGTTCGGGTGGCTGGAGCAGC 3519  
QY 2760 GCTTCTACTTCGGCACTCTCCAG 2785  
DB 3520 CCTTCGGTCCCAAGCAAGTCCAG 3545

RESULT 10  
US-11-174-307B-4053  
Sequence 4053, Application US/11174307B  
Publication No. US20060143729A1  
GENERAL INFORMATION:  
APPLICANT: ALEXANDROV, Nickolai  
APPLICANT: BROVER, Vyacheslav  
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND POLYPEPTIDES ENCODED THEREBY  
FILE REFERENCE: 2750-1601PUS2  
CURRENT APPLICATION NUMBER: US/11/174,307B  
CURRENT FILING DATE: 2005-06-30  
PRIOR APPLICATION NUMBER: 60/583,671  
PRIOR FILING DATE: 2004-06-30  
PRIOR APPLICATION NUMBER: 60/583,781  
PRIOR FILING DATE: 2004-06-30  
PRIOR APPLICATION NUMBER: 60/583,651  
PRIOR FILING DATE: 2004-06-30  
NUMBER OF SEQ ID NOS: 5544  
SEQ ID NO 4053  
LENGTH: 1189  
TYPE: DNA  
ORGANISM: Zea mays  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)..(1189)  
OTHER INFORMATION: Ceres cdna ID no. 21666056  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)..(1189)  
OTHER INFORMATION: Ceres CLONE ID no. 1277411  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)..(1189)  
OTHER INFORMATION: Also known as Ceres CDNA ID no. 24358413  
US-11-174-307B-4053

Query Match 0.8%; Score 39.2; DB 9; Length 1189;  
Best Local Similarity 56.1%; Pred. No. 0.77;  
Matches 74; Conservative 0; Mismatches 58; Indels 0; Gaps 0;



QY 1880 GCGCAGTTCCGCACTCGAACCGGTTCAACTGGCTGTTCTCGCGCTCGGCTCGCAGGCC 1939  
Db 863 GGGCTGTTCCGCGCTGTCGCGCTGTCCTCATCGCAGCGTGTGCGCGCTCGCGCGGGGCC 922  
QY 1940 TCGGCGGAGGACCGCGCATGCTCGACGTGCTGCACTGCATCCTCATCGACTCGCGCTGAA 1999  
Db 923 GGGGACGACGGCGCTGCGCTGCTCGGCTCAACTGGTTCCTCCTCGGCTGCTCACC 982  
QY 2000 GCGCTCAATATG 2011  
Db 983 TCGCCCATGCTG 994

RESULT 11  
US-11-218-305-4140  
; Sequence 4140, Application US/11218305  
; Publication No. US20060141495A1  
; GENERAL INFORMATION:  
; APPLICANT: MONSANTO TECHNOLOGY, LLC  
; APPLICANT: McLaird, Paul L.  
; APPLICANT: Tao, Nengbing  
; APPLICANT: Wu, Kunsheng  
; TITLE OF INVENTION: Polymorphic Markers and Methods of Genotyping  
; FILE REFERENCE: 38-21 (53660)B  
; CURRENT APPLICATION NUMBER: US/11/218,305  
; CURRENT FILING DATE: 2005-09-01  
; PRIOR APPLICATION NUMBER: US 60/606,880  
; PRIOR FILING DATE: 2004-09-01  
; NUMBER OF SEQ ID NOS: 25043  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 4140  
; LENGTH: 2294  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (18)..(18)  
; OTHER INFORMATION: n is a, c, g, or t  
US-11-218-305-4140

Query Match 0.8%; Score 39.2; DB 9; Length 2294;  
Best Local Similarity 56.1%; Pred. No. 1.2; Mismatches 58; Indels 0; Gaps 0;  
Matches 74; Conservative 0;  
QY 1880 GCGCAGTTCCGCACTCGAACCGGTTCAACTGGCTGTTCTCGCGCTCGGCTCGCAGGCC 1939  
Db 245 GGGCTGTTCCGCGCTGTCGCGCTGTCCTCATCGCAGCGTGTGCGCGCTCGCGGGGCC 304  
QY 1940 TCGGCGGAGGACCGCGCATGCTCGACGTGCTGCACTGCATCCTCATCGACTCGCGCTGAA 1999  
Db 305 GGGGACGACGGCGCTGCGCTGCTCGGCTCAACTGGTTCCTCCTCGGCTGCTCACC 364  
QY 2000 GCGCTCAATATG 2011  
Db 365 TCGCCCATGCTG 376

RESULT 12  
US-11-218-305-12749  
; Sequence 12749, Application US/11218305  
; Publication No. US20060141495A1  
; GENERAL INFORMATION:  
; APPLICANT: MONSANTO TECHNOLOGY, LLC  
; APPLICANT: McLaird, Paul L.  
; APPLICANT: Tao, Nengbing  
; APPLICANT: Wu, Kunsheng  
; TITLE OF INVENTION: Polymorphic Markers and Methods of Genotyping  
; FILE REFERENCE: 38-21 (53660)B  
; CURRENT APPLICATION NUMBER: US/11/218,305  
; CURRENT FILING DATE: 2005-09-01

; PRIOR APPLICATION NUMBER: US 60/606,880  
; PRIOR FILING DATE: 2004-09-01  
; NUMBER OF SEQ ID NOS: 25043  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 12749  
; LENGTH: 895  
; TYPE: DNA  
; ORGANISM: Zea mays  
US-11-218-305-12749  
Query Match 0.8%; Score 39; DB 9; Length 895;  
Best Local Similarity 54.5%; Pred. No. 0.74;  
Matches 78; Conservative 0; Mismatches 65; Indels 0; Gaps 0;  
QY 1853 ATATAAAGGCAACCAACGACTGCGCGAGTTCGGAACCTCGAACCGGTTCAACTGG 1912  
Db 296 ATGAAGCAGGACCTCAAGATCAGGACACGAGATCGAGATCCTCGCGGATCATCAAT 355  
QY 1913 CTGTTCTCGGCGCTCGGCTCGCAGGCTCGGCGGAGGCGCACCGCATGCTCGAGCTGCTG 1972  
Db 356 ATCTACTCGTCTGCTGCTCGCGCGGCGGCGGACGCTCGACTGGCTCGGCGGCGG 415  
QY 1973 CACTGCATCTCATCGACTCGCC 1995  
Db 416 TACACCATGCTGCTCGCGGGGC 438

RESULT 13  
US-11-174-307B-3341  
; Sequence 3341, Application US/11174307B  
; Publication No. US20060143729A1  
; GENERAL INFORMATION:  
; APPLICANT: ALEXANDROV, Nikolai  
; APPLICANT: BROVER, Vyacheslav  
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND POLYPEPTIDES ENCODED THEREBY  
; FILE REFERENCE: 2750-1601PUS2  
; CURRENT APPLICATION NUMBER: US/11/174,307B  
; CURRENT FILING DATE: 2005-06-30  
; PRIOR APPLICATION NUMBER: 60/583,671  
; PRIOR FILING DATE: 2004-06-30  
; PRIOR APPLICATION NUMBER: 60/583,781  
; PRIOR FILING DATE: 2004-06-30  
; PRIOR APPLICATION NUMBER: 60/583,651  
; PRIOR FILING DATE: 2004-06-30  
; NUMBER OF SEQ ID NOS: 5544  
; SEQ ID NO 3341  
; LENGTH: 1739  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)..(1739)  
; OTHER INFORMATION: Ceres cdna ID no. 21572848  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)..(1739)  
; OTHER INFORMATION: Ceres CLONE ID no. 1532145  
; NAME/KEY: misc\_feature  
; LOCATION: (1)..(1739)  
; OTHER INFORMATION: Also known as Ceres CDNA ID no. 24359342  
US-11-174-307B-3341

Query Match 0.8%; Score 39; DB 9; Length 1739;  
Best Local Similarity 54.5%; Pred. No. 1.2; Mismatches 65; Indels 0; Gaps 0;  
Matches 78; Conservative 0;  
QY 1853 ATATAAAGGCAACCAACGACTGCGCGAGTTCGGAACCTCGAACCGGTTCAACTGG 1912  
Db 243 ATGAAGCAGGACCTCAAGATCAGGACACGAGATCGAGATCCTCGCGGATCATCAAT 302  
QY 1913 CTGTTCTCGGCGCTCGGCTCGCAGGCTCGGCGGAGGCGCACCGGATGCTCGAGCTGCTG 1972

Db 303 ATCTACTCGCTCGTGGCTCGCTCGGGGGGGCGGACGTCGACTGGCTCGCGCGCGG 362  
Qy 1973 CACTGCATCCTCATCGACTCGCC 1995  
Db 363 TACACCATGGTGTCTCGCGCGGC 385

RESULT 14

US-11-218-305-12750  
; Sequence 12750, Application US/11218305  
; Publication No. US20060141495A1  
; GENERAL INFORMATION:  
; APPLICANT: MONSANTO TECHNOLOGY, LLC  
; APPLICANT: McLaird, Paul L.  
; APPLICANT: Tao, Nengbing  
; APPLICANT: Wu, Kunsheng  
; TITLE OF INVENTION: Polymorphic Markers and Methods of Genotyping  
; FILE OF INVENTION: Corn.  
; FILE REFERENCE: 38-21 (53660)B  
; CURRENT APPLICATION NUMBER: US/11/218,305  
; CURRENT FILING DATE: 2005-09-01  
; PRIOR APPLICATION NUMBER: US 60/606,880  
; PRIOR FILING DATE: 2004-09-01  
; NUMBER OF SEQ ID NOS: 25043  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 12750  
; LENGTH: 1847  
; TYPE: DNA  
; ORGANISM: Zea mays  
US-11-218-305-12750

Query Match 0.8%; Score 39; DB 9; Length 1847;  
Best Local Similarity 54.3%; Pred. No. 1.2; Mismatches 0; Gaps 0;  
Matches 78; Conservative 0; Indels 65; Indels 0; Gaps 0;  
Qy 1853 ATATAAAGGCAACACACAGAACTCGCGCGAGTTCGCGAATCTCGAATCTCGAACCGGTTCAAATCG 1912  
Db 228 ATGACGAGGACCTCAAGATCAGGACACGACATCGAGATCTCTCGCGGCATCATCAAT 287  
Qy 1913 CTGTTCTCGCGCTCGGCTCGAGGCTCGGGGAGGCGACCGGATGCTCGACGTGCTG 1972  
Db 288 ATCTACTCGCTCGTGGCTCGCTCGGGGGGGCGGACGTCGACTGGCTCGCGCGCGG 347  
Qy 1973 CACTGCATCCTCATCGACTCGCC 1995  
Db 348 TACACCATGGTGTCTCGCGCGGC 370

RESULT 15

US-11-292-078-9801  
; Sequence 9801, Application US/11292078  
; Publication No. US20060195941A1  
; GENERAL INFORMATION:  
; APPLICANT: Deikman, Jill  
; APPLICANT: Feng, Paul C.C.  
; APPLICANT: Fincher, Karen L.  
; APPLICANT: Ziegler, Todd E.  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
; TITLE OF INVENTION: Plants  
; FILE REFERENCE: 16517,346 - 38-21(52274)C  
; CURRENT APPLICATION NUMBER: US/11/292,078  
; CURRENT FILING DATE: 2005-12-02  
; PRIOR APPLICATION NUMBER: US 10/021,323  
; PRIOR FILING DATE: 2001-12-12  
; PRIOR APPLICATION NUMBER: US 60/255,619  
; PRIOR FILING DATE: 2000-12-14  
; NUMBER OF SEQ ID NOS: 17880  
; SEQ ID NO 9801  
; LENGTH: 604  
; TYPE: DNA  
; ORGANISM: Gossypium hirsutum  
; FEATURE:

; NAME/KEY: unsure  
; LOCATION: (1)..(604)  
; OTHER INFORMATION: unsure at all n locations  
; OTHER INFORMATION: Clone ID: LIB3828-028-Q6-K6-C7  
US-11-292-078-9801  
Query Match 0.8%; Score 38.8; DB 7; Length 604;  
Best Local Similarity 58.8%; Pred. No. 0.65;  
Matches 67; Conservative 0; Mismatches 47; Indels 0; Gaps 0;  
Qy 1346 AAGTCTTACGAAACGAAGAAAGCGGTGGGTAAGTAGAAGAGAAGCAAGCGATTCTC 1405  
Db 369 AAGTTTGAAGAGCAAACTAGAGAGAGGTTAAGTTGAAGAGCAGGATGTGCTTCAG 428  
Qy 1405 CACGAGGAGGCAAGATGACGATGGCCTTCGACCTCTCCAGGTCAAGAGGAA 1459  
Db 429 CTTNAGAAGGAGAGGTTTCAGAAAGACCTCGAGATTTCTAGGCTAAAGAGGAA 482  
Search completed: October 11, 2006, 02:43:59  
Job time : 1555 secs

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